

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:13:31 ; Search time 54.6792 Seconds  
(without alignments)  
2460.550 Million cell updates/sec

Perfect score: 1657  
Sequence: 1 MARCESLVLLTSTWTRLL.....NPESKSPSKTVRCLEAEV 322

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications AA.Main.\*

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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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93	1657	100.0	322	4	US-10-223-085-32
94	1657	100.0	322	4	US-10-223-084-32
95	1657	100.0	322	4	US-10-223-088-32
96	1657	100.0	322	4	US-10-223-090-32
98	1657	100.0	322	4	US-10-223-087-32
101	1657	100.0	322	4	US-10-223-083-32
102	1657	100.0	322	4	US-10-079-111-1
103	1657	100.0	322	4	US-10-223-089-32
108	1657	100.0	322	4	US-10-299-976-201
136	1657	100.0	322	4	US-10-063-742-6
211	1657	100.0	322	4	US-10-299-937-201
214	1657	100.0	322	4	US-10-223-081-32
224	1657	100.0	322	4	US-10-223-082-32
230	1657	100.0	322	4	US-10-298-993-201
231	1657	100.0	322	4	US-10-305-654-32
232	1657	100.0	322	4	US-10-448-923-201
233	1657	100.0	322	4	US-10-449-656-201
234	1657	100.0	322	4	US-10-448-713-201
235	1657	100.0	322	4	US-10-425-447-201
236	1657	100.0	322	4	US-10-081-056-32
238	1657	100.0	322	4	US-10-215-371-201
239	1657	100.0	322	4	US-10-797-366-201
240	1657	100.0	322	4	US-10-771-187-201
241	1657	100.0	322	5	US-10-972-317-6
242	1657	100.0	322	5	US-10-963-467-201
243	1657	100.0	322	5	US-10-978-255-201
244	1657	100.0	322	5	US-10-820-474A-64

245	1657	100.0	322	5	US-10-756-149-5685	Sequence 5685, Ap
246	1657	100.0	322	5	US-10-970-823-201	Sequence 201, App
247	1654	99.8	344	4	US-10-276-774-2349	Sequence 2349, Ap
248	1651	99.6	322	4	US-10-281-634-2	Sequence 2, Appli
249	1651	99.6	322	4	US-10-284-237-2665	Sequence 2665, Ap
250	1638	98.9	322	4	US-10-723-860-3909	Sequence 3909, Ap
251	1511.5	91.2	297	4	US-10-138-588-2	Sequence 2, Appli
252	821	49.5	255	3	US-09-866-050A-700	Sequence 700, App
253	229	13.8	364	5	US-10-024-607-8	Sequence 8, Appli
254	224.5	13.5	339	4	US-10-281-634-3	Sequence 3, Appli
255	222.5	13.4	365	3	US-09-870-759-73	Sequence 73, Appli
256	222.5	13.4	365	3	US-09-751-708A-73	Sequence 73, Appli
257	222.5	13.4	365	4	US-10-428-817A-69	Sequence 69, Appli
258	222.5	13.4	365	5	US-10-937-758A-50	Sequence 50, Appli
259	208.5	12.6	668	4	US-10-741-601-341	Sequence 341, App
260	208.5	12.6	668	5	US-10-473-127-1285	Sequence 1285, Ap
261	208.5	12.6	668	5	US-10-741-600-1047	Sequence 1047, Ap
262	208.5	12.6	668	5	US-10-482-029-253	Sequence 253, App
263	207	12.5	361	3	US-09-836-544-32	Sequence 32, Appli
264	207	12.5	361	5	US-10-473-127-1276	Sequence 1276, Ap
265	207	12.5	361	5	US-10-473-127-1292	Sequence 1292, Ap
266	207	12.5	361	5	US-10-473-127-1296	Sequence 1296, Ap
267	207	12.5	361	5	US-10-473-127-1298	Sequence 1298, Ap
268	207	12.5	361	5	US-10-473-127-1300	Sequence 1300, Ap
269	207	12.5	361	5	US-10-473-127-1302	Sequence 1302, Ap
270	207	12.5	361	5	US-10-473-127-1304	Sequence 1304, Ap
271	205	12.4	361	5	US-10-473-127-1275	Sequence 1275, Ap
272	205	12.4	361	5	US-10-473-127-1309	Sequence 1309, Ap
273	205	12.4	361	5	US-10-473-127-1310	Sequence 1310, Ap
274	205	12.4	361	5	US-10-482-029-255	Sequence 255, App
275	205	12.4	361	5	US-10-852-335A-131	Sequence 131, App
276	204	12.3	361	4	US-10-741-601-340	Sequence 340, App
277	204	12.3	361	5	US-10-473-127-1288	Sequence 1288, Ap
278	204	12.3	361	5	US-10-741-600-1048	Sequence 1048, Ap
279	203.5	12.3	607	5	US-10-486-226-2	Sequence 2, Appli
280	203.5	12.3	700	5	US-10-473-127-1306	Sequence 1306, Ap
281	203.5	12.3	700	5	US-10-505-769-4	Sequence 4, Appli
282	203	12.3	361	5	US-10-505-769-2	Sequence 2, Appli
283	203	12.3	436	5	US-10-473-127-1308	Sequence 1308, Ap
284	203	12.3	742	4	US-10-648-593-176	Sequence 176, App
285	203	12.3	742	5	US-10-473-127-1282	Sequence 1282, Ap
286	203	12.3	742	5	US-10-473-127-1319	Sequence 1319, Ap
287	203	12.3	742	5	US-10-741-600-1054	Sequence 1054, Ap
288	203	12.3	742	5	US-10-287-436A-545	Sequence 545, App
289	203	12.3	742	5	US-10-287-436A-1236	Sequence 1236, Ap
290	202.5	12.2	431	5	US-10-473-127-1307	Sequence 1307, Ap
291	202	12.2	361	4	US-10-663-244-3	Sequence 3, Appli
292	202	12.2	361	5	US-10-473-127-1273	Sequence 1273, Ap
293	202	12.2	675	5	US-10-473-127-1284	Sequence 1284, Ap
294	202	12.2	691	4	US-10-741-601-344	Sequence 344, App
295	202	12.2	691	5	US-10-473-127-1287	Sequence 1287, Ap
296	202	12.2	691	5	US-10-741-600-1053	Sequence 1053, Ap
297	202	12.2	742	3	US-10-116-275-206	Sequence 16, Appli
298	202	12.2	742	4	US-10-663-244-1	Sequence 1, Appli
299	202	12.2	742	4	US-10-741-601-338	Sequence 338, App
300	202	12.2	742	4	US-10-741-601-339	Sequence 339, App
301	202	12.2	742	4	US-10-473-127-1286	Sequence 1286, Ap
302	202	12.2	742	5	US-10-473-127-1311	Sequence 1311, Ap
303	202	12.2	742	5	US-10-690-880-40	Sequence 40, Appli
304	202	12.2	742	5	US-10-741-600-1046	Sequence 1046, Ap
305	202	12.2	742	5	US-10-741-600-1049	Sequence 1049, Ap
306	202	12.2	742	5	US-10-652-981-16	Sequence 16, Appli
307	202	12.2	742	5	US-10-473-127-1283	Sequence 1283, Ap
308	201	12.1	425	5	US-10-505-769-6	Sequence 6, Appli
309	200.5	12.0	699	5	US-09-836-544-34	Sequence 34, Appli
310	199.5	12.0	493	3	US-10-663-244-2	Sequence 2, Appli
311	199.5	12.0	493	5	US-10-473-127-1278	Sequence 1278, Ap
312	199.5	12.0	493	5	US-10-473-127-1279	Sequence 1279, Ap
313	199.5	12.0	493	5	US-10-473-127-1289	Sequence 1289, Ap
314	199.5	12.0	493	5	US-10-473-127-1293	Sequence 1293, Ap
315	199.5	12.0	493	5	US-10-473-127-1297	Sequence 1297, Ap
316	199.5	12.0	493	5	US-10-473-127-1299	Sequence 1299, Ap
317	199.5	12.0	493	5	US-10-473-127-1299	Sequence 1299, Ap

318	199.5	12.0	493	5	US-10-473-127-1301	Sequence 1301, Ap	391	131	7.9	649	4	US-10-189-123-63	Sequence 63, Appl
319	199.5	12.0	493	5	US-10-473-127-1303	Sequence 1303, Ap	392	131	7.9	649	4	US-10-188-495-63	Sequence 63, Appl
320	199.5	12.0	493	5	US-10-473-127-1305	Sequence 1305, Ap	393	131	7.9	649	4	US-10-741-790-333	Sequence 333, App
321	199.5	12.0	493	6	US-11-037-713-34	Sequence 34, Appl	394	131	7.9	671	3	US-09-759-130B-331	Sequence 331, App
322	199.5	12.0	700	4	US-10-013-969C-2	Sequence 2, Appl	395	131	7.9	671	4	US-10-189-123-61	Sequence 61, Appl
323	199	12.0	338	5	US-10-473-127-1271	Sequence 1271, Ap	396	131	7.9	671	4	US-10-188-495-61	Sequence 61, Appl
324	199	12.0	338	5	US-10-473-127-1315	Sequence 1315, Ap	397	131	7.9	671	4	US-10-741-790-331	Sequence 331, App
325	198	11.9	395	5	US-10-473-127-1281	Sequence 1281, Ap	406	131	7.9	911	4	US-10-237-535-52	Sequence 52, Appl
326	197	11.9	719	5	US-10-473-127-1270	Sequence 1270, Ap	415	131	7.9	911	4	US-10-239-196-52	Sequence 52, Appl
327	197	11.9	719	5	US-10-473-127-1316	Sequence 1316, Ap	506	131	7.9	911	4	US-10-312-352-24	Sequence 24, Appl
328	196.5	11.9	535	4	US-10-741-601-336	Sequence 336, App	507	131	7.9	911	5	US-10-936-626-89	Sequence 89, Appl
329	196.5	11.9	535	5	US-10-741-600-1044	Sequence 1044, Ap	508	131	7.9	911	5	US-10-938-061-89	Sequence 89, Appl
330	196.5	11.9	699	5	US-10-473-127-1274	Sequence 1274, Ap	509	131	7.9	911	5	US-10-983-340-21	Sequence 21, Appl
331	196.5	11.9	699	5	US-10-473-127-1280	Sequence 1280, Ap	510	130.5	7.9	883	3	US-09-759-130B-342	Sequence 342, App
332	196.5	11.9	699	5	US-10-473-127-1313	Sequence 1313, Ap	511	130.5	7.9	883	4	US-10-195-970-6	Sequence 6, Appl
333	196.5	11.9	699	5	US-10-696-639-71	Sequence 71, Appl	512	130.5	7.9	883	4	US-10-189-123-72	Sequence 72, Appl
334	196	11.8	293	5	US-10-473-127-1277	Sequence 1277, Ap	513	130.5	7.9	883	4	US-10-188-495-72	Sequence 72, Appl
335	196	11.8	294	5	US-10-473-127-1290	Sequence 1290, Ap	514	130.5	7.9	883	4	US-10-453-420-6	Sequence 6, Appl
336	196	11.8	294	5	US-10-473-127-1312	Sequence 1312, Ap	515	130.5	7.9	883	4	US-10-741-790-342	Sequence 342, App
337	196	11.8	395	4	US-10-741-601-345	Sequence 345, App	516	130.5	7.9	1082	4	US-10-284-237-2725	Sequence 2725, App
338	196	11.8	395	5	US-10-741-600-1052	Sequence 1052, Ap	517	130.5	7.9	2316	5	US-10-287-436A-566	Sequence 566, App
339	196	11.8	425	4	US-10-741-601-337	Sequence 337, App	518	129.5	7.8	457	5	US-10-960-275-5	Sequence 5, Appl
340	196	11.8	425	5	US-10-741-600-1045	Sequence 1045, Ap	519	129.5	7.8	2157	5	US-10-960-275-2	Sequence 2, Appl
341	196	11.8	493	4	US-10-741-601-343	Sequence 343, App	520	129.5	7.8	2570	4	US-10-028-248A-42	Sequence 42, Appl
342	196	11.8	493	5	US-10-741-600-1051	Sequence 1051, Ap	521	129.5	7.8	2570	4	US-10-107-782-42	Sequence 42, Appl
343	194.5	11.7	742	5	US-10-450-763-47430	Sequence 47430, A	522	128.5	7.8	95	5	US-10-473-127-1291	Sequence 1291, Ap
344	191.5	11.6	676	5	US-10-473-127-1368	Sequence 1368, Ap	523	128	7.7	2212	4	US-10-028-248A-43	Sequence 43, Appl
345	191.5	11.6	676	5	US-10-473-127-1318	Sequence 1318, Ap	524	128	7.7	2212	4	US-10-107-782-43	Sequence 43, Appl
346	191	11.5	271	5	US-10-473-127-1318	Sequence 1318, Ap	525	127.5	7.7	671	3	US-09-983-000A-14	Sequence 14, Appl
347	191	11.5	271	5	US-10-473-127-1314	Sequence 1314, Ap	526	127.5	7.7	671	5	US-10-652-981-14	Sequence 14, Appl
348	191	11.5	470	5	US-10-473-127-1269	Sequence 1269, Ap	527	127.5	7.7	671	5	US-10-936-626-90	Sequence 90, Appl
349	191	11.5	470	5	US-10-473-127-1317	Sequence 1317, Ap	528	127.5	7.7	671	5	US-10-938-061-90	Sequence 90, Appl
350	187	11.3	112	5	US-10-487-620-12	Sequence 2, Appl	529	127.5	7.7	671	5	US-10-852-335A-97	Sequence 97, Appl
351	186.5	11.3	113	5	US-10-487-620-6	Sequence 6, Appl	530	127.5	7.7	911	4	US-10-453-420-8	Sequence 8, Appl
352	185	11.2	112	5	US-10-487-620-8	Sequence 8, Appl	531	127.5	7.7	911	4	US-10-295-027-260	Sequence 260, App
353	183	11.0	112	5	US-10-487-620-10	Sequence 10, Appl	532	127	7.7	277	4	US-10-295-027-294	Sequence 294, App
354	182	11.0	112	5	US-10-487-620-4	Sequence 4, Appl	533	127	7.7	277	4	US-10-755-889-118	Sequence 118, App
355	181	10.9	112	5	US-10-487-620-12	Sequence 12, Appl	534	126.5	7.6	457	3	US-09-774-639-108	Sequence 108, App
356	180	10.9	920	5	US-10-450-763-47426	Sequence 47426, A	535	126.5	7.6	457	3	US-09-969-730-110	Sequence 110, App
357	170	10.3	34	3	US-09-864-761-47905	Sequence 47905, A	536	126.5	7.6	457	4	US-10-621-363-110	Sequence 110, App
358	161	9.7	90	3	US-09-799-118-3	Sequence 3, Appl	537	124.5	7.5	482	4	US-10-104-047-3794	Sequence 3794, Ap
359	153.5	9.3	90	3	US-09-927-463-8	Sequence 8, Appl	540	121.5	7.3	360	3	US-09-905-291A-213	Sequence 213, App
360	153.5	9.3	90	4	US-10-837-671-8	Sequence 8, Appl	1071	121.5	7.3	360	4	US-10-174-587-28	Sequence 28, Appl
361	150	9.1	510	4	US-10-104-047-2580	Sequence 2580, Ap	1106	121.5	7.3	360	4	US-10-299-976-213	Sequence 213, App
362	148.5	9.0	80	5	US-10-487-620-23	Sequence 23, Appl	1108	121.5	7.3	360	4	US-10-299-937-213	Sequence 213, App
363	145	8.8	277	3	US-09-799-118-2	Sequence 2, Appl	1112	121.5	7.3	360	4	US-10-298-993-213	Sequence 213, App
364	145	8.8	277	4	US-10-247-671-185	Sequence 185, App	1123	121.5	7.3	360	4	US-10-448-923-213	Sequence 213, App
365	145	8.8	277	4	US-10-295-027-232	Sequence 292, App	1124	121.5	7.3	360	4	US-10-448-656-213	Sequence 213, App
366	145	8.8	277	4	US-10-295-027-1237	Sequence 1237, App	1125	121.5	7.3	360	4	US-10-448-713-213	Sequence 213, App
367	145	8.8	277	5	US-10-723-860-4326	Sequence 4326, Ap	1127	121.5	7.3	360	4	US-10-425-447-213	Sequence 213, App
368	145	8.8	1069	4	US-10-028-248A-39	Sequence 39, Appl	1135	121.5	7.3	360	4	US-10-215-371-213	Sequence 213, App
369	145	8.8	1069	4	US-10-107-782-39	Sequence 39, Appl	1136	121.5	7.3	360	4	US-10-797-366-213	Sequence 213, App
370	145	8.8	2626	4	US-10-634-574-4	Sequence 4, Appl	1137	121.5	7.3	360	4	US-10-771-187-213	Sequence 213, App
371	144	8.7	275	5	US-10-960-275-12	Sequence 12, Appl	1138	121.5	7.3	360	5	US-10-963-467-213	Sequence 213, App
372	143.5	8.7	95	4	US-10-424-593-248857	Sequence 248857, A	1139	121.5	7.3	360	5	US-10-978-255-213	Sequence 213, App
373	134	8.1	897	4	US-10-028-248A-41	Sequence 41, Appl	1143	121.5	7.3	360	5	US-10-970-823-213	Sequence 213, App
374	134	8.1	897	4	US-10-028-248A-211	Sequence 211, App	1144	121	7.3	528	3	US-09-759-130B-341	Sequence 341, App
375	134	8.1	897	4	US-10-107-782-41	Sequence 41, Appl	1145	121	7.3	528	4	US-10-188-495-71	Sequence 71, Appl
376	134	8.1	897	4	US-10-107-782-211	Sequence 211, App	1146	121	7.3	528	4	US-10-188-495-71	Sequence 71, Appl
377	134	8.1	2675	4	US-10-028-248A-2	Sequence 2, Appl	1147	121	7.3	528	4	US-10-741-790-341	Sequence 341, App
378	134	8.1	2675	4	US-10-107-782-2	Sequence 2, Appl	1148	121	7.3	528	5	US-10-314-942-20	Sequence 20, Appl
379	133	8.0	1192	4	US-10-028-248A-40	Sequence 40, Appl	1149	118.5	7.2	1642	5	US-10-741-600-1176	Sequence 1176, Ap
380	133	8.0	1192	4	US-10-107-782-40	Sequence 40, Appl	1150	118.5	7.2	1642	5	US-10-741-600-1178	Sequence 1178, Ap
381	133	8.0	1394	3	US-09-842-930A-25	Sequence 25, Appl	1151	118.5	7.2	3396	4	US-10-788-792-170	Sequence 170, App
382	133	8.0	1394	5	US-10-990-844-25	Sequence 25, Appl	1152	118.5	7.2	3396	5	US-10-741-600-1172	Sequence 1172, Ap
383	133	8.0	1416	4	US-10-133-172-4	Sequence 4, Appl	1153	118.5	7.2	3396	5	US-10-741-600-1173	Sequence 1173, Ap
384	133	8.0	1431	3	US-09-842-930A-2	Sequence 2, Appl	1154	118.5	7.2	3396	5	US-10-631-467-773	Sequence 773, App
385	133	8.0	1431	5	US-10-133-172-2	Sequence 2, Appl	1155	117	7.1	340	4	US-10-112-944-397	Sequence 397, App
386	133	8.0	1431	5	US-10-990-844-2	Sequence 2, Appl	1156	116	7.0	2397	5	US-10-631-467-1518	Sequence 1518, Ap
387	133	8.0	1653	4	US-10-133-172-20	Sequence 20, Appl	1157	114.5	6.9	1257	4	US-10-698-190-22	Sequence 22, Appl
388	131.5	7.9	883	4	US-10-195-970-3	Sequence 3, Appl	1158	113.5	6.8	97	3	US-09-799-118-5	Sequence 5, Appl
389	131.5	7.9	883	4	US-10-453-420-3	Sequence 3, Appl	1159	112.5	6.8	287	3	US-09-764-853-576	Sequence 576, App
390	131	7.9	649	3	US-09-759-130B-333	Sequence 333, App	1160	111.5	6.7	402	4	US-10-282-122A-64209	Sequence 64209, A



1161	111	6.7	104	4	US-10-028-248A-46	Sequence 46, Appl	1234	99.5	6.0	402	5	US-10-481-698-17	Sequence 17, Appl
1162	111	6.7	104	4	US-10-107-782-46	Sequence 46, Appl	1235	99	6.0	201	4	US-10-120-907A-40	Sequence 40, Appl
1163	111	6.7	655	4	US-10-270-253-2	Sequence 2, Appl	1236	99	6.0	201	4	US-10-120-907A-41	Sequence 41, Appl
1164	111	6.7	655	5	US-10-741-600-1174	Sequence 1174, Ap	1237	99	6.0	260	4	US-10-460-512-3	Sequence 3, Appl
1165	111	6.7	2409	4	US-10-177-293-90	Sequence 90, Appl	1238	99	6.0	260	5	US-10-897-911-3	Sequence 3, Appl
1166	111	6.7	2409	5	US-10-741-600-1175	Sequence 1175, Ap	1239	99	6.0	260	5	US-10-898-615-3	Sequence 3, Appl
1167	111	6.7	2409	5	US-10-741-600-1177	Sequence 1177, Ap	1240	99	6.0	1428	6	US-11-097-143-37923	Sequence 37923, A
1168	111	6.7	2409	5	US-10-482-029-194	Sequence 194, Ap	1241	99	6.0	5376	4	US-10-028-248A-74	Sequence 74, Appl
1169	111	6.7	2409	5	US-10-852-335A-184	Sequence 184, Ap	1242	99	6.0	5376	4	US-10-107-782-74	Sequence 74, Appl
1170	110	6.6	341	3	US-09-948-820-48	Sequence 48, Appl	1243	98.5	5.9	1126	6	US-11-097-143-35952	Sequence 35952, A
1171	110	6.6	341	5	US-10-613-076-48	Sequence 48, Appl	1244	98	5.9	2112	6	US-11-097-143-8001	Sequence 8001, Ap
1172	109	6.6	353	5	US-10-960-275-11	Sequence 11, Appl	1245	95.5	5.8	376	3	US-09-801-368-206	Sequence 206, App
1173	109	6.6	1321	4	US-10-241-220-82	Sequence 82, Appl	1246	95.5	5.8	585	5	US-10-868-381-58	Sequence 58, Appl
1174	109	6.6	1321	4	US-10-295-027-262	Sequence 262, App	1247	95.5	5.8	1217	4	US-10-437-963-183891	Sequence 183891,
1175	109	6.6	1321	4	US-10-408-765A-1421	Sequence 1421, Ap	1248	95.5	5.8	5374	4	US-10-028-248A-75	Sequence 75, Appl
1176	109	6.6	1321	4	US-10-698-190-18	Sequence 18, Appl	1249	95.5	5.8	5374	4	US-10-107-782-75	Sequence 75, Appl
1177	109	6.6	1321	5	US-10-872-972-82	Sequence 82, Appl	1250	93.5	5.6	258	3	US-09-764-853-840	Sequence 840, App
1178	109	6.6	1321	5	US-10-872-991-82	Sequence 82, Appl	1251	93.5	5.6	258	4	US-10-091-438-205	Sequence 205, App
1179	108	6.5	322	4	US-10-120-907A-32	Sequence 32, Appl	1252	93.5	5.6	261	3	US-09-764-853-669	Sequence 669, App
1180	108	6.5	322	4	US-10-120-907A-33	Sequence 33, Appl	1253	93.5	5.6	261	4	US-10-091-438-144	Sequence 144, App
1181	108	6.5	354	4	US-10-120-907A-3	Sequence 3, Appl	1254	93.5	5.6	320	5	US-10-450-763-31869	Sequence 31869, A
1182	108	6.5	354	4	US-10-120-907A-7	Sequence 7, Appl	1255	93.5	5.6	339	5	US-10-391-939A-2	Sequence 2, Appl
1183	108	6.5	354	4	US-10-120-907A-9	Sequence 9, Appl	1256	93.5	5.6	339	5	US-10-391-939A-28	Sequence 28, Appl
1184	108	6.5	354	4	US-10-120-907A-11	Sequence 11, Appl	1257	93.5	5.6	359	4	US-10-188-012-17	Sequence 17, Appl
1185	108	6.5	354	4	US-10-120-907A-13	Sequence 13, Appl	1258	93.5	5.6	359	4	US-10-188-012-19	Sequence 19, Appl
1186	108	6.5	354	4	US-10-120-907A-15	Sequence 15, Appl	1259	93.5	5.6	359	4	US-10-188-012-23	Sequence 23, Appl
1187	108	6.5	354	4	US-10-120-907A-17	Sequence 17, Appl	1260	93.5	5.6	359	4	US-10-295-027-302	Sequence 302, App
1188	108	6.5	354	4	US-10-120-907A-19	Sequence 19, Appl	1261	93.5	5.6	359	4	US-10-188-832-64	Sequence 64, Appl
1189	108	6.5	354	4	US-10-120-907A-21	Sequence 21, Appl	1262	93.5	5.6	359	5	US-10-391-939A-4	Sequence 4, Appl
1190	108	6.5	354	4	US-10-120-907A-23	Sequence 23, Appl	1263	93.5	5.6	359	5	US-10-663-497-17	Sequence 17, Appl
1191	108	6.5	354	4	US-10-120-907A-24	Sequence 24, Appl	1264	93.5	5.6	359	5	US-10-663-497-19	Sequence 19, Appl
1192	108	6.5	354	4	US-10-120-907A-28	Sequence 28, Appl	1265	93.5	5.6	359	5	US-10-663-497-23	Sequence 23, Appl
1193	108	6.5	354	4	US-10-120-907A-29	Sequence 29, Appl	1266	93.5	5.6	359	5	US-10-718-321-8	Sequence 8, Appl
1194	108	6.5	354	4	US-10-120-907A-30	Sequence 30, Appl	1267	93.5	5.6	359	5	US-10-847-918-25	Sequence 25, Appl
1195	108	6.5	354	4	US-10-120-907A-36	Sequence 36, Appl	1268	93.5	5.6	366	5	US-10-450-763-38282	Sequence 38282, A
1196	108	6.5	354	4	US-10-120-907A-38	Sequence 38, Appl	1269	93.5	5.6	1595	5	US-10-484-218-20	Sequence 20, Appl
1197	108	6.5	354	4	US-10-120-907A-42	Sequence 42, Appl	1270	92.5	5.6	40	5	US-10-487-620-26	Sequence 26, Appl
1198	108	6.5	354	4	US-10-120-907A-64	Sequence 64, Appl	1271	92.5	5.6	300	3	US-09-953-499-10	Sequence 10, Appl
1199	108	6.5	354	4	US-10-120-907A-66	Sequence 66, Appl	1272	92.5	5.6	300	4	US-10-365-542-10	Sequence 10, Appl
1200	108	6.5	354	5	US-10-754-473-19	Sequence 19, Appl	1273	92.5	5.6	300	4	US-10-633-008-10	Sequence 10, Appl
1201	108	6.5	354	5	US-10-754-473-22	Sequence 22, Appl	1274	92.5	5.6	300	4	US-10-785-220-10	Sequence 10, Appl
1202	108	6.5	721	4	US-10-120-907A-5	Sequence 5, Appl	1275	92.5	5.6	300	4	US-10-785-221-10	Sequence 10, Appl
1203	108	6.5	721	4	US-10-120-907A-25	Sequence 25, Appl	1276	92.5	5.6	300	4	US-10-785-433-10	Sequence 10, Appl
1204	108	6.5	721	4	US-10-120-907A-43	Sequence 43, Appl	1277	92.5	5.6	300	4	US-10-767-904-10	Sequence 10, Appl
1205	108	6.5	721	4	US-10-120-907A-65	Sequence 65, Appl	1278	92.5	5.6	300	5	US-10-785-607-10	Sequence 10, Appl
1206	108	6.5	721	4	US-10-120-907A-67	Sequence 67, Appl	1279	92.5	5.6	300	5	US-10-785-351-12	Sequence 12, Appl
1207	107	6.5	93	4	US-10-133-172-5	Sequence 5, Appl	1280	92.5	5.6	300	5	US-10-663-497-21	Sequence 21, Appl
1208	107	6.5	315	4	US-10-667-723-4	Sequence 4, Appl	1281	92.5	5.6	365	4	US-10-663-497-21	Sequence 21, Appl
1209	107	6.5	339	5	US-10-754-473-21	Sequence 21, Appl	1282	92.5	5.6	365	5	US-10-282-122A-60442	Sequence 60442, A
1210	107	6.5	354	4	US-10-120-907A-39	Sequence 39, Appl	1283	92.5	5.6	569	4	US-10-188-012-25	Sequence 25, Appl
1211	107	6.5	355	4	US-10-120-907A-31	Sequence 31, Appl	1284	92.5	5.6	966	4	US-10-663-497-25	Sequence 25, Appl
1212	107	6.5	355	5	US-10-754-473-20	Sequence 20, Appl	1285	92.5	5.6	966	4	US-09-801-368-372	Sequence 372, App
1213	107	6.5	355	5	US-10-667-275-9	Sequence 9, Appl	1286	92	5.6	966	4	US-10-451-467A-52	Sequence 52, Appl
1214	107	6.5	1268	4	US-10-698-190-34	Sequence 34, Appl	1287	92	5.6	966	4	US-09-764-853-777	Sequence 777, App
1215	107	6.5	1795	6	US-11-097-143-36210	Sequence 36210, A	1288	92	5.6	166	3	US-10-091-438-181	Sequence 181, App
1216	107	6.5	2420	4	US-10-028-248A-4	Sequence 4, Appl	1289	91.5	5.5	166	4	US-10-239-431A-6	Sequence 6, Appl
1217	107	6.5	2420	4	US-10-107-782-4	Sequence 4, Appl	1290	91.5	5.5	350	4	US-10-239-431A-2	Sequence 2, Appl
1218	107	6.5	354	4	US-10-120-907A-37	Sequence 37, Appl	1291	91.5	5.5	350	4	US-10-825-144-9	Sequence 9, Appl
1219	105	6.3	354	5	US-10-754-473-18	Sequence 18, Appl	1292	91.5	5.5	610	4	US-09-823-240-5	Sequence 5, Appl
1220	104	6.3	98	3	US-09-799-118-4	Sequence 4, Appl	1293	91.5	5.5	639	3	US-10-353-856-23	Sequence 23, Appl
1221	104	6.3	139	5	US-10-741-601-342	Sequence 342, App	1294	91.5	5.5	639	3	US-10-369-493-3228	Sequence 3228, Ap
1222	104	6.3	139	5	US-10-473-127-2037	Sequence 2037, Ap	1295	91.5	5.5	681	4	US-10-437-963-189767	Sequence 189767,
1223	104	6.3	139	5	US-10-473-127-2040	Sequence 2040, Ap	1296	91.5	5.5	1103	4	Sequence 4, Appl	Sequence 4, Appl
1224	104	6.3	139	5	US-10-741-600-1050	Sequence 1050, Ap	1297	91.5	5.5	246	4	Sequence 3, Appl	Sequence 3, Appl
1225	104	6.3	1712	6	US-11-097-143-8400	Sequence 8400, Ap	1298	91	5.5	463	4	Sequence 66913, A	Sequence 66913, A
1226	102.5	6.2	183	6	US-11-097-143-24753	Sequence 24753, A	1299	91	5.5	463	4	Sequence 322413	Sequence 322413
1227	102	6.2	309	4	US-10-425-114-41494	Sequence 41494, A	1300	91	5.5	505	4	Sequence 17, Appl	Sequence 17, Appl
1228	101.5	6.1	380	4	US-10-369-493-6206	Sequence 6206, Ap	1301	91	5.5	1714	6	Sequence 7350, Ap	Sequence 7350, Ap
1229	101.5	6.1	590	3	US-09-957-187-12	Sequence 12, Appl	1302	90.5	5.5	1976	6	Sequence 35049, A	Sequence 35049, A
1230	101.5	6.1	590	6	US-11-058-709-12	Sequence 12, Appl	1303	90.5	5.5				
1231	100.5	6.1	402	4	US-10-343-953-2	Sequence 2, Appl	1304	90.5	5.5				
1232	100.5	6.1	402	4	US-10-257-174-47	Sequence 47, Appl	1305	90.5	5.5				
1233	100.5	6.1	1379	6	US-11-097-143-33612	Sequence 33612, A	1306	90.5	5.5				

1307	90	5.4	364	4	US-10-188-012-27	Sequence 27, Appl	1380	86.5	5.2	714	5	US-10-450-763-45506	Sequence 45506, A
1308	90	5.4	364	5	US-10-663-497-27	Sequence 27, Appl	1381	86.5	5.2	714	5	US-10-450-763-46006	Sequence 46006, A
1309	90	5.4	629	6	US-11-097-143-5313	Sequence 5313, Ap	1382	86.5	5.2	1579	5	US-10-504-582-158	Sequence 158, App
1310	90	5.4	957	3	US-09-840-746-19	Sequence 19, Appl	1383	86.5	5.2	2781	4	US-10-263-929-122	Sequence 122, App
1311	90	5.4	1130	4	US-10-425-115-339478	Sequence 1324, App	1384	86.5	5.2	2781	4	US-10-754-342-10	Sequence 10, Appl
1312	90	5.4	1217	4	US-10-734-564-122	Sequence 1227, App	1385	86.5	5.2	2781	4	US-10-723-860-1472	Sequence 1472, Ap
1313	90	5.4	1367	3	US-09-801-368-108	Sequence 108, App	1386	86.5	5.2	2907	4	US-10-754-342-1	Sequence 1, Appli
1314	89.5	5.4	195	4	US-10-074-978A-350	Sequence 350, App	1387	86	5.2	390	5	US-10-732-923-20210	Sequence 20210, A
1315	89.5	5.4	305	4	US-10-188-012-5	Sequence 5, Appli	1388	86	5.2	857	4	US-10-425-114-45539	Sequence 45539, A
1316	89.5	5.4	305	4	US-10-188-012-7	Sequence 7, Appli	1389	86	5.2	1086	4	US-10-205-219-62	Sequence 62, Appl
1317	89.5	5.4	305	5	US-10-663-497-5	Sequence 5, Appli	1390	86	5.2	1086	5	US-10-450-763-58747	Sequence 58747, A
1318	89.5	5.4	305	5	US-10-663-497-7	Sequence 7, Appli	1391	86	5.2	1190	5	US-10-450-763-36034	Sequence 36034, A
1319	89.5	5.4	1368	5	US-10-732-923-13518	Sequence 13518, A	1392	85.5	5.2	346	4	US-10-416-328-6	Sequence 6, Appli
1320	89.5	5.4	1369	5	US-10-732-923-13517	Sequence 13517, A	1393	85.5	5.2	346	4	US-10-432-230-11	Sequence 11, Appl
1321	89	5.4	307	6	US-11-097-143-24429	Sequence 24429, A	1394	85.5	5.2	346	5	US-10-498-778-6	Sequence 6, Appli
1322	89	5.4	416	4	US-10-371-525-26	Sequence 26, Appl	1395	85.5	5.2	652	4	US-10-467-490-5	Sequence 5, Appl
1323	89	5.4	416	4	US-10-371-069-26	Sequence 26, Appl	1396	85.5	5.2	686	4	US-10-425-115-230245	Sequence 230245, A
1324	89	5.4	416	4	US-10-371-645-26	Sequence 26, Appl	1397	85.5	5.2	686	4	US-10-283-122A-43763	Sequence 43763, A
1325	89	5.4	416	4	US-10-371-260-26	Sequence 26, Appl	1398	85.5	5.2	781	4	US-10-074-978A-286	Sequence 286, App
1326	89	5.4	416	5	US-10-684-422-68	Sequence 68, Appl	1399	85.5	5.2	781	4	US-10-664-456-16	Sequence 16, Appl
1327	89	5.4	416	5	US-10-287-436A-533	Sequence 533, App	1400	85.5	5.2	792	3	US-09-803-207-27	Sequence 27, Appl
1328	89	5.4	416	5	US-10-287-436A-1224	Sequence 1224, Ap	1401	85.5	5.2	841	4	US-10-467-490-2	Sequence 2, Appli
1329	89	5.4	846	6	US-11-097-143-36909	Sequence 36909, A	1402	85.5	5.2	843	6	US-11-097-143-39828	Sequence 39828, A
1330	89	5.4	882	6	US-11-097-143-28098	Sequence 28098, A	1403	85.5	5.2	862	4	US-10-437-963-115723	Sequence 115723, A
1331	89	5.4	1441	4	US-10-437-963-138354	Sequence 138354, A	1404	85.5	5.2	862	4	US-10-467-490-3	Sequence 3, Appli
1332	89	5.4	2588	4	US-10-437-963-138279	Sequence 138279, A	1405	85.5	5.2	1794	3	US-09-965-738-299	Sequence 299, App
1333	88.5	5.3	165	4	US-10-424-599-216371	Sequence 216371, A	1406	85.5	5.2	1799	3	US-09-965-738-149	Sequence 149, App
1334	88.5	5.3	358	5	US-10-450-763-45673	Sequence 45673, A	1407	85.5	5.2	1821	3	US-09-965-738-82	Sequence 82, App
1335	88.5	5.3	481	6	US-11-097-143-17043	Sequence 17043, A	1408	85.5	5.2	2055	4	US-10-193-874-20	Sequence 20, Appl
1336	88.5	5.3	615	4	US-10-239-818-14	Sequence 14, Appl	1409	85.5	5.2	2586	3	US-09-729-485A-11	Sequence 11, Appl
1337	88	5.3	125	4	US-10-424-598-221671	Sequence 221671, A	1410	85.5	5.2	2586	3	US-09-729-485A-14	Sequence 14, Appl
1338	88	5.3	995	3	US-09-984-130-48	Sequence 48, Appl	1411	85.5	5.2	2586	3	US-09-803-318-11	Sequence 11, Appl
1339	88	5.3	995	3	US-09-836-353A-48	Sequence 48, Appl	1412	85.5	5.2	2586	3	US-09-803-318-14	Sequence 14, Appl
1340	88	5.3	3507	4	US-10-369-493-5784	Sequence 5784, Ap	1413	85.5	5.2	2586	3	US-09-905-129-11	Sequence 11, Appl
1341	87.5	5.3	536	4	US-10-218-743-15	Sequence 21, Appl	1414	85.5	5.2	2586	3	US-09-905-129-14	Sequence 14, Appl
1342	87.5	5.3	555	4	US-10-218-743-15	Sequence 15, Appl	1415	85.5	5.2	2586	3	US-09-991-630-11	Sequence 11, Appl
1343	87.5	5.3	555	4	US-10-218-743-18	Sequence 18, Appl	1416	85.5	5.2	2586	3	US-09-991-630-14	Sequence 14, Appl
1344	87.5	5.3	649	4	US-10-425-115-295178	Sequence 295178, A	1417	85.5	5.2	2586	4	US-10-454-351-11	Sequence 11, Appl
1345	87.5	5.3	717	4	US-10-104-047-3100	Sequence 3100, Ap	1418	85.5	5.2	2587	4	US-10-454-351-14	Sequence 14, Appl
1346	87.5	5.3	1085	4	US-10-159-339-10	Sequence 10, Ap	1419	85.5	5.2	2587	3	US-09-729-485A-16	Sequence 16, Appl
1347	87.5	5.3	1085	4	US-10-041-615-108	Sequence 108, App	1420	85.5	5.2	2587	3	US-09-802-318-16	Sequence 16, Appl
1348	87.5	5.3	1085	4	US-10-436-715-21	Sequence 21, Appl	1421	85.5	5.2	2587	3	US-09-905-129-16	Sequence 16, Appl
1349	87.5	5.3	1085	4	US-10-436-715-75	Sequence 75, Appl	1422	85.5	5.2	2587	3	US-09-991-630-16	Sequence 16, Appl
1350	87.5	5.3	1322	4	US-10-369-493-13040	Sequence 13040, A	1423	85.5	5.2	2587	4	US-10-454-351-16	Sequence 16, Appl
1351	87	5.3	288	3	US-09-216-393-341	Sequence 341, App	1424	85.5	5.2	2589	3	US-09-991-630-24	Sequence 24, Appl
1352	87	5.3	288	3	US-09-216-393-344	Sequence 344, App	1425	85.5	5.2	2589	4	US-10-454-351-24	Sequence 24, Appl
1353	87	5.3	288	4	US-10-321-856-341	Sequence 341, App	1426	85.5	5.2	2589	4	US-10-142-515-11	Sequence 11, Appl
1354	87	5.3	288	4	US-10-321-856-344	Sequence 344, App	1427	85.5	5.2	2589	4	US-10-243-243A-8	Sequence 8, Appli
1355	87	5.3	363	5	US-10-926-543-87	Sequence 87, Appl	1428	85.5	5.2	2595	5	US-10-983-340-4	Sequence 4, Appli
1356	87	5.3	363	5	US-10-631-467-1565	Sequence 1565, Ap	1429	85.5	5.2	11721	3	US-09-965-738-162	Sequence 162, App
1357	87	5.3	611	4	US-10-425-114-54378	Sequence 54378, A	1430	85.5	5.2	22152	4	US-10-715-066-5	Sequence 5, Appli
1358	87	5.3	631	3	US-09-841-132-325	Sequence 325, App	1431	85	5.1	326	6	US-11-097-143-41430	Sequence 41430, A
1359	87	5.3	631	5	US-10-872-155-325	Sequence 325, App	1432	85	5.1	472	5	US-10-746-264-7	Sequence 7, Appli
1360	87	5.3	650	4	US-10-425-115-353793	Sequence 353793, A	1433	85	5.1	472	5	US-10-976-042-25	Sequence 25, Appl
1361	87	5.3	664	5	US-10-197-220-168	Sequence 168, App	1434	85	5.1	472	5	US-10-995-266-7	Sequence 7, Appli
1362	87	5.3	664	6	US-11-109-468-168	Sequence 168, App	1435	85	5.1	573	4	US-10-437-963-142231	Sequence 142231, A
1363	87	5.3	1016	3	US-09-841-260-95	Sequence 95, Appl	1436	85	5.1	627	4	US-10-369-493-18499	Sequence 18499, A
1364	87	5.3	1016	4	US-10-007-693-95	Sequence 95, Appl	1437	85	5.1	635	4	US-10-425-114-58558	Sequence 58558, A
1365	87	5.3	1016	4	US-10-467-534-41	Sequence 41, Appl	1438	85	5.1	637	4	US-10-094-749-2621	Sequence 2621, Ap
1366	87	5.3	1016	4	US-10-762-058-95	Sequence 95, Appl	1439	85	5.1	1049	6	US-10-739-930-6279	Sequence 6279, Ap
1367	87	5.3	1016	5	US-10-197-220-95	Sequence 95, Appl	1440	85	5.1	1061	4	US-11-097-143-7953	Sequence 7953, Ap
1368	87	5.3	1016	5	US-10-498-327-95	Sequence 95, Appl	1441	85	5.1	1061	4	US-10-291-285-347	Sequence 347, App
1369	87	5.3	1016	6	US-11-109-468-95	Sequence 95, Appl	1442	85	5.1	1091	4	US-10-291-285-348	Sequence 348, App
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1371	87	5.3	1537	4	US-10-369-493-1398	Sequence 1398, Ap	1444	85	5.1	1354	6	US-11-097-143-36711	Sequence 36711, A
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270	72.5	4.4	2244	7	US-11-131-263-41	Sequence 41, Appl	343	70	4.2	485	6	US-10-501-035-349	Sequence 349, App
271	72.5	4.4	2314	7	US-11-097-728-2	Sequence 2, Appli	344	70	4.2	531	7	US-11-096-568A-19343	Sequence 19343, A
272	72.5	4.4	2353	7	US-11-097-728-6	Sequence 6, Appli	345	70	4.2	578	6	US-10-821-234-1039	Sequence 1039, Ap
273	72.5	4.4	2801	7	US-11-124-368A-305	Sequence 305, App	346	70	4.2	609	7	US-11-110-082-40	Sequence 40, Appl
274	72.5	4.4	2801	7	US-11-124-367A-433	Sequence 433, App	347	70	4.2	733	7	US-11-096-568A-29645	Sequence 29645, A
275	72.5	4.4	2896	7	US-11-124-368A-306	Sequence 306, App	348	70	4.2	735	7	US-11-096-568A-29645	Sequence 29645, A
276	72.5	4.4	2896	7	US-11-124-367A-434	Sequence 434, App	349	70	4.2	735	7	US-11-096-568A-31569	Sequence 31569, A
277	72.5	4.4	2910	6	US-10-330-773-39	Sequence 39, Appl	350	70	4.2	768	7	US-11-096-568A-29644	Sequence 29644, A
278	72.5	4.4	3256	7	US-11-124-367A-432	Sequence 304, App	351	70	4.2	768	7	US-11-096-568A-31568	Sequence 31568, A
279	72.5	4.4	3256	7	US-11-124-367A-432	Sequence 432, App	352	70	4.2	770	7	US-11-096-568A-31567	Sequence 31567, A
280	72	4.3	245	7	US-11-087-099-299	Sequence 299, App	353	70	4.2	1256	6	US-10-517-695-111	Sequence 111, App
281	72	4.3	245	7	US-11-096-568A-33799	Sequence 33799, A	354	70	4.2	1416	7	US-11-128-059-60	Sequence 60, Appl
282	72	4.3	255	7	US-11-096-568A-7533	Sequence 7533, Ap	355	70	4.2	2011	7	US-11-080-991-56	Sequence 56, Appl
283	72	4.3	308	7	US-11-072-512-3898	Sequence 3898, Ap	356	69.5	4.2	106	7	US-11-096-568A-19298	Sequence 19298, A
284	72	4.3	458	6	US-10-540-091-24	Sequence 24, Appl	357	69.5	4.2	162	7	US-11-096-568A-641	Sequence 641, App
285	72	4.3	545	7	US-11-201-916-8	Sequence 8, Appli	358	69.5	4.2	173	7	US-11-096-568A-452	Sequence 452, App
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287	72	4.3	784	6	US-10-467-657-5968	Sequence 5968, Ap	360	69.5	4.2	175	7	US-11-087-099-6466	Sequence 6466, Ap
288	72	4.3	1009	6	US-10-514-531-11	Sequence 11, Appl	361	69.5	4.2	215	6	US-10-467-657-476	Sequence 476, App
289	71.5	4.3	232	6	US-10-884-730-366	Sequence 366, App	363	69.5	4.2	312	6	US-10-973-115B-336	Sequence 336, App
290	71.5	4.3	308	7	US-11-096-568A-20980	Sequence 20980, A	364	69.5	4.2	349	7	US-11-096-568A-10641	Sequence 10641, A
291	71.5	4.3	330	7	US-11-098-686-10903	Sequence 10903, A	365	69.5	4.2	453	7	US-11-052-554A-224	Sequence 224, App
292	71.5	4.3	348	7	US-11-096-568A-20979	Sequence 20979, A	366	69.5	4.2	461	7	US-11-096-568A-10640	Sequence 10640, A
293	71.5	4.3	353	7	US-11-096-568A-12810	Sequence 12810, A	367	69.5	4.2	497	7	US-11-072-512-3773	Sequence 3773, Ap
294	71.5	4.3	368	7	US-11-096-568A-20978	Sequence 20978, A	368	69.5	4.2	519	7	US-11-087-099-9352	Sequence 9352, Ap
295	71.5	4.3	447	6	US-10-641-678-58	Sequence 58, Appl	369	69.5	4.2	537	6	US-10-330-773-666	Sequence 666, App
296	71.5	4.3	1340	7	US-11-098-686-11135	Sequence 11135, A	370	69.5	4.2	567	7	US-11-016-503-2	Sequence 2, Appli
297	71	4.3	250	7	US-11-128-059-62	Sequence 62, Appl	371	69.5	4.2	618	7	US-11-087-099-9161	Sequence 9161, Ap
298	71	4.3	343	7	US-11-080-091-4	Sequence 4, Appli	372	69.5	4.2	626	7	US-11-072-512-2827	Sequence 2827, Ap
299	71	4.3	345	7	US-11-087-177-19	Sequence 19, Appl	373	69.5	4.2	646	7	US-11-087-099-6754	Sequence 6754, Ap
300	71	4.3	354	7	US-11-189-817-2	Sequence 2, Appli	374	69.5	4.2	713	6	US-10-330-773-668	Sequence 668, App
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302	71	4.3	578	7	US-11-087-099-542	Sequence 542, App	376	69.5	4.2	1007	7	US-11-051-720-1445	Sequence 1445, Ap
303	71	4.3	579	7	US-11-087-099-6979	Sequence 6979, Ap	377	69.5	4.2	1120	7	US-11-051-720-1733	Sequence 1733, Ap
304	71	4.3	579	7	US-11-087-099-7852	Sequence 7852, Ap	378	69.5	4.2	1305	7	US-11-051-720-1370	Sequence 1370, Ap
305	71	4.3	581	7	US-11-087-099-2154	Sequence 2154, Ap	379	69.5	4.2	1690	7	US-11-173-689-7	Sequence 7, Appli
306	71	4.3	581	7	US-11-087-099-2375	Sequence 2375, Ap	380	69	4.2	1473	7	US-11-096-568A-8463	Sequence 8463, Ap
307	71	4.3	581	7	US-11-087-099-2375	Sequence 2375, Ap	381	69	4.2	180	7	US-11-096-568A-12758	Sequence 12758, A
308	71	4.3	581	7	US-11-087-099-3070	Sequence 3070, Ap	382	69	4.2	443	7	US-11-087-099-7683	Sequence 7683, Ap
309	71	4.3	581	7	US-11-087-099-3327	Sequence 3227, Ap	383	69	4.2	476	7	US-11-055-823-540	Sequence 540, App
310	71	4.3	581	7	US-11-087-099-3736	Sequence 3736, Ap	384	69	4.2	476	7	US-11-055-823-542	Sequence 542, App
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314	71	4.3	581	7	US-11-087-099-10957	Sequence 10957, A	388	69	4.2	696	7	US-11-096-568A-29818	Sequence 29818, A
315	71	4.3	581	7	US-11-087-099-11208	Sequence 11208, A	389	69	4.2	696	7	US-11-256-548-23	Sequence 23, Appl
316	71	4.3	581	7	US-11-087-099-11354	Sequence 11354, A	390	69	4.2	705	7	US-11-087-099-10564	Sequence 10564, A
317	71	4.3	581	7	US-11-087-099-12146	Sequence 12146, A	391	69	4.2	720	7	US-11-256-548-6	Sequence 6, Appli
318	71	4.3	581	7	US-11-087-099-4567	Sequence 4567, Ap	392	69	4.2	761	6	US-10-485-517-252	Sequence 252, App
319	71	4.3	626	7	US-11-010-748A-1	Sequence 1, Appli	393	69	4.2	802	7	US-11-087-099-4882	Sequence 4882, Ap
320	71	4.3	1118	7	US-11-113-751-42	Sequence 42, Appl	394	69	4.2	820	7	US-11-087-099-13246	Sequence 13246, A
321	71	4.3	1153	7	US-11-113-751-44	Sequence 44, Appl	395	69	4.2	910	7	US-11-206-587-17	Sequence 17, Appli
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323	70.5	4.3	231	7	US-11-096-568A-1421	Sequence 1421, Ap	397	68.5	4.1	2145	7	US-11-096-568A-21710	Sequence 21710, A

398	68.5	4.1	339	7	US-11-096-568A-21709	Sequence 21709, A	471	758	7	US-11-096-568A-26595	Sequence 26595, A	
399	68.5	4.1	341	7	US-11-096-568A-21708	Sequence 21708, A	472	961	7	US-11-113-424-35	Sequence 35, App	
400	68.5	4.1	411	7	US-11-096-568A-7197	Sequence 7197, App	473	1026	7	US-11-169-041-205	Sequence 205, App	
401	68.5	4.1	436	7	US-11-124-368A-236	Sequence 236, App	474	4.1	1122	7	US-11-191-374-3	Sequence 3, Appli
402	68.5	4.1	451	7	US-11-096-568A-7196	Sequence 7196, App	475	4.1	1122	7	US-11-191-375-3	Sequence 3, Appli
403	68.5	4.1	455	7	US-11-087-099-10931	Sequence 10931, A	476	4.1	1122	7	US-11-191-588-3	Sequence 3, Appli
404	68.5	4.1	464	7	US-11-096-568A-7196	Sequence 7196, App	477	4.1	1267	7	US-11-096-568A-28960	Sequence 28960, A
405	68.5	4.1	467	7	US-11-096-568A-7195	Sequence 7195, App	478	4.1	1274	7	US-11-096-568A-28959	Sequence 28959, A
406	68.5	4.1	467	7	US-11-096-568A-7529	Sequence 7529, App	479	4.1	1574	7	US-11-096-568A-28958	Sequence 28958, A
407	68.5	4.1	509	7	US-11-096-568A-7528	Sequence 7528, App	480	4.1	1678	7	US-11-124-367A-340	Sequence 340, App
408	68.5	4.1	529	7	US-11-210-316-28	Sequence 28, Appl	481	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
409	68.5	4.1	557	7	US-11-016-503-4	Sequence 4, Appli	482	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
410	68.5	4.1	567	7	US-11-016-503-10	Sequence 10, Appl	483	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
411	68.5	4.1	589	7	US-11-096-568A-9189	Sequence 9189, App	484	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
412	68.5	4.1	589	7	US-11-096-568A-9191	Sequence 9191, App	485	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
413	68.5	4.1	605	7	US-11-096-568A-9188	Sequence 9188, App	486	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
414	68.5	4.1	696	7	US-11-052-554A-101	Sequence 101, App	487	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
415	68.5	4.1	696	7	US-11-052-554A-101	Sequence 101, App	488	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
416	68.5	4.1	709	7	US-11-072-512-2349	Sequence 2349, App	489	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
417	68.5	4.1	748	6	US-10-330-773-394	Sequence 394, App	490	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
418	68.5	4.1	798	6	US-10-770-726-64	Sequence 64, Appl	491	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
419	68.5	4.1	825	7	US-11-087-099-1341	Sequence 1341, App	492	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
420	68.5	4.1	886	7	US-11-087-099-11456	Sequence 11456, A	493	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
421	68.5	4.1	897	7	US-11-137-465-35	Sequence 35, Appl	494	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
422	68.5	4.1	1070	7	US-11-087-099-5657	Sequence 5657, App	495	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
423	68.5	4.1	1344	7	US-11-072-512-2452	Sequence 2452, App	496	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
424	68.5	4.1	1669	6	US-10-330-773-392	Sequence 392, App	497	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
425	68	4.1	246	7	US-11-052-554A-50	Sequence 50, Appl	498	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
426	68	4.1	263	7	US-11-096-568A-9712	Sequence 9712, App	499	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
427	68	4.1	269	6	US-10-839-799-109	Sequence 109, App	500	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
428	68	4.1	312	6	US-10-986-501-124	Sequence 124, App	501	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
429	68	4.1	347	7	US-11-096-568A-16579	Sequence 16579, A	502	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
430	68	4.1	406	7	US-11-096-568A-15346	Sequence 15346, A	503	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
431	68	4.1	435	7	US-11-096-568A-15345	Sequence 15345, A	504	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
432	68	4.1	422	7	US-11-169-041-224	Sequence 224, App	505	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
433	68	4.1	472	7	US-11-165-211-4	Sequence 4, Appli	506	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
434	68	4.1	472	7	US-11-165-226-4	Sequence 4, Appli	507	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
435	68	4.1	550	7	US-11-087-099-5463	Sequence 5463, App	508	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
436	68	4.1	648	7	US-11-096-568A-27576	Sequence 27576, App	509	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
437	68	4.1	633	6	US-10-714-995-24	Sequence 24, Appl	510	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
438	68	4.1	1078	7	US-11-096-568A-30451	Sequence 30451, A	511	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
439	68	4.1	1116	7	US-11-096-568A-30450	Sequence 30450, A	512	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
440	68	4.1	1123	7	US-11-096-568A-30449	Sequence 30449, A	513	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
441	68	4.1	1323	6	US-10-517-939-312	Sequence 312, App	514	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
442	68	4.1	2053	7	US-11-013-759-9	Sequence 9, Appli	515	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
443	68	4.1	2426	7	US-11-203-806A-11	Sequence 11, Appl	516	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
444	68	4.1	3712	7	US-11-019-711-48	Sequence 48, Appl	517	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
445	68	4.1	3712	7	US-11-019-711-51	Sequence 51, Appl	518	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
446	67.5	4.1	96	7	US-11-096-568A-6177	Sequence 6177, App	519	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
447	67.5	4.1	163	7	US-11-096-568A-9622	Sequence 9622, App	520	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
448	67.5	4.1	173	7	US-11-096-568A-9621	Sequence 9621, App	521	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
449	67.5	4.1	176	7	US-11-096-568A-9620	Sequence 9620, App	522	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
450	67.5	4.1	238	7	US-11-096-568A-26721	Sequence 26721, App	523	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
451	67.5	4.1	400	7	US-11-096-568A-3236	Sequence 3236, App	524	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
452	67.5	4.1	403	7	US-11-169-041-185	Sequence 185, App	525	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
453	67.5	4.1	411	7	US-11-024-959-330	Sequence 330, App	526	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
454	67.5	4.1	413	7	US-11-096-568A-20771	Sequence 20771, App	527	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
455	67.5	4.1	418	7	US-11-096-568A-3235	Sequence 3235, App	528	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
456	67.5	4.1	433	7	US-11-098-686-10135	Sequence 10135, A	529	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
457	67.5	4.1	436	7	US-11-096-568A-3234	Sequence 3234, App	530	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
458	67.5	4.1	532	7	US-11-087-099-8860	Sequence 8860, App	531	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
459	67.5	4.1	577	7	US-11-201-916-31	Sequence 31, Appl	532	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
460	67.5	4.1	600	7	US-11-072-512-3397	Sequence 3397, App	533	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
461	67.5	4.1	608	6	US-10-763-712A-16	Sequence 16, Appl	534	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
462	67.5	4.1	608	6	US-10-763-712A-90	Sequence 90, Appl	535	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
463	67.5	4.1	618	7	US-11-087-099-6625	Sequence 6625, App	536	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
464	67.5	4.1	630	7	US-11-096-568A-26597	Sequence 26597, A	537	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
465	67.5	4.1	637	7	US-11-236-198-5	Sequence 5, Appli	538	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
466	67.5	4.1	637	7	US-11-096-568A-27876	Sequence 27876, A	539	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
467	67.5	4.1	649	7	US-11-236-198-3	Sequence 3, Appli	540	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
468	67.5	4.1	704	7	US-11-096-568A-27875	Sequence 27875, A	541	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
469	67.5	4.1	725	7	US-11-096-568A-26596	Sequence 26596, A	542	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
470	67.5	4.1	732	7	US-11-096-568A-27874	Sequence 27874, A	543	4.1	1678	7	US-11-124-367A-341	Sequence 341, App
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548	66.5	4.0	319	7	US-11-096-568A-24347	Sequence 24347, A	623	65.5	4.0	485	7	US-11-096-568A-26552	Sequence 13552, A
549	66.5	4.0	362	7	US-11-256-548-3	Sequence 3, Appli	624	65.5	4.0	539	7	US-11-096-568A-13358	Sequence 13358, A
550	66.5	4.0	380	7	US-11-087-099-1300	Sequence 1300, App	625	65.5	4.0	541	7	US-11-201-916-17	Sequence 17, Appl
551	66.5	4.0	388	7	US-11-096-568A-27930	Sequence 27930, A	626	65.5	4.0	560	7	US-11-018-868-40	Sequence 40, Appl
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555	66.5	4.0	786	6	US-10-330-773-674	Sequence 674, App	630	65.5	4.0	683	7	US-11-124-368A-243	Sequence 243, App
556	66.5	4.0	812	7	US-10-467-962B-103	Sequence 103, App	631	65.5	4.0	707	7	US-11-072-512-3162	Sequence 3162, App
557	66.5	4.0	812	7	US-11-120-308-126	Sequence 126, App	632	65.5	4.0	777	7	US-11-124-368A-238	Sequence 238, App
558	66.5	4.0	897	7	US-11-087-099-11042	Sequence 11042, A	633	65.5	4.0	778	7	US-11-124-368A-240	Sequence 240, App
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561	66.5	4.0	3100	7	US-11-235-732-7	Sequence 7, Appli	636	65.5	4.0	876	7	US-10-485-517-200	Sequence 200, App
562	66	4.0	149	7	US-11-087-099-7791	Sequence 7791, App	637	65.5	4.0	925	6	US-10-453-372-1124	Sequence 1124, App
563	66	4.0	212	7	US-11-025-834A-16	Sequence 16, Appl	638	65.5	4.0	966	6	US-10-877-346-32	Sequence 32, Appl
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582	66	4.0	462	7	US-11-177-648-94	Sequence 94, Appl	657	65	3.9	305	6	US-10-055-877-264	Sequence 264, App
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594	66	4.0	690	6	US-10-880-881-23	Sequence 23, Appl	669	65	3.9	462	6	US-10-973-115B-224	Sequence 224, App
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846	63.5	3.8	871	7	US-11-077-550-8	Sequence 8, Appl1	919	63	3.8	615	7	US-11-096-568A-401	Sequence 401, App
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873	63.5	3.8	2176	7	US-11-193-806-25	Sequence 25, Appl	946	63	3.8	1966	6	US-10-480-330-6	Sequence 6, Appl1
874	63.5	3.8	2176	7	US-11-193-857-25	Sequence 25, Appl	947	63	3.8	1966	6	US-10-480-330-8	Sequence 8, Appl1
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877	63.5	3.8	2296	7	US-11-193-771-23	Sequence 23, Appl	950	63	3.8	1966	6	US-10-480-330-14	Sequence 14, Appl
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887	63	3.8	257	7	US-11-067-121-18	Sequence 18, Appl	960	63	3.8	2221	7	US-11-126-313-30	Sequence 30, Appl
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899	63	3.8	363	7	US-11-087-099-9842	Sequence 9842, Ap	973	63	3.8	299	7	US-11-000-463-747	Sequence 747, App
900	63	3.8	371	7	US-11-096-568A-31340	Sequence 31340, A	974	63	3.8	299	7	US-11-000-463-748	Sequence 748, App
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909	63	3.8	476	7	US-11-139-499-12	Sequence 12, Appl	983	63	3.8	446	7	US-11-096-568A-28876	Sequence 28876, A
910	63	3.8	485	7	US-11-043-889-52	Sequence 52, Appl	984	63	3.8	457	7	US-11-096-568A-32234	Sequence 32234, A
911	63	3.8	488	7	US-11-072-512-2639	Sequence 2639, Ap	985	63	3.8	464	7	US-11-087-099-7754	Sequence 7754, Ap
912	63	3.8	497	6	US-10-501-035-337	Sequence 337, App	986	63	3.8	467	7	US-11-096-568A-7912	Sequence 7912, Ap
913	63	3.8	501	6	US-10-485-517-381	Sequence 381, App	987	63	3.8	489	7	US-11-096-568A-32213	Sequence 32213, A
914	63	3.8	513	6	US-10-641-678-66	Sequence 66, Appl	988	63	3.8	499	7	US-11-096-568A-25749	Sequence 25749, A





1136	61.5	3.7	454	7	US-11-196-475-116	Sequence 116, App	1209	61	3.7	379	7	US-11-087-039-5014	Sequence 5014, Ap
1137	61.5	3.7	455	7	US-11-096-568A-29406	Sequence 29406, A	1210	61	3.7	380	7	US-11-087-039-5011	Sequence 5011, Ap
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1139	61.5	3.7	457	7	US-11-096-568A-29405	Sequence 29405, A	1212	61	3.7	395	6	US-10-330-773-661	Sequence 661, App
1140	61.5	3.7	459	7	US-11-087-099-3380	Sequence 3380, Ap	1213	61	3.7	405	7	US-11-096-568A-28005	Sequence 28005, A
1141	61.5	3.7	495	7	US-11-052-554A-258	Sequence 258, App	1214	61	3.7	424	7	US-11-024-959-459	Sequence 499, App
1142	61.5	3.7	510	6	US-10-641-678-43	Sequence 43, App1	1215	61	3.7	432	7	US-11-096-568A-30110	Sequence 30110, A
1143	61.5	3.7	511	6	US-10-641-678-42	Sequence 42, App1	1216	61	3.7	440	7	US-11-096-568A-31383	Sequence 31383, A
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1145	61.5	3.7	517	7	US-11-096-568A-31871	Sequence 31871, A	1219	61	3.7	463	6	US-10-973-115B-360	Sequence 360, App
1146	61.5	3.7	516	7	US-11-096-568A-31882	Sequence 31882, A	1220	61	3.7	473	7	US-11-096-568A-21002	Sequence 21002, A
1147	61.5	3.7	540	6	US-10-641-678-44	Sequence 44, App1	1221	61	3.7	474	7	US-11-096-568A-21001	Sequence 21001, A
1148	61.5	3.7	540	7	US-11-212-443-168	Sequence 168, App	1222	61	3.7	474	7	US-11-096-568A-21505	Sequence 21505, A
1149	61.5	3.7	541	7	US-11-169-041-136	Sequence 136, App	1223	61	3.7	513	6	US-10-641-678-64	Sequence 64, App1
1150	61.5	3.7	549	7	US-11-096-568A-33577	Sequence 33577, A	1225	61	3.7	523	6	US-10-973-115B-246	Sequence 246, App
1151	61.5	3.7	583	7	US-11-024-959-268	Sequence 268, App	1226	61	3.7	529	7	US-11-096-568A-31382	Sequence 31382, A
1152	61.5	3.7	610	7	US-11-096-568A-26675	Sequence 26675, A	1227	61	3.7	533	7	US-11-072-512-3718	Sequence 3718, Ap
1153	61.5	3.7	621	7	US-11-096-568A-26674	Sequence 26674, A	1228	61	3.7	544	7	US-11-096-568A-21504	Sequence 21504, A
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1155	61.5	3.7	640	7	US-11-212-443-20	Sequence 20, App1	1230	61	3.7	545	7	US-11-087-099-951	Sequence 951, App
1156	61.5	3.7	643	7	US-11-072-512-2737	Sequence 2737, Ap	1231	61	3.7	547	7	US-11-087-039-3034	Sequence 3034, Ap
1157	61.5	3.7	669	7	US-11-096-568A-31870	Sequence 31870, A	1232	61	3.7	557	7	US-11-096-568A-21000	Sequence 21000, A
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1160	61.5	3.7	690	7	US-11-096-568A-31869	Sequence 31869, A	1235	61	3.7	597	7	US-11-051-720-1354	Sequence 1354, Ap
1161	61.5	3.7	730	7	US-11-082-389-358	Sequence 358, App	1236	61	3.7	610	7	US-11-096-568A-31381	Sequence 31381, A
1162	61.5	3.7	731	7	US-11-098-686-10415	Sequence 10415, A	1237	61	3.7	665	7	US-11-124-368A-289	Sequence 289, App
1163	61.5	3.7	737	6	US-10-055-877-156	Sequence 156, App	1238	61	3.7	685	7	US-11-072-512-2916	Sequence 2916, Ap
1164	61.5	3.7	863	7	US-11-077-550-38	Sequence 38, App1	1239	61	3.7	718	7	US-11-074-176-306	Sequence 306, App
1165	61.5	3.7	875	7	US-11-077-550-10	Sequence 10, App1	1240	61	3.7	723	7	US-11-074-176-18	Sequence 18, App1
1166	61.5	3.7	877	7	US-11-077-550-157	Sequence 157, App	1241	61	3.7	745	6	US-10-793-626-1742	Sequence 1742, Ap
1167	61.5	3.7	877	7	US-11-074-176-322	Sequence 322, App	1242	61	3.7	797	6	US-10-330-773-663	Sequence 663, App
1168	61.5	3.7	883	7	US-11-074-176-88	Sequence 88, App1	1243	61	3.7	810	6	US-10-453-372-1116	Sequence 1116, Ap
1169	61.5	3.7	992	7	US-11-098-686-10761	Sequence 10761, A	1244	61	3.7	843	7	US-11-123-104-89	Sequence 89, App1
1170	61.5	3.7	1076	7	US-11-098-686-11338	Sequence 11338, A	1245	61	3.7	852	7	US-11-087-099-4834	Sequence 4834, Ap
1171	61.5	3.7	1107	6	US-10-485-517-115	Sequence 145, App	1246	61	3.7	873	7	US-11-087-099-7920	Sequence 7920, Ap
1172	61.5	3.7	1127	7	US-11-077-550-50	Sequence 50, App1	1247	61	3.7	899	7	US-11-124-368A-290	Sequence 290, App
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1174	61.5	3.7	1171	7	US-11-087-099-2303	Sequence 2303, Ap	1249	61	3.7	1064	7	US-11-087-039-10112	Sequence 10112, A
1175	61.5	3.7	1171	7	US-11-087-099-3806	Sequence 3806, Ap	1250	61	3.7	1071	6	US-10-467-657-1654	Sequence 1654, Ap
1176	61.5	3.7	1171	7	US-11-087-099-7445	Sequence 7445, Ap	1251	61	3.7	1075	6	US-10-821-234-1202	Sequence 1202, Ap
1177	61.5	3.7	1171	7	US-11-087-099-9917	Sequence 9917, Ap	1252	61	3.7	1139	7	US-11-096-568A-27582	Sequence 27582, A
1178	61.5	3.7	1308	6	US-10-912-971-12	Sequence 12, App1	1253	61	3.7	1224	7	US-11-096-568A-27581	Sequence 27580, A
1179	61.5	3.7	1308	6	US-11-113-202-16	Sequence 16, App1	1254	61	3.7	1240	7	US-11-096-568A-27580	Sequence 27580, A
1180	61.5	3.7	1596	6	US-11-060-005-4	Sequence 4, App1	1255	61	3.7	1439	7	US-11-124-368A-291	Sequence 291, App
1181	61.5	3.7	3623	6	US-10-995-561-593	Sequence 593, App	1256	61	3.7	1493	7	US-11-183-136-26	Sequence 26, App1
1182	61	3.7	139	6	US-10-467-657-2748	Sequence 2748, Ap	1257	61	3.7	1579	6	US-10-330-773-939	Sequence 939, App
1183	61	3.7	154	7	US-11-096-568A-11923	Sequence 11923, A	1258	61	3.7	1613	7	US-11-108-528-84	Sequence 84, App1
1184	61	3.7	168	6	US-10-714-887-68	Sequence 68, App1	1259	61	3.7	1751	7	US-11-103-957-45	Sequence 45, App1
1185	61	3.7	265	7	US-11-087-099-5324	Sequence 5324, Ap	1260	61	3.7	1751	7	US-11-018-868-16	Sequence 16, App1
1186	61	3.7	273	6	US-10-995-561-917	Sequence 917, App	1261	61	3.7	2214	7	US-11-080-991-94	Sequence 94, App1
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1188	61	3.7	277	7	US-11-098-686-11027	Sequence 11027, A	1263	61	3.7	2723	7	US-11-129-741-388	Sequence 388, App
1189	61	3.7	288	7	US-11-052-554A-353	Sequence 353, App	1264	61	3.7	2828	7	US-11-080-991-54	Sequence 54, App1
1190	61	3.7	293	7	US-11-096-568A-15588	Sequence 15588, A	1265	61	3.7	2828	7	US-11-186-284-49	Sequence 49, App1
1191	61	3.7	295	7	US-11-096-568A-30519	Sequence 30519, A	1266	60.5	3.7	53	7	US-11-096-568A-6179	Sequence 6179, Ap
1192	61	3.7	297	6	US-10-967-527A-17	Sequence 17, App1	1267	60.5	3.7	101	7	US-11-096-568A-26972	Sequence 26972, A
1193	61	3.7	297	7	US-11-096-568A-15587	Sequence 15587, A	1268	60.5	3.7	132	7	US-11-087-099-3992	Sequence 3992, Ap
1194	61	3.7	307	7	US-11-096-568A-28007	Sequence 28007, A	1269	60.5	3.7	154	6	US-10-475-075-802	Sequence 802, App
1195	61	3.7	315	7	US-11-096-568A-21620	Sequence 21620, A	1270	60.5	3.7	161	7	US-10-475-075-802	Sequence 802, App
1196	61	3.7	317	6	US-10-674-767-2	Sequence 2, App1	1271	60.5	3.7	171	7	US-11-096-568A-6182	Sequence 6182, Ap
1197	61	3.7	329	7	US-11-096-568A-30518	Sequence 30518, A	1272	60.5	3.7	221	7	US-11-112-481C-2	Sequence 2, App1
1198	61	3.7	330	7	US-11-096-568A-21618	Sequence 21618, A	1273	60.5	3.7	237	6	US-10-884-730-336	Sequence 336, App
1199	61	3.7	336	7	US-11-096-568A-15586	Sequence 15586, A	1274	60.5	3.7	245	7	US-11-186-284-167	Sequence 167, App
1200	61	3.7	336	7	US-11-096-568A-28006	Sequence 28006, A	1275	60.5	3.7	248	7	US-11-176-830-528	Sequence 528, App
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1202	61	3.7	338	7	US-11-055-822-286	Sequence 286, App	1277	60.5	3.7	266	7	US-11-087-099-5491	Sequence 5491, Ap
1203	61	3.7	338	7	US-11-055-822-622	Sequence 622, App	1278	60.5	3.7	266	7	US-11-087-099-7758	Sequence 7758, Ap
1204	61	3.7	342	7	US-11-174-751-19	Sequence 19, App1	1279	60.5	3.7	272	7	US-11-087-099-8109	Sequence 8109, Ap
1205	61	3.7	344	7	US-11-087-099-6649	Sequence 6649, Ap	1280	60.5	3.7	272	7	US-11-087-099-9485	Sequence 9485, Ap
1206	61	3.7	350	6	US-10-467-657-5824	Sequence 5824, Ap	1281	60.5	3.7	276	7	US-11-020-602-224	Sequence 224, App
1207	61	3.7	375	7	US-11-096-568A-21506	Sequence 21506, A	1282	60.5	3.7	276	6	US-11-092-587-20	Sequence 20, App1
1208	61	3.7	379	7	US-11-087-099-1412	Sequence 1412, Ap	1283	60.5	3.7	278	6	US-10-861-934-16	Sequence 16, App1

1284	60.5	3.7	278	6	US-10-861-934-26	Sequence 26, Appl	1358	60	3.6	112	7	US-11-096-568A-7599	Sequence 7599, Ap
1285	60.5	3.7	279	6	US-10-861-934-24	Sequence 24, Appl	1359	60	3.6	135	7	US-11-077-619-106	Sequence 106, App
1286	60.5	3.7	279	6	US-10-861-934-32	Sequence 32, Appl	1360	60	3.6	142	7	US-11-186-284-105	Sequence 105, App
1287	60.5	3.7	279	6	US-11-032-797-5	Sequence 5, Appl	1361	60	3.6	150	6	US-10-467-657-2040	Sequence 2040, Ap
1288	60.5	3.7	283	7	US-11-096-568A-30112	Sequence 30112, A	1362	60	3.6	190	7	US-11-096-568A-26722	Sequence 26722, A
1289	60.5	3.7	293	6	US-10-821-234-1374	Sequence 1374, Ap	1363	60	3.6	203	7	US-11-096-568A-30022	Sequence 30022, A
1290	60.5	3.7	306	7	US-11-096-568A-16235	Sequence 16235, A	1364	60	3.6	214	7	US-11-096-568A-30021	Sequence 30021, A
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1294	60.5	3.7	315	7	US-11-096-568A-1902	Sequence 1902, Ap	1368	60	3.6	262	7	US-11-096-568A-21488	Sequence 21488, A
1295	60.5	3.7	317	7	US-11-096-568A-5836	Sequence 5836, Ap	1369	60	3.6	264	7	US-11-087-099-772	Sequence 772, App
1296	60.5	3.7	333	7	US-11-096-568A-1901	Sequence 1901, Ap	1370	60	3.6	266	6	US-10-884-730-114	Sequence 114, App
1297	60.5	3.7	338	7	US-11-096-568A-5835	Sequence 5835, Ap	1371	60	3.6	277	7	US-11-132-285-3	Sequence 12, Appl
1298	60.5	3.7	340	7	US-11-143-980-43	Sequence 43, Appl	1372	60	3.6	277	7	US-11-182-946-12	Sequence 12, Appl
1299	60.5	3.7	343	6	US-10-793-626-1626	Sequence 1626, Ap	1373	60	3.6	289	7	US-11-087-099-8567	Sequence 8567, Ap
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1301	60.5	3.7	357	7	US-11-241-347-10	Sequence 10, Appl	1375	60	3.6	303	7	US-11-096-568A-21487	Sequence 21487, A
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1304	60.5	3.7	379	6	US-10-973-115B-216	Sequence 216, App	1377	60	3.6	312	6	US-10-498-026-56	Sequence 56, Appl
1305	60.5	3.7	380	7	US-11-052-554A-369	Sequence 369, App	1378	60	3.6	324	7	US-11-087-099-8018	Sequence 8018, Ap
1306	60.5	3.7	383	7	US-11-031-206-199	Sequence 199, App	1379	60	3.6	324	7	US-11-087-099-9180	Sequence 9180, Ap
1307	60.5	3.7	417	6	US-10-793-626-950	Sequence 950, App	1380	60	3.6	330	7	US-11-087-099-11267	Sequence 11267, A
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1309	60.5	3.7	444	7	US-11-004-590-232	Sequence 232, App	1382	60	3.6	332	6	US-10-973-115B-386	Sequence 386, App
1310	60.5	3.7	446	7	US-11-117-667-2	Sequence 2, Appl	1384	60	3.6	339	7	US-11-087-099-6189	Sequence 6189, Ap
1311	60.5	3.7	461	7	US-11-096-568A-29257	Sequence 29257, A	1385	60	3.6	342	7	US-11-087-099-10231	Sequence 10231, A
1312	60.5	3.7	463	7	US-11-052-554A-261	Sequence 261, App	1386	60	3.6	344	7	US-11-016-564-13	Sequence 13, Appl
1313	60.5	3.7	468	7	US-11-086-289-22	Sequence 22, Appl	1387	60	3.6	344	7	US-11-016-564-16	Sequence 16, Appl
1314	60.5	3.7	472	6	US-10-467-657-6774	Sequence 6774, Ap	1388	60	3.6	348	7	US-11-087-099-7041	Sequence 7041, Ap
1315	60.5	3.7	473	7	US-11-096-568A-148	Sequence 148, App	1389	60	3.6	349	7	US-11-016-564-9	Sequence 9, Appl
1316	60.5	3.7	476	7	US-11-024-959-385	Sequence 385, App	1390	60	3.6	356	7	US-11-096-568A-32647	Sequence 32647, A
1317	60.5	3.7	477	7	US-11-024-959-261	Sequence 261, App	1391	60	3.6	361	7	US-11-087-099-2191	Sequence 2191, Ap
1318	60.5	3.7	510	7	US-11-096-568A-147	Sequence 147, App	1392	60	3.6	361	7	US-11-096-568A-32646	Sequence 32646, A
1319	60.5	3.7	511	7	US-11-096-568A-146	Sequence 146, App	1393	60	3.6	362	7	US-11-052-554A-77	Sequence 77, Appl
1320	60.5	3.7	521	7	US-11-096-568A-29256	Sequence 29256, A	1394	60	3.6	362	7	US-11-052-554A-204	Sequence 204, App
1321	60.5	3.7	540	7	US-11-212-443-167	Sequence 167, App	1395	60	3.6	362	7	US-11-096-568A-32491	Sequence 32491, A
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1324	60.5	3.7	585	7	US-11-241-347-15	Sequence 15, Appl	1398	60	3.6	380	7	US-11-087-099-6231	Sequence 6231, Ap
1325	60.5	3.7	608	7	US-11-226-701-8	Sequence 8, Appl	1399	60	3.6	380	7	US-11-087-099-8371	Sequence 8371, Ap
1326	60.5	3.7	608	7	US-11-241-347-9	Sequence 9, Appl	1400	60	3.6	387	7	US-11-096-568A-31873	Sequence 31873, A
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1328	60.5	3.7	664	6	US-10-624-932-10	Sequence 10, Appl	1402	60	3.6	389	7	US-11-096-568A-32491	Sequence 32491, A
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1334	60.5	3.7	728	6	US-10-517-696-112	Sequence 112, App	1408	60	3.6	431	7	US-11-074-176-132	Sequence 1285, Ap
1335	60.5	3.7	761	7	US-11-212-443-22	Sequence 22, Appl	1409	60	3.6	438	7	US-11-074-176-152	Sequence 152, App
1336	60.5	3.7	773	6	US-10-995-561-852	Sequence 852, Appl	1410	60	3.6	440	7	US-11-096-568A-32490	Sequence 32490, A
1337	60.5	3.7	803	6	US-10-821-234-1643	Sequence 1643, Ap	1411	60	3.6	450	7	US-11-072-512-3499	Sequence 3499, Ap
1338	60.5	3.7	803	6	US-10-962-951-2	Sequence 2, Appl	1412	60	3.6	456	7	US-11-000-463-451	Sequence 451, App
1339	60.5	3.7	840	7	US-11-108-172-1102	Sequence 1102, Ap	1413	60	3.6	456	7	US-11-000-463-923	Sequence 923, App
1340	60.5	3.7	858	6	US-10-995-561-854	Sequence 854, App	1414	60	3.6	468	7	US-11-087-099-11555	Sequence 11555, A
1341	60.5	3.7	860	7	US-11-019-711-59	Sequence 59, Appl	1415	60	3.6	472	7	US-11-165-226-9	Sequence 9, Appl
1342	60.5	3.7	873	7	US-11-077-550-167	Sequence 167, App	1416	60	3.6	479	7	US-11-096-568A-19818	Sequence 19818, A
1343	60.5	3.7	907	7	US-11-087-099-3272	Sequence 3272, Ap	1417	60	3.6	485	6	US-10-467-657-946	Sequence 946, App
1344	60.5	3.7	964	7	US-11-137-465-58	Sequence 58, Appl	1418	60	3.6	491	7	US-11-072-512-3243	Sequence 3243, Ap
1345	60.5	3.7	965	7	US-11-147-047-51	Sequence 51, Appl	1419	60	3.6	496	7	US-11-072-512-3006	Sequence 3006, Ap
1346	60.5	3.7	1137	7	US-11-012-762-70	Sequence 70, Appl	1420	60	3.6	497	6	US-10-641-678-10	Sequence 10, Appl
1347	60.5	3.7	1178	6	US-10-995-561-851	Sequence 851, Appl	1421	60	3.6	515	7	US-11-087-099-4483	Sequence 4483, Ap
1348	60.5	3.7	1178	7	US-11-044-899-29	Sequence 29, Appl	1422	60	3.6	533	7	US-11-087-099-7375	Sequence 7375, Ap
1349	60.5	3.7	1196	6	US-11-072-512-2933	Sequence 2933, Ap	1423	60	3.6	533	7	US-11-147-047-33	Sequence 33, Appl
1350	60.5	3.7	1263	6	US-10-485-517-127	Sequence 127, App	1424	60	3.6	536	7	US-11-096-568A-10893	Sequence 10893, A
1351	60.5	3.7	1337	7	US-11-112-304A-33	Sequence 33, Appl	1425	60	3.6	538	7	US-11-096-568A-10892	Sequence 10892, A
1352	60.5	3.7	1332	7	US-11-212-443-62	Sequence 62, Appl	1426	60	3.6	548	7	US-11-052-554A-324	Sequence 324, App
1353	60.5	3.7	1395	7	US-11-069-834-60	Sequence 60, Appl	1427	60	3.6	550	7	US-11-087-099-11870	Sequence 11870, A
1354	60.5	3.7	2314	7	US-11-013-759-11	Sequence 11, Appl	1428	60	3.6	554	7	US-11-096-568A-10891	Sequence 10891, A
1355	60.5	3.7	2766	6	US-10-877-346-62	Sequence 62, Appl	1429	60	3.6	556	7	US-11-124-368A-303	Sequence 303, App
1356	60.5	3.7	8746	7	US-11-098-686-10232	Sequence 10232, A	1430	60	3.6	562	7	US-11-065-943-24	Sequence 24, Appl
1357	60	3.6	109	6	US-10-517-696-115	Sequence 115, App	1431	60	3.6	611	6	US-10-517-939-156	Sequence 156, App

1432	60	3.6	663	6	US-10-467-945A-1	Sequence 1, Appli
1433	60	3.6	663	7	US-11-216-245-1	Sequence 1, Appli
1434	60	3.6	682	7	US-11-072-175-154	Sequence 154, App
1436	60	3.6	690	6	US-10-973-115B-306	Sequence 306, App
1437	60	3.6	741	7	US-11-087-099-6883	Sequence 6883, Ap
1438	60	3.6	749	7	US-11-096-568A-32687	Sequence 32687, A
1439	60	3.6	750	7	US-11-096-568A-32686	Sequence 32686, A
1440	60	3.6	755	7	US-11-037-243-82	Sequence 82, Appl
1441	60	3.6	771	7	US-11-147-047-34	Sequence 34, Appl
1442	60	3.6	813	7	US-11-096-568A-31851	Sequence 31851, A
1443	60	3.6	839	7	US-11-076-431-2	Sequence 2, Appli
1444	60	3.6	839	7	US-11-076-431-4	Sequence 4, Appli
1445	60	3.6	839	7	US-11-076-431-6	Sequence 6, Appli
1446	60	3.6	839	7	US-11-076-431-8	Sequence 8, Appli
1447	60	3.6	851	7	US-11-096-568A-31850	Sequence 31850, A
1448	60	3.6	878	7	US-11-077-550-12	Sequence 12, Appl
1449	60	3.6	902	7	US-11-096-568A-31849	Sequence 31849, A
1450	60	3.6	907	7	US-11-077-550-16	Sequence 16, Appl
1451	60	3.6	937	6	US-10-512-544-1	Sequence 1, Appli
1452	60	3.6	953	7	US-11-077-550-14	Sequence 14, Appl
1453	60	3.6	1000	7	US-11-098-686-10907	Sequence 10907, A
1454	60	3.6	1013	7	US-11-077-550-18	Sequence 18, Appl
1455	60	3.6	1103	7	US-11-096-568A-27585	Sequence 27585, A
1456	60	3.6	1122	6	US-10-995-561-705	Sequence 705, App
1457	60	3.6	1129	6	US-10-995-561-706	Sequence 706, App
1458	60	3.6	1145	7	US-11-096-568A-27584	Sequence 27584, A
1459	60	3.6	1157	6	US-10-330-773-936	Sequence 936, App
1460	60	3.6	1613	7	US-11-108-528-86	Sequence 86, Appl
1461	59.5	3.6	106	5	US-09-978-360A-551	Sequence 551, App
1462	59.5	3.6	106	5	US-09-978-360A-701	Sequence 701, App
1463	59.5	3.6	148	7	US-11-087-099-539	Sequence 539, App
1464	59.5	3.6	148	7	US-11-096-568A-20684	Sequence 20684, A
1465	59.5	3.6	152	7	US-11-096-568A-7426	Sequence 7426, Ap
1466	59.5	3.6	162	7	US-11-096-568A-7425	Sequence 7425, Ap
1467	59.5	3.6	175	7	US-11-096-568A-3912	Sequence 3912, Ap
1468	59.5	3.6	180	7	US-11-096-568A-7424	Sequence 7424, Ap
1469	59.5	3.6	188	7	US-11-087-099-9413	Sequence 9413, Ap
1470	59.5	3.6	198	7	US-11-087-099-2043	Sequence 2043, Ap
1471	59.5	3.6	198	7	US-11-087-099-5351	Sequence 5351, Ap
1472	59.5	3.6	198	7	US-11-087-099-7609	Sequence 7609, Ap
1473	59.5	3.6	219	7	US-11-112-481C-4	Sequence 4, Appli
1474	59.5	3.6	221	5	US-09-995-493-130	Sequence 130, App
1475	59.5	3.6	236	7	US-11-096-568A-22845	Sequence 22845, A
1476	59.5	3.6	248	7	US-11-176-830-538	Sequence 538, App
1477	59.5	3.6	251	7	US-11-096-568A-1074	Sequence 1074, Ap
1478	59.5	3.6	251	7	US-11-096-568A-16236	Sequence 16236, A
1479	59.5	3.6	265	7	US-11-087-099-5951	Sequence 5951, Ap
1480	59.5	3.6	266	7	US-11-087-099-3608	Sequence 3608, Ap
1481	59.5	3.6	266	7	US-11-087-099-4585	Sequence 4585, Ap
1482	59.5	3.6	266	7	US-11-087-099-6865	Sequence 6865, Ap
1483	59.5	3.6	276	7	US-11-096-568A-12522	Sequence 12522, A
1484	59.5	3.6	298	7	US-11-096-568A-25291	Sequence 25291, A
1485	59.5	3.6	298	7	US-11-096-568A-25290	Sequence 25290, A
1486	59.5	3.6	299	7	US-11-096-568A-25289	Sequence 25289, A
1487	59.5	3.6	312	7	US-11-096-568A-34393	Sequence 34393, A
1488	59.5	3.6	313	6	US-10-485-517-123	Sequence 123, App
1489	59.5	3.6	313	6	US-10-485-517-293	Sequence 293, App
1490	59.5	3.6	316	7	US-11-152-811-4	Sequence 4, Appli
1491	59.5	3.6	316	7	US-11-072-512-2455	Sequence 2455, Ap
1492	59.5	3.6	317	7	US-11-096-568A-12521	Sequence 12521, A
1493	59.5	3.6	320	7	US-11-096-568A-5457	Sequence 5457, Ap
1494	59.5	3.6	321	7	US-11-096-568A-5456	Sequence 5456, Ap
1495	59.5	3.6	325	7	US-11-096-568A-5455	Sequence 5455, Ap
1496	59.5	3.6	331	7	US-11-096-568A-3911	Sequence 3911, Ap
1497	59.5	3.6	335	7	US-11-087-099-1878	Sequence 1878, Ap
1498	59.5	3.6	342	6	US-10-467-657-4232	Sequence 4232, Ap
1499	59.5	3.6	347	6	US-10-821-234-1379	Sequence 1379, Ap
1500	59.5	3.6	353	7	US-11-207-626A-42	Sequence 42, Appl

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OM protein - protein search, using sw model  
Run on: March 20, 2006, 14:17:31 ; Search time 64.5519 Seconds  
(without alignments)  
2191.725 Million cell updates/sec

Title: US-10-063-510-6  
Perfect score: 1657  
Sequence: 1 MARCFSLVLLTSTWTRLL.....NPESKSPSKTTRVCLEAEV 322  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	AA13379	standard; protein; 322 AA.		
DE	Amino acid sequence of protein PRO263.			
PN	WO9914328-A2.			
PD	25-MAR-1999.			
PA	(GETH ) GENENTECH INC.			
Query Match				
Best Local Similarity	100.0%;	Score 1657; DB 2;	Length 322;	
RESULT 2				
ID	AA87287	standard; protein; 322 AA.		
DE	Human signal peptide containing protein HSPP-64 SEQ ID NO:64.			
PN	WO20000610-A2.			
PD	06-JAN-2000.			
PA	(INCY-) INCYTE PHARM INC.			
Query Match				
Best Local Similarity	100.0%;	Score 1657; DB 3;	Length 322;	
RESULT 3				
ID	ADC78521	standard; protein; 322 AA.		
DE	Human PRO263 protein.			
PN	WO200015796-A2.			
PD	23-MAR-2000.			
PA	(GETH ) GENENTECH INC.			
Query Match				
Best Local Similarity	100.0%;	Score 1657; DB 3;	Length 322;	
RESULT 4				
ID	AA880247	standard; protein; 322 AA.		
DE	Human PRO263 protein.			
PN	WO200104311-A1.			
PD	18-JAN-2001.			
PA	(GETH ) GENENTECH INC.			
Query Match				
Best Local Similarity	100.0%;	Score 1657; DB 4;	Length 322;	
RESULT 5				
ID	AA887528	standard; protein; 322 AA.		
DE	Human PRO263.			
PN	WO200116318-A2.			
PD	08-MAR-2001.			
PA	(GETH ) GENENTECH INC.			
Query Match				
Best Local Similarity	100.0%;	Score 1657; DB 4;	Length 322;	
RESULT 6				
ID	AA888391	standard; protein; 322 AA.		
DE	Human membrane or secretory protein clone PSEC0135.			

PN EPI067182-A2.  
PD 10-JAN-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 100.0%; Score 1657; DB 4; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 7  
ID ABG95853 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 5; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 8  
ID ABB84832 standard; protein; 322 AA.  
DE Human PRO263 protein sequence SEQ ID NO:32.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 5; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 9  
ID ABB95438 standard; protein; 322 AA.  
DE Human angiogenesis related protein PRO263 SEQ ID NO: 32.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1657; DB 5; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 10  
ID ABU71625 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 11  
ID ABU71480 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 12  
ID ABU71926 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 13  
ID ABO01809 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2002197671-A1.  
PD 26-DEC-2002.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 14  
ID ABU90878 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 15  
ID AB033937 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 16  
ID AB071954 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 17  
ID ABU54382 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 18  
ID AB047397 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO263.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 19  
ID AB071508 standard; protein; 322 AA.  
DE Human secreted polypeptide PRO263.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 20  
ID ABU72289 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 21  
ID ABU90962 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 22  
ID AB027283 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO263.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 23  
ID ABU64534 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #38.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 24  
ID ABU67380 standard; protein; 322 AA.  
DE Human secreted protein PRO263.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 25  
ID ABU92478 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 26  
ID ABO14900 standard; protein; 322 AA.  
DE Human secreted / transmembrane polypeptide PRO263.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 27  
ID ABU81148 standard; protein; 322 AA.  
DE Human secreted polypeptide PRO263.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 28  
ID ABO53263 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 29  
ID ABU98265 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 30  
ID ABU89270 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 31  
ID ABU82477 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 32



Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 32  
ID ABO69657 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 33  
ID ABO96441 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 34  
ID ABO72111 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 35  
ID ABO14839 standard; protein; 322 AA.  
DE Human secreted / transmembrane polypeptide PRO263.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 36  
ID ADB29406 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 37  
ID ABO17063 standard; protein; 322 AA.  
DE Human transmembrane PRO polypeptide (SeqID 6).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 38  
ID ABO44241 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO 263.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 39  
ID ADA18262 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 40  
ID ABO32791 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;

RESULT 41  
ID ADA19868 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003089394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 42  
ID ADB17251 standard; protein; 322 AA.  
DE Human transmembrane PRO polypeptide (SeqID 6).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 43  
ID ABO34851 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 44  
ID ADA16237 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 45  
ID ADA20040 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 46  
ID ABO34169 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO 263.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 47  
ID ADA42382 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 48  
ID ABO17529 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 49  
ID ADA00337 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO 263.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 50  
ID ABO32791 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;

ID ADA16661 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 51  
ID ADA13090 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 52  
ID ADA41958 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 53  
ID ADA17305 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 54  
ID ADA42808 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 55  
ID AB017590 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 56  
ID AD885579 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 57  
ID ADB77727 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 58  
ID ADB74863 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 59  
ID ADB68258 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 60  
ID ADB68065 standard; protein; 322 AA.  
DE Human PRO263 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 61  
ID ADB90882 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 62  
ID ADC28509 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 63  
ID ADC39709 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 64  
ID ADC40223 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 65  
ID ADC19047 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 66  
ID ADC34347 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 67  
ID ADC29402 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 68  
ID ADC28933 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.

PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 69  
ID ADC40818 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 70  
ID ADC19475 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054411-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 71  
ID ADC06962 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 72  
ID ADC17141 standard; protein; 322 AA.  
DE Mammalian PRO polypeptide (SeqID 6).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 73  
ID ADC33923 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 74  
ID ADC12993 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 75  
ID ADC14839 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 76  
ID ADC52334 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 77  
ID ADC12445 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003082541-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 78  
ID ADD10321 standard; protein; 322 AA.  
DE Human secreted/transmembrane PRO polypeptide #16.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 79  
ID ADD05000 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 80  
ID ADD11281 standard; protein; 322 AA.  
DE Human secreted/transmembrane PRO polypeptide #16.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 81  
ID ADD04006 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 82  
ID ADD03582 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003108993-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 83  
ID ADD37074 standard; protein; 322 AA.  
DE Human secreted/transmembrane PRO polypeptide #16.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 84  
ID ADD36010 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 85  
ID ADE34834 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 86  
ID ADG01011 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003078387-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 87  
ID ADG08564 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 88  
ID ADG95185 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 89  
ID ADH24038 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 90  
ID ADH34064 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 91  
ID ADH29897 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 92  
ID ADH23868 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 93  
ID ADG85272 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 94  
ID ADH24548 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 95  
ID ADH37404 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 96  
ID ADH01993 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 97  
ID ADH37574 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 98  
ID ADG85612 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 99  
ID ADH24208 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 100  
ID ADH38502 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 101  
ID ADG83623 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 102  
ID ADH29431 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 103  
ID ADH27547 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 104  
ID ADH37744 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;

Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 105  
ID ADH37921 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 106  
ID ADH57341 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 107  
ID ADH59317 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 108  
ID ADH53483 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 109  
ID ADH53653 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 110  
ID ADH51989 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 111  
ID ADH49844 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 112  
ID ADI25354 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 113  
ID ADH90147 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;

RESULT 114  
ID ADI25524 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 115  
ID ADH97698 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 116  
ID ADI38096 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 117  
ID ADI03546 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 118  
ID ADI11903 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 119  
ID ADH89977 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 120  
ID ADH98378 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 121  
ID ADI11053 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 122  
ID ADI11563 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 123  
ID ADI11563 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;

ID ADH98208 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 124  
ID ADH98548 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 125  
ID ADH98038 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 126  
ID ADI05026 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 127  
ID ADI03376 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 128  
ID ADI04771 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 129  
ID ADH78225 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
FN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 130  
ID ADI19569 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 131  
ID ADH90317 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 132  
ID ADI03036 standard; protein; 322 AA.

DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 133  
ID ADH77885 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
FN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 134  
ID ADH97868 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 135  
ID ADI01253 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 136  
ID ADI01948 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 137  
ID ADI03206 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 138  
ID ADI11393 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
FN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 139  
ID ADI02295 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 140  
ID ADI11733 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
FN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 141  
ID ADI05370 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.



PN US2003190716-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 142  
ID ADH79442 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 143  
ID ADI19399 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 144  
ID ADI05200 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 145  
ID ADH79612 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 146  
ID ADI01438 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 147  
ID ADI01608 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 148  
ID ADI01778 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 149  
ID ADH79782 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 150  
ID ADI04600 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003171550-A1.

PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 151  
ID ADI02736 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 152  
ID ADH78055 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 153  
ID ADI25694 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 154  
ID ADI25864 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 155  
ID ADK65376 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 156  
ID ADH98718 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 157  
ID ADH79959 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 158  
ID ADJ26364 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 159  
ID ADL93690 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003040013-A1.  
PD 27-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 160  
ID ADE52144 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 161  
ID ADE79279 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 162  
ID ADE79703 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 163  
ID ADE73379 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 164  
ID ADE41282 standard; protein; 322 AA.  
DE Human secreted/transmembrane PRO polypeptide #16.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 165  
ID ADE71444 standard; protein; 322 AA.  
DE Human PDEBC incyte 3044710CD1.  
PN US2003124543-A1.  
PD 03-JUL-2003.  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 166  
ID ADE73914 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 167  
ID ADE99468 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 168  
ID ADE98587 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003211569-A1.  
PD 13-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 169  
ID ADE99014 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 170  
ID ADG40484 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 171  
ID ADF73878 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 172  
ID ADF73454 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US200316051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 173  
ID ADH06576 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 174  
ID ADH06406 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 175  
ID ADG68827 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 176  
ID ADG68827 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 177  
ID ADH27717 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;



DE Human PRO polypeptide #3.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 196  
ID ADH01070 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 197  
ID ADG69677 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 198  
ID ADH02163 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 199  
ID ADG69167 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 200  
ID ADG85952 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 201  
ID ADH24888 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 202  
ID ADH39505 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 203  
ID ADH02503 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 204  
ID ADG68997 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.

PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 205  
ID ADH07600 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 206  
ID ADG86122 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 207  
ID ADH24718 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 208  
ID ADH25766 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 209  
ID ADH38332 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 210  
ID ADH20513 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 211  
ID ADH57171 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 212  
ID ADH43465 standard; protein; 322 AA.  
DE Human PRO polypeptide #16.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 213  
ID ADH07368 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004006211-A1.

PD 08-JAN-2004.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 214  
 ID ADH52159 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003180921-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 215  
 ID ADH59913 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003215904-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 216  
 ID ADH49525 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003180857-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 217  
 ID ADH06941 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2004005665-A1.  
 PD 08-JAN-2004.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 218  
 ID ADH90487 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003181700-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 219  
 ID ADI11223 standard; protein; 322 AA.  
 DE Human PRO polypeptide #3.  
 PN US2003181683-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 220  
 ID ADI18683 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003152999-A1.  
 PD 14-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 221  
 ID ADJ99630 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003187238-A1.

ID ADH9888 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003190698-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 222  
 ID ADI65403 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003148419-A1.  
 PD 07-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 223  
 ID ADI02118 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003190699-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 224  
 ID ADH90657 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003181701-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 225  
 ID ADI37666 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003096340-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 226  
 ID ADH97462 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003190610-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 227  
 ID ADI65830 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003148371-A1.  
 PD 07-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 228  
 ID ADH60573 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2004023331-A1.  
 PD 05-FEB-2004.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match  
 Best Local Similarity 100.0%; Score 1657; DB 8; Length 322;  
 RESULT 229  
 ID ADJ99630 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003187238-A1.

PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 230  
ID ADL08823 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 231  
ID ADJ98532 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 232  
ID ADJ98702 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 233  
ID ADH7861 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 234  
ID ADJ99095 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 235  
ID ADJ99265 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 236  
ID ADJ98883 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 237  
ID ADH79031 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 238  
ID ADK00891 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GERB ) GERBER H.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 239  
ID ADK14412 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 240  
ID ADM25164 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 241  
ID ADM29914 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 242  
ID ADK82810 standard; protein; 322 AA.  
DE Human PRO polypeptide #16.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 243  
ID ADM80861 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 244  
ID ADO06236 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 245  
ID ADR11088 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004137561-A1.  
PD 15-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 246  
ID ADR17997 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK ) ASHKENAZI A.  
PA (BOTS ) BOTSTEIN D.  
PA (DESN ) DESNOYERS L.  
PA (EATO ) EATON D L.  
PA (FERR ) FERRARA N.  
PA (FILV ) FILVAROFF E.  
PA (FONG ) FONG S.  
PA (GAOW ) GAO W.  
PA (GERB ) GERBER H.

(GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 247  
ID ADS74636 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein #40.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 248  
ID ADT03673 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003152922-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 249  
ID ADY77701 standard; protein; 322 AA.  
DE Neoplastic disease detection protein PRO263.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (FILV/) FILVAROFF E.  
PA (GERB/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1657; DB 9; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 250  
(GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1657; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 251  
ID AEA37911 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1657; DB 9; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
RESULT 252  
ID ADR41495 standard; protein; 344 AA.  
DE Human CD-like molecule HEMFC27, SEQ ID NO:294.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 1657; DB 5; Length 344;  
Best Local Similarity 100.0%; Pred. No. 1.1e-147;  
RESULT 253  
ID ABB11979 standard; peptide; 344 AA.  
DE Human PRO263 homologue, SEQ ID NO:2349.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 99.8%; Score 1654; DB 4; Length 344;  
Best Local Similarity 99.7%; Pred. No. 2.1e-147;  
RESULT 254  
ID AAM56249 standard; protein; 322 AA.  
DE Amino acid sequence of a CD44-like protein.  
PN WO9806839-A1.  
PD 19-FEB-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 99.6%; Score 1651; DB 2; Length 322;  
Best Local Similarity 99.7%; Pred. No. 3.7e-147;  
RESULT 255  
ID ABB90289 standard; protein; 322 AA.  
DE Human polypeptide SEQ ID NO 2665.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 99.6%; Score 1651; DB 5; Length 322;  
Best Local Similarity 99.7%; Pred. No. 3.7e-147;  
RESULT 256  
ID ADN05866 standard; protein; 322 AA.  
DE Antipsoriatic protein sequence #1096.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 98.9%; Score 1638; DB 8; Length 322;  
Best Local Similarity 99.1%; Pred. No. 6.3e-146;  
RESULT 257  
ID ADQ21089 standard; protein; 322 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3909.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 98.9%; Score 1638; DB 8; Length 322;  
Best Local Similarity 99.1%; Pred. No. 6.3e-146;  
RESULT 258  
ID ABU69126 standard; protein; 297 AA.  
DE Human NOVX polypeptide #1.  
PN WO200290504-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 91.2%; Score 1511.5; DB 6; Length 297;  
Best Local Similarity 92.2%; Pred. No. 5.1e-134;  
RESULT 259  
ID ADO08255 standard; protein; 297 AA.

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DE Human NOVX polypeptide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLER I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match
Best Local Similarity 90.6%; Score 1500.5; DB 8; Length 297;
RESULT 260
ID AAB34702 standard; protein; 250 AA.
DE Human secreted protein encoded by DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match
Best Local Similarity 73.5%; Score 1218.5; DB 3; Length 250;
RESULT 261
ID AA053364 standard; protein; 318 AA.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 66.6%; Score 1103; DB 4; Length 318;
RESULT 262
ID AB372376 standard; protein; 255 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 700.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 49.5%; Score 821; DB 5; Length 255;
RESULT 263
ID AAY12323 standard; protein; 116 AA.
DE Human 5' EST secreted protein SEQ ID NO:354.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 35.7%; Score 592; DB 2; Length 116;
RESULT 264
ID AA112853 standard; protein; 58 AA.
DE Human 5' EST secreted protein SEQ ID NO:443.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 16.7%; Score 277; DB 2; Length 58;
RESULT 265
ID AAY12170 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO: 483.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 15.8%; Score 261; DB 2; Length 69;
RESULT 266
ID ADW24431 standard; protein; 364 AA.
DE Rat CD44.
PN WO200024869-A2.
PD 04-MAY-2000.
PA (UYYA) UNIV YALE.
PA (VIGN/) VIGNERY A.
Query Match
Best Local Similarity 13.8%; Score 229; DB 3; Length 364;
RESULT 267
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match
Best Local Similarity 13.8%; Score 229; DB 5; Length 364;
RESULT 268
ID AAR07355 standard; protein; 362 AA.
DE B7 adhesion receptor.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Query Match
Best Local Similarity 13.4%; Score 222.5; DB 2; Length 362;
RESULT 269
ID ABU79109 standard; protein; 365 AA.
DE CD44 protein.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.
Query Match
Best Local Similarity 13.4%; Score 222.5; DB 6; Length 365;
RESULT 270
ID ADF43353 standard; protein; 365 AA.
DE CD44 receptor polypeptide seq id 73.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match
Best Local Similarity 13.4%; Score 222.5; DB 7; Length 365;
RESULT 271
ID AEA03024 standard; protein; 365 AA.
DE CD14 receptor amino acid sequence SEQ ID NO:50.
PN US2005112141-A1.
PD 26-MAY-2005.
PA (TERM/) TERMAN D S.
Query Match
Best Local Similarity 13.4%; Score 222.5; DB 9; Length 365;
RESULT 272
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match
Best Local Similarity 13.4%; Score 222; DB 2; Length 503;
RESULT 273
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.
```



PD 27-FEB-2003.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 Query Match 13.4%; Score 222; DB 7; Length 503;  
 Best Local Similarity 25.7%; Pred. No. 8.7e-12;  
 RESULT 274  
 ID AD251063 standard; protein; 778 AA.  
 DE Amino acid sequence of murine CD44.  
 PN WO2005034984-A1.  
 PD 21-APR-2005.  
 PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
 Query Match 12.7%; Score 210; DB 9; Length 778;  
 Best Local Similarity 32.3%; Pred. No. 2.1e-10;  
 RESULT 275  
 ID ABU04619 standard; protein; 668 AA.  
 DE Human expressed protein tag (EPT) #1285.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.6%; Score 208.5; DB 6; Length 668;  
 Best Local Similarity 29.3%; Pred. No. 2.4e-10;  
 RESULT 276  
 ID AQ039384 standard; protein; 668 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 12.6%; Score 208.5; DB 8; Length 668;  
 Best Local Similarity 29.3%; Pred. No. 2.4e-10;  
 RESULT 277  
 ID AAK20816 standard; protein; 361 AA.  
 DE Haematopoietic CD44 Antigen.  
 PN WO9201049-A.  
 PD 23-JAN-1992.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 12.5%; Score 207; DB 2; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 278  
 ID AAR91444 standard; protein; 361 AA.  
 DE Human haematopoietic CD44 antigen.  
 PN US5506126-A.  
 PD 03-APR-1996.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 12.5%; Score 207; DB 2; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 279  
 ID AAW80453 standard; protein; 361 AA.  
 DE Human CD44 antigen (membrane form).  
 PN US5830731-A.  
 PD 03-NOV-1998.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 12.5%; Score 207; DB 2; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 280  
 ID AAW86200 standard; protein; 361 AA.  
 DE Human CD44 antigen (membrane form).  
 PN US5849898-A.  
 PD 15-DEC-1998.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 12.5%; Score 207; DB 2; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 281  
 ID AAY96139 standard; protein; 361 AA.  
 DE Human haematopoietic CD44.5.  
 PN US6111093-A.  
 PD 23-AUG-2000.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 12.5%; Score 207; DB 3; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 282  
 ID AAU02448 standard; protein; 361 AA.  
 DE Human haematopoietic antigen CD44 polypeptide.  
 PN US6218525-B1.

PD 17-APR-2001.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 12.5%; Score 207; DB 4; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 283  
 ID ABU04632 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1298.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.5%; Score 207; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 284  
 ID ABU04610 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1276.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.5%; Score 207; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 285  
 ID ABU04638 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1304.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.5%; Score 207; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 286  
 ID ABU04634 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1300.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.5%; Score 207; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 287  
 ID ABU04626 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1292.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.5%; Score 207; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 288  
 ID ABU04630 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1296.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.5%; Score 207; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 289  
 ID ABU04636 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1302.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.5%; Score 207; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 290  
 ID ADO49373 standard; protein; 361 AA.  
 DE Human CD44 #1.  
 PN US2004072283-A1.  
 PD 15-APR-2004.  
 PA .. (SEED/) SEED B.  
 PA (ALIE/) ALLEN J.  
 PA (ARUF/) ARUFFO A.  
 PA (CAME/) CAMERINI D.  
 PA (LAUF/) LAUFFER L.  
 PA (OQUE/) OQUENDO C.  
 PA (SIMM/) SIMMONS D.  
 PA (STAW/) STAMENKOVIC I.

PA (STEN/) STENGELIN S.  
 PA (AMIO/) AMIOT M.  
 Query Match 12.5%; Score 207; DB 8; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 1.4e-10;  
 RESULT 291  
 ID AAY99851 standard; protein; 361 AA.  
 DE Human CD44 cell surface adhesion receptor.  
 PN WO200035935-A1.  
 PD 22-JUN-2000.  
 PA (ISIS-) ISIS PHARM INC.  
 Query Match 12.4%; Score 205; DB 3; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
 RESULT 292  
 ID ABU04643 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1309.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.4%; Score 205; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
 RESULT 293  
 ID ABU04609 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1275.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.4%; Score 205; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
 RESULT 294  
 ID ABU04644 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1310.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.4%; Score 205; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
 RESULT 295  
 ID ADV70207 standard; protein; 361 AA.  
 DE Tumor-associated antigenic target polypeptide TAT449.  
 PN WO2004112829-A2.  
 PD 29-DEC-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 205; DB 9; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
 RESULT 296  
 ID ADY19504 standard; protein; 361 AA.  
 DE PRO polypeptide SEQ ID NO 5310.  
 PN WO2005016962-A2.  
 PD 24-FEB-2005.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 205; DB 9; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
 RESULT 297  
 ID AEA63870 standard; protein; 361 AA.  
 DE Protein of human anti-CD44 antibody.  
 PN JP2005154389-A.  
 PD 16-JUN-2005.  
 PA (FUJY ) FUJI PHARM IND CO LTD.  
 Query Match 12.4%; Score 205; DB 9; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
 RESULT 298  
 ID ABU04622 standard; protein; 361 AA.  
 DE Human expressed protein tag (EPT) #1288.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.3%; Score 204; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.8e-10;  
 RESULT 299  
 ID AAE30338 standard; protein; 361 AA.  
 DE Human CD44 antigen.  
 PN WO200276510-A1.

PD 03-OCT-2002.  
 PA (AGYT-) AGY THERAPEUTICS INC.  
 Query Match 12.3%; Score 204; DB 6; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.8e-10;  
 RESULT 300  
 ID AQO39385 standard; protein; 361 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 12.3%; Score 204; DB 8; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.8e-10;  
 RESULT 301  
 ID ADY16699 standard; protein; 361 AA.  
 DE PRO polypeptide SEQ ID NO 2505.  
 PN WO2005016962-A2.  
 PD 24-FEB-2005.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.3%; Score 204; DB 9; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 2.8e-10;  
 RESULT 302  
 ID ABP72424 standard; protein; 608 AA.  
 DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.  
 PN WO2003014160-A2.  
 PD 20-FEB-2003.  
 PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 Query Match 12.3%; Score 203.5; DB 6; Length 608;  
 Best Local Similarity 21.8%; Pred. No. 6.3e-10;  
 RESULT 303  
 ID AAY97579 standard; protein; 700 AA.  
 DE Human CD44 splice variant (RA-CD44) protein sequence.  
 PN WO200075312-A1.  
 PD 14-DEC-2000.  
 PA (YISS ) YISSUM RES & DEV CO.  
 Query Match 12.3%; Score 203.5; DB 4; Length 700;  
 Best Local Similarity 21.8%; Pred. No. 7.7e-10;  
 RESULT 304  
 ID ABU04640 standard; protein; 700 AA.  
 DE Human expressed protein tag (EPT) #1306.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.3%; Score 203.5; DB 6; Length 700;  
 Best Local Similarity 21.8%; Pred. No. 7.7e-10;  
 RESULT 305  
 ID ADD90594 standard; protein; 700 AA.  
 DE Human CD44v glycoprotein SEQ ID NO:4.  
 PN WO2003072606-A2.  
 PD 04-SEP-2003.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 Query Match 12.3%; Score 203.5; DB 7; Length 700;  
 Best Local Similarity 21.8%; Pred. No. 7.7e-10;  
 RESULT 306  
 ID ADW43568 standard; protein; 700 AA.  
 DE CD44vRA.  
 PN WO2005007700-A1.  
 PD 27-JAN-2005.  
 PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 Query Match 12.3%; Score 203.5; DB 9; Length 700;  
 Best Local Similarity 21.8%; Pred. No. 7.7e-10;  
 RESULT 307  
 ID ADD90592 standard; protein; 361 AA.  
 DE Human CD44std glycoprotein SEQ ID NO:2.  
 PN WO2003072606-A2.  
 PD 04-SEP-2003.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 Query Match 12.3%; Score 203; DB 7; Length 361;  
 Best Local Similarity 24.4%; Pred. No. 3.4e-10;  
 RESULT 308  
 ID ADW43572 standard; protein; 361 AA.  
 DE CD44s.

PN WO2005007700-A1.  
PD 27-JAN-2005.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.3%; Score 203; DB 9; Length 361;  
Best Local Similarity 24.4%; Pred. No. 3.4e-10;  
RESULT 309  
ID AAY97651 standard; protein; 436 AA.  
DE CD44Hextra/tmfascyto protein sequence.  
PN WO200100854-A2.  
PD 04-JAN-2001.  
PA (ANGI-) ANGIOGENE PHARM LTD.  
Query Match 12.3%; Score 203; DB 4; Length 436;  
Best Local Similarity 25.4%; Pred. No. 4.5e-10;  
RESULT 310  
ID ABU04642 standard; protein; 436 AA.  
DE Human expressed protein tag (EPT) #1308.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.3%; Score 203; DB 6; Length 436;  
Best Local Similarity 25.4%; Pred. No. 4.5e-10;  
RESULT 311  
ID ABU04653 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1319.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.3%; Score 203; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 312  
ID ABU04616 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1282.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.3%; Score 203; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 313  
ID ADP65295 standard; protein; 742 AA.  
DE Human CD44 antigen (homolog function and Indian blood group system), CD44.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 12.3%; Score 203; DB 7; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 314  
ID ADL61252 standard; protein; 742 AA.  
DE Human protein tyrosine kinase biomarker CD44 antigen protein.  
PN WO2004020583-A2.  
PD 11-MAR-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 12.3%; Score 203; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 315  
ID ADQ39391 standard; protein; 742 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.3%; Score 203; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 316  
ID ADR67253 standard; protein; 742 AA.  
DE Human bladder cancer associated amino acid sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERZ/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (STAU/) STAUB E.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Query Match 12.3%; Score 203; DB 8; Length 742;

Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 317  
ID ADU06304 standard; protein; 742 AA.  
DE Novel bronchial cancer-associated human protein SeqID528.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
Query Match 12.3%; Score 203; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 318  
ID ADY15336 standard; protein; 742 AA.  
DE PRO polypeptide SEQ ID NO 1142.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 12.3%; Score 203; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 319  
ID ADY15338 standard; protein; 742 AA.  
DE PRO polypeptide SEQ ID NO 1144.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 12.3%; Score 203; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.2e-10;  
RESULT 320  
ID ADH18898 standard; protein; 330 AA.  
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 12.3%; Score 202.5; DB 8; Length 330;  
Best Local Similarity 25.1%; Pred. No. 3.4e-10;  
RESULT 321  
ID AAY97650 standard; protein; 431 AA.  
DE CD44HextraFASm/cyto protein sequence.  
PN WO200100854-A2.  
PD 04-JAN-2001.  
PA (ANGI-) ANGIOGENE PHARM LTD.  
Query Match 12.2%; Score 202.5; DB 4; Length 431;  
Best Local Similarity 24.7%; Pred. No. 4.9e-10;  
RESULT 322  
ID ABU04641 standard; protein; 431 AA.  
DE Human expressed protein tag (EPT) #1307.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.2%; Score 202.5; DB 6; Length 431;  
Best Local Similarity 24.7%; Pred. No. 4.9e-10;  
RESULT 323  
ID ABU04607 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1273.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.2%; Score 202; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 4.3e-10;  
RESULT 324  
ID ADL93508 standard; protein; 361 AA.  
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.  
PN WO2004024750-A2.  
PD 25-MAR-2004.  
PA (DYAX-) DYAX CORP.  
Query Match 12.2%; Score 202; DB 8; Length 361;  
Best Local Similarity 24.1%; Pred. No. 4.3e-10;  
RESULT 325  
ID ADS75483 standard; protein; 361 AA.  
DE Human cell surface glycoprotein CD44 amino acid sequence.  
PN JP2004275060-A.  
PD 07-OCT-2004.  
PA (SANY ) SANKYO CO LTD.

Query Match 12.2%; Score 202; DB 8; Length 361;  
Best Local Similarity 24.4%; Pred. No. 4.3e-10;  
RESULT 326  
ID ABU04618 standard; protein; 675 AA.  
DE Human expressed protein tag (EPT) #1284.  
FN W0200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.2%; Score 202; DB 6; Length 675;  
Best Local Similarity 26.0%; Pred. No. 1e-09;  
RESULT 327  
ID ABU04621 standard; protein; 691 AA.  
DE Human expressed protein tag (EPT) #1287.  
FN W0200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.2%; Score 202; DB 6; Length 691;  
Best Local Similarity 26.0%; Pred. No. 1e-09;  
RESULT 328  
ID ADQ39390 standard; protein; 691 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.  
FN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.2%; Score 202; DB 8; Length 691;  
Best Local Similarity 26.0%; Pred. No. 1e-09;  
RESULT 329  
ID ABU04620 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1286.  
FN W0200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.2%; Score 202; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 330  
ID ABU04645 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1311.  
FN W0200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.2%; Score 202; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 331  
ID ADN95511 standard; protein; 742 AA.  
DE Human BEC/LEC-related protein sequence SeqID434.  
FN W02003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN-) LICENTIA LTD.  
Query Match 12.2%; Score 202; DB 7; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 332  
ID ADL93506 standard; protein; 742 AA.  
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.  
FN W02004024750-A2.  
PD 25-MAR-2004.  
PA (DYAX-) DYAX CORP.  
Query Match 12.2%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 333  
ID AD055181 standard; protein; 742 AA.  
DE Protein #83 with increased gene expression in renal cell carcinoma.  
FN W02004032842-A2.  
PD 22-APR-2004.  
PA (VAND-) VAN ANDEL INST.  
Query Match 12.2%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 334  
ID ADQ39383 standard; protein; 742 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.  
FN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.

Query Match 12.2%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 335  
ID ADQ39386 standard; protein; 742 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.  
FN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.2%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 336  
ID ADW72142 standard; protein; 742 AA.  
DE Human CD44 protein as biomarker for colorectal cancer.  
FN US2005014165-A1.  
PD 20-JAN-2005.  
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.  
Query Match 12.2%; Score 202; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 337  
ID AD251062 standard; protein; 742 AA.  
DE Amino acid sequence of human CD44.  
FN W02005034984-A1.  
PD 21-APR-2005.  
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
Query Match 12.2%; Score 202; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 338  
ID ABU04617 standard; protein; 425 AA.  
DE Human expressed protein tag (EPT) #1283.  
FN W0200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.1%; Score 201; DB 6; Length 425;  
Best Local Similarity 22.0%; Pred. No. 6.6e-10;  
RESULT 339  
ID ADD90596 standard; protein; 699 AA.  
DE Human CD44v glycoprotein SEQ ID NO:6.  
FN W02003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.1%; Score 200.5; DB 7; Length 699;  
Best Local Similarity 25.2%; Pred. No. 1.5e-09;  
RESULT 340  
ID ADW43570 standard; protein; 699 AA.  
DE CD44v3-V10.  
FN W02005007700-A1.  
PD 27-JAN-2005.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.1%; Score 200.5; DB 9; Length 699;  
Best Local Similarity 25.2%; Pred. No. 1.5e-09;  
RESULT 341  
ID AAR20817 standard; protein; 493 AA.  
DE Epithelial CD44 Antigen.  
FN W09201049-A.  
PD 23-JAN-1992.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 12.0%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
RESULT 342  
ID AAR91445 standard; protein; 493 AA.  
DE Human epithelial CD44 antigen.  
FN US5506126-A.  
PD 09-APR-1996.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 12.0%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
RESULT 343  
ID AAW80454 standard; protein; 493 AA.  
DE Human CD44 antigen (epithelial form).  
FN US5830731-A.  
PD 03-NOV-1998.  
PA (GEHO) GEN HOSPITAL CORP.

Query Match 12.0%; Score 199.5; DB 2; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 344  
 ID AAW89151 standard; protein; 493 AA.  
 DE Human CD44 antigen (epithelial form).  
 PN US5849898-A.  
 PD 15-DEC-1998.  
 PA (GHO) GEN HOSPITAL CORP.  
 Query Match 12.0%; Score 199.5; DB 2; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 345  
 ID AAY96140 standard; protein; 493 AA.  
 DE Human epithelial CD44.  
 PN US6111093-A.  
 PD 29-AUG-2000.  
 PA (GHO) GEN HOSPITAL CORP.  
 Query Match 12.0%; Score 199.5; DB 3; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 346  
 ID AAU02449 standard; protein; 493 AA.  
 DE Human epithelial antigen CD44 polypeptide.  
 PN US6218525-B1.  
 PD 17-APR-2001.  
 PA (GHO) GEN HOSPITAL CORP.  
 Query Match 12.0%; Score 199.5; DB 4; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 347  
 ID AAU99123 standard; protein; 493 AA.  
 DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.  
 PN WO200244342-A2.  
 PD 06-JUN-2002.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Query Match 12.0%; Score 199.5; DB 5; Length 493;  
 Best Local Similarity 22.2%; Pred. No. 1.1e-09;  
 RESULT 348  
 ID ABU04637 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1303.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 349  
 ID ABU04627 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1293.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 350  
 ID ABU04639 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1305.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 351  
 ID ABU04623 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1289.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;  
 Best Local Similarity 22.2%; Pred. No. 1.1e-09;  
 RESULT 352  
 ID ABU04631 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1297.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;

Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 353  
 ID ABU04633 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1299.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 354  
 ID ABU04612 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1278.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;  
 Best Local Similarity 22.2%; Pred. No. 1.1e-09;  
 RESULT 355  
 ID ABU04635 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1301.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 356  
 ID ABU04613 standard; protein; 493 AA.  
 DE Human expressed protein tag (EPT) #1279.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 12.0%; Score 199.5; DB 6; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 357  
 ID ADL93507 standard; protein; 493 AA.  
 DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.  
 PN WO2004024750-A2.  
 PD 25-MAR-2004.  
 PA (DYAX-) DYAX CORP.  
 Query Match 12.0%; Score 199.5; DB 8; Length 493;  
 Best Local Similarity 22.2%; Pred. No. 1.1e-09;  
 RESULT 358  
 ID ADO49375 standard; protein; 493 AA.  
 DE Human CD44 #2.  
 PN US2004072283-A1.  
 PD 15-APR-2004.  
 PA (SEED/) SEED B.  
 PA (ALIE/) ALLEN J.  
 PA (ARUF/) ARUFFO A.  
 PA (CAME/) CAMERINI D.  
 PA (LAUF/) LAUFFER L.  
 PA (OQUE/) OQUENDO C.  
 PA (SIMM/) SIMMONS D.  
 PA (STAM/) STAMENKOVIC I.  
 PA (STEN/) STENGELIN S.  
 PA (AMIO/) AMIOT M.  
 Query Match 12.0%; Score 199.5; DB 8; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 359  
 ID AEB87764 standard; protein; 493 AA.  
 DE Human CD44, breast tumor marker.  
 PN WO2005071419-A2.  
 PD 04-AUG-2005.  
 PA (IPSO-) IPSOGEN.  
 PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.  
 PA (PAOL-) INST PAOLI CALMETTES.  
 Query Match 12.0%; Score 199.5; DB 9; Length 493;  
 Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
 RESULT 360  
 ID ABU04649 standard; protein; 338 AA.  
 DE Human expressed protein tag (EPT) #1315.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.

PA (ZYCO-) ZYCOS INC.  
Query Match 12.0%; Score 199; DB 6; Length 338;  
Best Local Similarity 24.6%; Pred. No. 7.5e-10;  
RESULT 361  
ID ABU04605 standard; protein; 338 AA.  
DE Human expressed protein tag (EPT) #1271.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.0%; Score 199; DB 6; Length 338;  
Best Local Similarity 24.6%; Pred. No. 7.5e-10;  
RESULT 362  
ID ABU04615 standard; protein; 395 AA.  
DE Human expressed protein tag (EPT) #1281.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.9%; Score 198; DB 6; Length 395;  
Best Local Similarity 23.0%; Pred. No. 1.2e-09;  
RESULT 363  
ID ABU04604 standard; protein; 719 AA.  
DE Human expressed protein tag (EPT) #1270.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.9%; Score 197; DB 6; Length 719;  
Best Local Similarity 26.3%; Pred. No. 3.3e-09;  
RESULT 364  
ID ABU04650 standard; protein; 719 AA.  
DE Human expressed protein tag (EPT) #1316.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.9%; Score 197; DB 6; Length 719;  
Best Local Similarity 26.3%; Pred. No. 3.3e-09;  
RESULT 365  
ID ABM83594 standard; protein; 535 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.  
FN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 11.9%; Score 196.5; DB 8; Length 535;  
Best Local Similarity 25.4%; Pred. No. 2.4e-09;  
RESULT 366  
ID ADQ39381 standard; protein; 535 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.  
FN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 11.9%; Score 196.5; DB 8; Length 535;  
Best Local Similarity 25.4%; Pred. No. 2.4e-09;  
RESULT 367  
ID ABU56470 standard; protein; 699 AA.  
DE Lung cancer-associated polypeptide #63.  
FN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 11.9%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 3.5e-09;  
RESULT 368  
ID ABU04647 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1313.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.9%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 3.5e-09;  
RESULT 369  
ID ABU04614 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1280.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.8%; Score 196; DB 8; Length 425;  
Best Local Similarity 30.9%; Pred. No. 1.8e-09;  
RESULT 370  
ID ABU04608 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1274.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.9%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 3.5e-09;  
RESULT 371  
ID ADV73230 standard; protein; 699 AA.  
DE Human colon tumor cell upregulated protein SEQ ID NO 71.  
FN WO2004110345-A2.  
PD 23-DEC-2004.  
PA (PHAA) PHARMACIA CORP.  
Query Match 11.9%; Score 196.5; DB 9; Length 699;  
Best Local Similarity 25.4%; Pred. No. 3.5e-09;  
RESULT 372  
ID ADY16689 standard; protein; 699 AA.  
DE PRO polypeptide SEQ ID NO 2495.  
FN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 11.8%; Score 196; DB 7; Length 261;  
Best Local Similarity 30.9%; Pred. No. 1e-09;  
RESULT 374  
ID ABU04611 standard; protein; 293 AA.  
DE Human expressed protein tag (EPT) #1277.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.8%; Score 196; DB 6; Length 293;  
Best Local Similarity 30.9%; Pred. No. 1.2e-09;  
RESULT 375  
ID ABU04624 standard; protein; 294 AA.  
DE Human expressed protein tag (EPT) #1290.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.8%; Score 196; DB 6; Length 294;  
Best Local Similarity 30.9%; Pred. No. 1.2e-09;  
RESULT 376  
ID ABU04646 standard; protein; 294 AA.  
DE Human expressed protein tag (EPT) #1312.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.8%; Score 196; DB 6; Length 294;  
Best Local Similarity 30.9%; Pred. No. 1.2e-09;  
RESULT 377  
ID ADQ39389 standard; protein; 395 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.  
FN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 11.8%; Score 196; DB 8; Length 395;  
Best Local Similarity 30.9%; Pred. No. 1.8e-09;  
RESULT 378  
ID ADQ39382 standard; protein; 425 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.  
FN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.

Best Local Similarity 30.9%; Pred. No. 2e-09;  
RESULT 379  
ID ABU04651 standard; protein; 493 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 11.8%; Score 196; DB 8; Length 493;  
Best Local Similarity 30.9%; Pred. No. 2.4e-09;  
RESULT 380  
ID ABG17071 standard; protein; 742 AA.  
DE Novel human diagnostic protein #17062.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.7%; Score 194.5; DB 4; Length 742;  
Best Local Similarity 25.4%; Pred. No. 5.9e-09;  
RESULT 381  
ID AAM48306 standard; protein; 194 AA.  
DE Protein R2 SEQ ID 29.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 11.7%; Score 194; DB 5; Length 194;  
Best Local Similarity 30.8%; Pred. No. 1e-09;  
RESULT 382  
ID AAM48307 standard; protein; 200 AA.  
DE Protein R3 SEQ ID 30.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 11.7%; Score 194; DB 5; Length 200;  
Best Local Similarity 30.8%; Pred. No. 1.1e-09;  
RESULT 383  
ID AAM48308 standard; protein; 273 AA.  
DE Protein R4 SEQ ID 31.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 11.7%; Score 194; DB 5; Length 273;  
Best Local Similarity 30.8%; Pred. No. 1.7e-09;  
RESULT 384  
ID ABU04602 standard; protein; 676 AA.  
DE Human expressed protein tag (EPT) #1268.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.6%; Score 191.5; DB 6; Length 676;  
Best Local Similarity 25.8%; Pred. No. 9.9e-09;  
RESULT 385  
ID ABU04652 standard; protein; 676 AA.  
DE Human expressed protein tag (EPT) #1318.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.6%; Score 191.5; DB 6; Length 676;  
Best Local Similarity 25.8%; Pred. No. 9.9e-09;  
RESULT 386  
ID ABU04648 standard; protein; 271 AA.  
DE Human expressed protein tag (EPT) #1314.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.5%; Score 191; DB 6; Length 271;  
Best Local Similarity 31.5%; Pred. No. 3.2e-09;  
RESULT 387  
ID ABU04606 standard; protein; 271 AA.  
DE Human expressed protein tag (EPT) #1272.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.5%; Score 191; DB 6; Length 271;  
Best Local Similarity 31.5%; Pred. No. 3.2e-09;

RESULT 388  
ID ABU04651 standard; protein; 470 AA.  
DE Human expressed protein tag (EPT) #1317.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.5%; Score 191; DB 6; Length 470;  
Best Local Similarity 31.5%; Pred. No. 6.7e-09;  
RESULT 389  
ID ABU04603 standard; protein; 470 AA.  
DE Human expressed protein tag (EPT) #1269.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.5%; Score 191; DB 6; Length 470;  
Best Local Similarity 31.5%; Pred. No. 6.7e-09;  
RESULT 390  
ID AAM48305 standard; protein; 170 AA.  
DE Protein R1 SEQ ID 28.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 11.3%; Score 188; DB 5; Length 170;  
Best Local Similarity 35.7%; Pred. No. 3.2e-09;  
RESULT 391  
ID ABP73148 standard; protein; 112 AA.  
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGEMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.3%; Score 187; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 2.2e-09;  
RESULT 392  
ID ABP73150 standard; protein; 113 AA.  
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGEMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.3%; Score 186.5; DB 6; Length 113;  
Best Local Similarity 36.3%; Pred. No. 2.5e-09;  
RESULT 393  
ID ABP73151 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGEMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.2%; Score 185; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 3.5e-09;  
RESULT 394  
ID ABP73152 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGEMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.0%; Score 183; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 5.4e-09;  
RESULT 395  
ID ABP73149 standard; protein; 112 AA.  
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGEMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.0%; Score 182; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 5.4e-09;



Best Local Similarity 34.2%; Pred. No. 6.7e-09;  
RESULT 396  
ID ABP73153 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
FN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match  
Best Local Similarity 10.9%; Score 181; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 8.3e-09;  
RESULT 397  
ID ABG17067 standard; protein; 920 AA.  
DE Novel human diagnostic protein #17058.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 10.9%; Score 180; DB 4; Length 920;  
Best Local Similarity 25.6%; Pred. No. 1.9e-07;  
RESULT 398  
ID AD160410 standard; protein; 920 AA.  
DE Secreted polypeptide encoded by gene splice variant #46.  
FN WO2003025142-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 10.9%; Score 180; DB 7; Length 920;  
Best Local Similarity 25.6%; Pred. No. 1.9e-07;  
RESULT 399  
ID AAM28056 standard; protein; 34 AA.  
DE Peptide #2093 encoded by probe for measuring placental gene expression.  
FN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 10.3%; Score 170; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
RESULT 400  
ID ABG37308 standard; peptide; 34 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.  
FN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 10.3%; Score 170; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
RESULT 401  
ID AD864426 standard; protein; 510 AA.  
DE Human protein encoded by clone FEBRA20038970.  
FN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 9.1%; Score 150; DB 7; Length 510;  
Best Local Similarity 23.6%; Pred. No. 5.7e-05;  
RESULT 402  
ID ABP73154 standard; protein; 80 AA.  
DE Deletion mutant of a CD44-hyaluronic acid binding domain.  
FN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match  
Best Local Similarity 9.0%; Score 148.5; DB 6; Length 80;  
Best Local Similarity 37.0%; Pred. No. 6.2e-06;  
RESULT 403  
ID ADP07712 standard; protein; 162 AA.  
DE Human secreted protein, seq id 195.  
FN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 8; Length 162;  
Best Local Similarity 33.0%; Pred. No. 3.5e-05;  
RESULT 404  
ID ADM80807 standard; protein; 237 AA.  
DE Human CADECM-36 protein SEQ ID NO:36.

PN WO2004015396-A2.  
PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 8; Length 237;  
Best Local Similarity 33.0%; Pred. No. 5.9e-05;  
RESULT 405  
ID AAR26044 standard; protein; 277 AA.  
DE Tumour necrosis factor-induced glycoprotein TSG-6.  
FN WO9212175-A1.  
PD 23-JUL-1992.  
PA (UNIV ) UNIV NEW YORK STATE.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 406  
ID AAM13654 standard; protein; 277 AA.  
DE Tumour necrosis factor-stimulated gene-6 protein.  
FN WO9704075-A1.  
PD 06-FEB-1997.  
PA (UNIV ) UNIV NEW YORK STATE.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 407  
ID AAM84087 standard; protein; 277 AA.  
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.  
FN US5846763-A.  
PD 08-DEC-1998.  
PA (UNIV ) UNIV NEW YORK STATE.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 408  
ID AAE02361 standard; protein; 277 AA.  
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.  
FN US6210905-B1.  
PD 03-APR-2001.  
PA (UNIV ) UNIV NEW YORK STATE.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 4; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 409  
ID ABG70870 standard; protein; 277 AA.  
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.  
FN US2002090708-A1.  
PD 11-JUL-2002.  
PA (UNIV ) UNIV NEW YORK STATE.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 5; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 410  
ID ABR58556 standard; protein; 277 AA.  
DE Human cancer related protein SEQ ID NO:213.  
FN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 6; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 411  
ID ABU56653 standard; protein; 277 AA.  
DE Lung cancer-associated polypeptide #246.  
FN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 6; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 412  
ID ADE25781 standard; protein; 277 AA.  
DE Human protein differentially expressed in foam cells #58.  
FN US2003194721-A1.  
PD 16-OCT-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 8.8%; Score 145; DB 7; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 413  
ID ADN39919 standard; protein; 277 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.  
FN WO2003042661-A2.

PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 8.8%; Score 145; DB 7; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 414  
ID ADN38974 standard; protein; 277 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.  
FN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 8.8%; Score 145; DB 7; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 415  
ID ADQ21506 standard; protein; 277 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.  
FN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 8.8%; Score 145; DB 8; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 416  
ID ADR51534 standard; protein; 277 AA.  
DE Human lipopolysaccharide-sensitive polypeptide #14.  
FN WO2004069870-A2.  
PD 19-AUG-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 8.8%; Score 145; DB 8; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 417  
ID ADW38508 standard; protein; 277 AA.  
DE Immunomodulatory Gene TNFa induced protein 6.  
FN WO200500099-A2.  
PD 06-JAN-2005.  
PA (GENZ-) GENZYME CORP.  
Query Match 8.8%; Score 145; DB 9; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 418  
ID ARA23596 standard; protein; 277 AA.  
DE Human PRO polypeptide SEQ ID NO 138.  
FN WO2005051988-A2.  
PD 09-JUN-2005.  
PA (GETH-) GENENTECH INC.  
Query Match 8.8%; Score 145; DB 9; Length 277;  
Best Local Similarity 33.0%; Pred. No. 7.3e-05;  
RESULT 419  
ID ADK67822 standard; protein; 2626 AA.  
DE Human BRCC300 polypeptide.  
FN WO2004012755-A1.  
PD 12-FEB-2004.  
PA (WIST-) WISTAR INST.  
Query Match 8.8%; Score 145; DB 8; Length 2626;  
Best Local Similarity 33.0%; Pred. No. 0.0016;  
RESULT 420  
ID ADS85081 standard; protein; 275 AA.  
DE Mouse atopic dermatitis-related protein sequence SeqID83.  
FN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 8.7%; Score 144; DB 8; Length 275;  
Best Local Similarity 33.0%; Pred. No. 9e-05;  
RESULT 421  
ID ADO09968 standard; protein; 897 AA.  
DE Human NOVIC cDNA.  
FN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHIMKETS R. A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (WALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
Query Match 8.1%; Score 134; DB 5; Length 2675;  
Best Local Similarity 17.8%; Pred. No. 0.018;  
RESULT 426  
ID ADO09971 standard; protein; 2675 AA.  
DE Human NOVA variant.  
FN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHIMKETS R. A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (WALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (BOLD/) BOLDOG F L.  
PA (LILL/) LI L.  
PA (TAUP/) TAUPIER R J.  
PA (KEKU/) KERUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERR/) ZERHUSEN B D.  
PA (LIUX/) LIU X.  
PA (COLM/) COLMAN S D.

PA (GANG/) GANGOLLI E A.  
PA (MILL/) MILLER C E.  
PA (BOLD/) BOLDOG F L.  
PA (LILL/) LI L.  
PA (TAUP/) TAUPIER R J.  
PA (KEKU/) KERUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERR/) ZERHUSEN B D.  
PA (LIUX/) LIU X.  
PA (COLM/) COLMAN S D.  
PA (TCHE/) TCHERNEV V T.  
PA (SIJG/) SI J.  
PA (EDIN/) EDINGER S R.  
PA (STON/) STONE D J.  
PA (SCIO/) SCIORE P.  
PA (MILL/) MILLET I.  
PA (ROTH/) ROTHENBERG M E.  
Query Match 8.2%; Score 136; DB 8; Length 897;  
Best Local Similarity 21.2%; Pred. No. 0.0026;  
RESULT 422  
ID ABJ10588 standard; protein; 897 AA.  
DE Human novel protein NOVIC SEQ ID NO: 211.  
FN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 134; DB 5; Length 897;  
Best Local Similarity 20.7%; Pred. No. 0.004;  
RESULT 423  
ID ADH71312 standard; protein; 897 AA.  
DE Human protein of the invention NOV9a SEQ ID NO:208.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 134; DB 8; Length 897;  
Best Local Similarity 20.7%; Pred. No. 0.004;  
RESULT 424  
ID ADH71356 standard; protein; 1502 AA.  
DE Human protein of the invention NOV9w SEQ ID NO:252.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 134; DB 8; Length 1502;  
Best Local Similarity 20.7%; Pred. No. 0.0081;  
RESULT 425  
ID ABJ10586 standard; protein; 2675 AA.  
DE Human novel protein NOVA SEQ ID NO: 2.  
FN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 134; DB 5; Length 2675;  
Best Local Similarity 17.8%; Pred. No. 0.018;  
RESULT 426  
ID ADO09971 standard; protein; 2675 AA.  
DE Human NOVA variant.  
FN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHIMKETS R. A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (WALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (BOLD/) BOLDOG F L.  
PA (LILL/) LI L.  
PA (TAUP/) TAUPIER R J.  
PA (KEKU/) KERUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERR/) ZERHUSEN B D.  
PA (LIUX/) LIU X.  
PA (COLM/) COLMAN S D.

PA (TCHE/) TCHERNEV V T.  
 PA (SIJJ/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (MILL/) MILLET I.  
 PA (ROTH/) ROTHENBERG M E.  
 Query Match  
 Best Local Similarity 8.1%; Score 134; DB 8; Length 2675;  
 Pred. No. 0.018;  
 RESULT 427  
 ID ADO09836 standard; protein; 2675 AA.  
 DE Human NOV1a.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTRAJAN M.  
 PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJJ/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (MILL/) MILLET I.  
 PA (ROTH/) ROTHENBERG M E.  
 Query Match  
 Best Local Similarity 8.1%; Score 134; DB 8; Length 2675;  
 Pred. No. 0.018;  
 RESULT 428  
 ID AAM47684 standard; protein; 1394 AA.  
 DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.  
 PN WO200181544-A2.  
 PD 01-NOV-2001.  
 PA (WEIG/) WEIGEL P A.  
 PA (ZHOU/) ZHOU B.  
 PA (WEIG/) WEIGEL J A.  
 Query Match  
 Best Local Similarity 8.0%; Score 133; DB 5; Length 1394;  
 Pred. No. 0.0091;  
 RESULT 429  
 ID ABG72499 standard; protein; 1416 AA.  
 DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #1.  
 PN WO200286093-A2.  
 PD 31-OCT-2002.  
 PA (WEIG/) WEIGEL P H.  
 PA (WEIG/) WEIGEL J A.  
 Query Match  
 Best Local Similarity 8.0%; Score 133; DB 6; Length 1416;  
 Pred. No. 0.0093;  
 RESULT 430  
 ID AAM47675 standard; protein; 1431 AA.  
 DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.  
 PN WO200181544-A2.  
 PD 01-NOV-2001.  
 PA (WEIG/) WEIGEL P A.  
 PA (ZHOU/) ZHOU B.  
 PA (WEIG/) WEIGEL J A.  
 Query Match  
 Best Local Similarity 8.0%; Score 133; DB 5; Length 1431;  
 Pred. No. 0.0095;  
 RESULT 431  
 ID ABG72498 standard; protein; 1431 AA.  
 DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).  
 PN WO200286093-A2.

PD 31-OCT-2002.  
 PA (WEIG/) WEIGEL P H.  
 PA (WEIG/) WEIGEL J A.  
 Query Match  
 Best Local Similarity 8.0%; Score 133; DB 6; Length 1431;  
 Pred. No. 0.0095;  
 RESULT 432  
 ID ADH71358 standard; protein; 1510 AA.  
 DE Human protein of the invention NOV9x SEQ ID NO:254.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 8.0%; Score 133; DB 8; Length 1510;  
 Pred. No. 0.01;  
 RESULT 433  
 ID ABG72514 standard; protein; 1653 AA.  
 DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.  
 PN WO200286093-A2.  
 PD 31-OCT-2002.  
 PA (WEIG/) WEIGEL P H.  
 PA (WEIG/) WEIGEL J A.  
 Query Match  
 Best Local Similarity 8.0%; Score 133; DB 6; Length 1653;  
 Pred. No. 0.012;  
 RESULT 434  
 ID ADM90835 standard; protein; 1895 AA.  
 DE Human pharmaceutically useful protein SeqID 228.  
 PN WO2004020595-A2.  
 PD 11-MAR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
 PA (DNAF-) DNAFORM KK.  
 Query Match  
 Best Local Similarity 8.0%; Score 133; DB 8; Length 1895;  
 Pred. No. 0.014;  
 RESULT 435  
 ID ADH71360 standard; protein; 2551 AA.  
 DE Human protein of the invention NOV9y SEQ ID NO:256.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 8.0%; Score 133; DB 8; Length 2551;  
 Pred. No. 0.021;  
 RESULT 436  
 ID ABM84174 standard; protein; 2285 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:4423.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 8.0%; Score 132.5; DB 8; Length 2285;  
 Pred. No. 0.02;  
 RESULT 437  
 ID ABM84173 standard; protein; 2384 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:4422.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 8.0%; Score 132.5; DB 8; Length 2384;  
 Pred. No. 0.021;  
 RESULT 438  
 ID ABF72603 standard; protein; 883 AA.  
 DE Rat mutant brain-enriched hyaluronan binding protein.  
 PN WO2003007880-A2.  
 PD 30-JAN-2003.  
 PA (UYIA) UNIV YALE.  
 PA (HOCK/) HOCKFIELD S.  
 PA (MATT/) MATTHEWS R T.  
 Query Match  
 Best Local Similarity 7.9%; Score 131.5; DB 6; Length 883;  
 Pred. No. 0.0068;  
 RESULT 439  
 ID ADK67779 standard; protein; 883 AA.  
 DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.  
 PN WO2004013356-A1.  
 PD 12-FEB-2004.  
 PA (UYIA) UNIV YALE.  
 Query Match  
 Best Local Similarity 7.9%; Score 131.5; DB 8; Length 883;  
 Pred. No. 0.0068;

Best Local Similarity 24.3%; Pred. No. 0.0068;  
RESULT 440  
ID AEB34752 standard; protein; 883 AA.  
DE Mammalian mutant BEHAB protein.  
PN WO2005069852-A2.  
PD 04-AUG-2005.  
PA (UYIA ) UNIV YALE.  
Query Match 7.9%; Score 131.5; DB 9; Length 883;  
Best Local Similarity 24.3%; Pred. No. 0.0068;  
RESULT 441  
ID AAB61236 standard; protein; 649 AA.  
DE Mature human TANGO 332 protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 131; DB 4; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0049;  
RESULT 442  
ID ABO32673 standard; protein; 649 AA.  
DE Secreted polypeptide-related protein #74.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARW/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (WACK/) WACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 7.9%; Score 131; DB 6; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0049;  
RESULT 443  
ID ADB90778 standard; protein; 649 AA.  
DE Human TANGO 332 mature protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 131; DB 7; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0049;  
RESULT 444  
ID ADF71513 standard; protein; 649 AA.  
DE Human TANGO 332 mature protein.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 131; DB 7; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0049;  
RESULT 445  
ID ADQ10331 standard; protein; 649 AA.  
DE Human polypeptide #167.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 131; DB 8; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0049;  
RESULT 446  
ID AAB61234 standard; protein; 671 AA.  
DE Human TANGO 332 protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 131; DB 4; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0052;  
RESULT 447  
ID ABO32671 standard; protein; 671 AA.  
DE Secreted polypeptide-related protein #73.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.

PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (WACK/) WACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 7.9%; Score 131; DB 6; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0052;  
RESULT 448  
ID ADB90776 standard; protein; 671 AA.  
DE Human TANGO 332 protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 131; DB 7; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0052;  
RESULT 449  
ID ADF71511 standard; protein; 671 AA.  
DE Human TANGO 332.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 131; DB 7; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0052;  
RESULT 450  
ID ADQ10329 standard; protein; 671 AA.  
DE Human polypeptide #165.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.9%; Score 131; DB 8; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0052;  
RESULT 451  
ID ADH18892 standard; protein; 806 AA.  
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 7.9%; Score 131; DB 8; Length 806;  
Best Local Similarity 20.4%; Pred. No. 0.0066;  
RESULT 452  
ID AAY97583 standard; protein; 911 AA.  
DE Human secreted protein PRO6018.  
PN WO200075317-A2.  
PD 14-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 4; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 453  
ID ABG34055 standard; protein; 911 AA.  
DE Human Pro peptide #26.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 5; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 454  
ID ADI28032 standard; protein; 911 AA.  
DE ECMCAD protein 6755002CD1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.9%; Score 131; DB 5; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 455  
ID ADA01320 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003068779-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC. 7.9%; Score 131; DB 6; Length 911;  
Query Match 20.4%; Pred. No. 0.0079;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 456  
ID ADA43749 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 6; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 457  
ID ADA43517 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003073196-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 6; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 458  
ID ADA01192 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003068782-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 6; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 459  
ID ADA01076 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003068780-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 460  
ID ADA43633 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003073190-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 461  
ID ADA06895 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003068781-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 462  
ID ADA08383 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003068783-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 463  
ID ADB99676 standard; protein; 911 AA.  
DE Human PRO polypeptide SEQ ID 52.  
PN US2003082728-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 464  
ID ADB86959 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003082726-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 465  
ID ADB66114 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003082729-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 466  
ID ADB99792 standard; protein; 911 AA.  
DE Human PRO polypeptide SEQ ID 52.  
PN US2003073192-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 467  
ID ADB99447 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003082731-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 468  
ID ADB65998 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003082732-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 469  
ID ADC23396 standard; protein; 911 AA.  
DE Human transmembrane PRO polypeptide (SeqID 52).  
PN US2003073193-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 470  
ID ADC26089 standard; protein; 911 AA.  
DE Human PRO6018 protein.  
PN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 471  
ID ADE62583 standard; protein; 911 AA.  
DE Human Protein NP 068767, SEQ ID NO 8514.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 472  
ID ADE04916 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 7; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 473  
ID ADE11222 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 474				
ID	ADB8153 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003082733-A1.			
PD	01-MAY-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 475				
ID	ADP95448 standard; protein;	911 AA.		
DE	Human secreted/transmembrane polypeptide PRO6018.			
PN	US2003064473-A1.			
PD	03-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 476				
ID	AD806378 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003073195-A1.			
PD	17-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 477				
ID	ADE38153 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003119120-A1.			
PD	26-JUN-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 478				
ID	ADD88269 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003073189-A1.			
PD	17-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 479				
ID	ADD90850 standard; protein;	911 AA.		
DE	Human secreted/transmembrane polypeptide PRO6018.			
PN	US2003073188-A1.			
PD	17-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 480				
ID	ADP99405 standard; protein;	911 AA.		
DE	Human secreted/transmembrane polypeptide PRO6018.			
PN	US2003078401-A1.			
PD	24-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 481				
ID	ADG06498 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003077742-A1.			
PD	24-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 482				
ID	ADG05449 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003077741-A1.			
PD	24-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 483				
ID	ADG05449 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003077741-A1.			
PD	24-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 484				
ID	ADG05449 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003077741-A1.			
PD	24-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 485				
ID	ADG05449 standard; protein;	911 AA.		
DE	Human PRO polypeptide #26.			
PN	US2003077741-A1.			
PD	24-APR-2003.			
PA	(GETH ) GENENTECH INC.			
Query Match	7.9%;	Score 131;	DB 7;	Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0079;		
RESULT 486				
ID				

RESULT 492  
ID ADE504248 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide #26.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 493  
ID ADE39845 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 494  
ID ADE19710 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 495  
ID ADE77288 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003124666-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 496  
ID ADE65396 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119116-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 497  
ID ADE76005 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003124663-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 498  
ID ADE37916 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 499  
ID ADE64526 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119114-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 500  
ID ADE38861 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003096363-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 501  
ID ADE51935 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104562-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 502  
ID ADE0966 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003138902-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 503  
ID ADE38745 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003108996-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 504  
ID ADE37445 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104563-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 505  
ID ADE06262 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003138898-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 506  
ID ADE90121 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 507  
ID ADE38629 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 508  
ID ADE39560 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 509  
ID ADE89165 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 510  
ID ADE88932 standard; protein; 911 AA.



DE Human PRO polypeptide #26.  
PN US2003138899-A1.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 511  
ID ADE19826 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 512  
ID ADE77404 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 513  
ID ADE65280 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 514  
ID ADE39328 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 515  
ID ADE38513 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 516  
ID ADG11066 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 517  
ID ADG10950 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 518  
ID ADH31478 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 519  
ID ADH38726 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119132-A1.

PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 520  
ID ADH29361 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 521  
ID ADH23664 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 522  
ID ADH26994 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 523  
ID ADH38262 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 524  
ID ADH26878 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 525  
ID ADH38146 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 526  
ID ADH38842 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 527  
ID ADH23780 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 131; DB 8; Length 911;  
Pred. No. 0.0079;  
RESULT 528  
ID ADH40156 standard; protein; 911 AA.  
DE Human PRO6018 protein.  
PN US2003119132-A1.

PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 529  
ID ADH40040 standard; protein; 911 AA.  
DE Human PRO6018 protein.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 530  
ID ADH31362 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 531  
ID ADH29240 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 532  
ID ADH49455 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 533  
ID ADH51919 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 534  
ID ADH49774 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 535  
ID ADH52375 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 536  
ID ADH52491 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 537  
ID ADH58488 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119121-A1.  
PD 26-JUN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 538  
ID ADH51803 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 539  
ID ADH58364 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 540  
ID ADI13561 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 541  
ID ADK00817 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 542  
ID ADL08558 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 543  
ID AEM80156 standard; protein; 911 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 544  
ID AEA00137 standard; protein; 911 AA.  
DE Human TAT145 protein SEQ ID NO:89.  
PN US2005106644-A1.  
PD 19-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 9; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 545  
ID AEA00657 standard; protein; 911 AA.  
DE Human TAT145 protein sequence SeqID89.  
PN US2005107595-A1.  
PD 19-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 7.9%; Score 131; DB 9; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0079;  
RESULT 546  
ID AAB61242 standard; protein; 883 AA.  
DE Murine brevidin protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.

Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 4; Length 883;  
RESULT 547  
ID ABO32678 standard; protein; 883 AA.  
DE Secreted polypeptide-related protein #119.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (WACK/) WACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 6; Length 883;  
RESULT 548  
ID ABB72604 standard; protein; 883 AA.  
DE Rat brain-enriched hyaluronan binding protein.  
PN WO2003007880-A2.  
PD 30-JAN-2003.  
PA (UYIA ) UNIV YALE.  
PA (HOCK/) HOCKFIELD S.  
PA (MATT/) MATTHEWS R T.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 6; Length 883;  
RESULT 549  
ID ADB90787 standard; protein; 883 AA.  
DE Mouse brevicain protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 7; Length 883;  
RESULT 550  
ID ADE62581 standard; protein; 883 AA.  
DE Rat Protein P55068, SEQ ID NO 8512.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 7; Length 883;  
RESULT 551  
ID ADF71522 standard; protein; 883 AA.  
DE Murine brevidin protein.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 7; Length 883;  
RESULT 552  
ID ADK67782 standard; protein; 883 AA.  
DE Rat glycosylation-variant BEHAB isoform.  
PN WO2004033356-A1.  
PD 12-FEB-2004.  
PA (UYIA ) UNIV YALE.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 8; Length 883;  
RESULT 553  
ID ADQ10338 standard; protein; 883 AA.  
DE Human polypeptide #172.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 8; Length 883;  
RESULT 554  
ID ABB34755 standard; protein; 883 AA.

DE Rat poly-sialylated brain-enriched hyaluronan binding protein.  
PN WO2005069852-A2.  
PD 04-AUG-2005.  
PA (UYIA ) UNIV YALE.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 9; Length 883;  
RESULT 555  
ID ABB90349 standard; protein; 1082 AA.  
DE Human polypeptide SEQ ID NO 2725.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 5; Length 1082;  
RESULT 556  
ID ADX15811 standard; protein; 2316 AA.  
DE Human aggregan.  
PN WO2005012512-A1.  
PD 10-FEB-2005.  
PA (NAKA/) NAKAMURA N.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 9; Length 2316;  
RESULT 557  
ID ABB80463 standard; protein; 2570 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENTECH INC.  
Query Match  
Best Local Similarity 7.9%; Score 130.5; DB 8; Length 2570;  
RESULT 558  
ID AAY93911 standard; protein; 457 AA.  
DE A human hyaluronan-binding protein, designated WF-HABP.  
PN WO200039166-A1.  
PD 06-JUL-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (AMNA-) AMERICAN NAT RED CROSS.  
Query Match  
Best Local Similarity 7.8%; Score 129.5; DB 3; Length 457;  
RESULT 559  
ID ABB83434 standard; protein; 761 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 7.8%; Score 129.5; DB 8; Length 761;  
RESULT 560  
ID AAY93910 standard; protein; 2157 AA.  
DE A human hyaluronan-binding protein, designated WF-HABP.  
PN WO200039166-A1.  
PD 06-JUL-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (AMNA-) AMERICAN NAT RED CROSS.  
Query Match  
Best Local Similarity 7.8%; Score 129.5; DB 3; Length 2157;  
RESULT 561  
ID ABR82200 standard; protein; 2570 AA.  
DE Human CLEVER-1 protein SEQ ID NO:1.  
PN WO2003057130-A2.  
PD 17-JUL-2003.  
PA (JALK/) JALKANEN S.  
PA (IRJA/) IRJALA H.  
PA (SALM/) SALMI M.  
Query Match  
Best Local Similarity 7.8%; Score 129.5; DB 6; Length 2570;  
RESULT 562  
ID AAB08023 standard; protein; 95 AA.  
DE The domain of hyaluronic acid which interacts with CD44.  
PN WO200047163-A2.  
PD 17-AUG-2000.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
--Query Match  
7.8%; Score 128.5; DB 3; Length 95;

Best Local Similarity 28.7%; Pred. No. 0.00061;  
RESULT 563  
ID AB004625 standard; protein; 95 AA.  
DE Human expressed protein tag (SPT) #1291.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 7.8%; Score 128.5; DB 6; Length 95;  
Best Local Similarity 28.7%; Pred. No. 0.00061;  
RESULT 564  
ID AAR85442 standard; protein; 912 AA.  
DE Bovine brevicin core protein.  
FN WO9526201-A1.  
PD 05-OCT-1995.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Query Match 7.8%; Score 128.5; DB 2; Length 912;  
Best Local Similarity 22.0%; Pred. No. 0.014;  
RESULT 565  
ID ADV70173 standard; protein; 671 AA.  
DE Tumor-associated antigenic target polypeptide TAT152.  
FN WO2004112829-A2.  
PD 29-DEC-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 7.7%; Score 127.5; DB 9; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.011;  
RESULT 566  
ID AEA00138 standard; protein; 671 AA.  
DE Human TAT152 protein SEQ ID NO:90.  
FN US2005106644-A1.  
PD 19-MAY-2005.  
PA (GETH-) GENENTECH INC.  
Query Match 7.7%; Score 127.5; DB 9; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.011;  
RESULT 567  
ID AEA00558 standard; protein; 671 AA.  
DE Human TAT152 protein sequence SeqID90.  
FN US2005107595-A1.  
PD 19-MAY-2005.  
PA (GETH-) GENENTECH INC.  
Query Match 7.7%; Score 127.5; DB 9; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.011;  
RESULT 568  
ID ABW83431 standard; protein; 825 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.  
FN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.7%; Score 127.5; DB 8; Length 825;  
Best Local Similarity 24.7%; Pred. No. 0.015;  
RESULT 569  
ID ABW83430 standard; protein; 863 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.  
FN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.7%; Score 127.5; DB 8; Length 863;  
Best Local Similarity 24.7%; Pred. No. 0.016;  
RESULT 570  
ID AAE30340 standard; protein; 911 AA.  
DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.  
FN WO200276510-A1.  
PD 03-OCT-2002.  
PA (AGYT-) AGY THERAPEUTICS INC.  
Query Match 7.7%; Score 127.5; DB 6; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.017;  
RESULT 571  
ID ADN38942 standard; protein; 911 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.  
FN WO2003042861-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.7%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.017;  
RESULT 572  
ID ADK67784 standard; protein; 911 AA.  
DE Human glycosylation-variant BEHAB isoform.  
FN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYYA-) UNIV YALE.  
Query Match 7.7%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.017;  
RESULT 573  
ID AEB34757 standard; protein; 911 AA.  
DE Human poly-sialylated brain-enriched hyaluronan binding protein.  
FN WO2005069852-A2.  
PD 04-AUG-2005.  
PA (UYYA-) UNIV YALE.  
Query Match 7.7%; Score 127.5; DB 9; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.017;  
RESULT 574  
ID ABR58557 standard; protein; 277 AA.  
DE Human cancer related protein SEQ ID NO:214.  
FN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.7%; Score 127; DB 6; Length 277;  
Best Local Similarity 30.7%; Pred. No. 0.0037;  
RESULT 575  
ID ABU56654 standard; protein; 277 AA.  
DE Lung cancer-associated polypeptide #247.  
FN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.7%; Score 127; DB 6; Length 277;  
Best Local Similarity 30.7%; Pred. No. 0.0037;  
RESULT 576  
ID ADN38976 standard; protein; 277 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.  
FN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.7%; Score 127; DB 7; Length 277;  
Best Local Similarity 30.7%; Pred. No. 0.0037;  
RESULT 577  
ID ADO24439 standard; protein; 277 AA.  
DE Human PRO87335 protein SEQ ID NO:78.  
FN WO2004043397-A2.  
PD 27-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 7.7%; Score 127; DB 8; Length 277;  
Best Local Similarity 30.7%; Pred. No. 0.0037;  
RESULT 578  
ID ADR14117 standard; protein; 277 AA.  
DE Human NF-kappaB pathway-associated protein SeqID118.  
FN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 7.7%; Score 127; DB 8; Length 277;  
Best Local Similarity 30.7%; Pred. No. 0.0037;  
RESULT 579  
ID ADB47827 standard; protein; 457 AA.  
DE Novel human secreted protein #3.  
FN US2003054443-A1.  
PD 20-MAR-2003.  
PA (RUBE-) RUBEN S M.  
PA (SOPP-) SOPPET D R.  
PA (EENE-) EENNER R.  
PA (OLSE-) OLSEN H S.  
PA (YOUN-) YOUNG P E.  
PA (GREE-) GREENE J M.  
PA (FEER-) FERRIE A M.  
PA (YUGG-) YU G.  
PA (NIJY-) NI J.  
PA (ROSE-) ROSEN C A.  
PA (BREW-) BREWER L A.  
PA (JANA-) JANAT F.

PA (BIRS/) BIRSE C E.  
Query Match 7.6%; Score 126.5; DB 7; Length 457;  
Best Local Similarity 20.6%; Pred. No. 0.0081;  
RESULT 580  
ID ADJ55382 standard; protein; 457 AA.  
DE Novel human secreted protein #3.  
PN US2004023283-A1.  
PD 05-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.6%; Score 126.5; DB 8; Length 457;  
Best Local Similarity 20.6%; Pred. No. 0.0081;  
RESULT 581  
ID ADO24485 standard; protein; 277 AA.  
DE Human PRO87343 protein SEQ ID NO:124.  
PN WO2004043397-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.6%; Score 126; DB 8; Length 277;  
Best Local Similarity 34.1%; Pred. No. 0.0046;  
RESULT 582  
ID ADB65640 standard; protein; 482 AA.  
DE Human protein encoded by clone THYM20143230.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
Query Match 7.5%; Score 124.5; DB 7; Length 482;  
Best Local Similarity 22.1%; Pred. No. 0.014;  
RESULT 583  
ID ADM80804 standard; protein; 259 AA.  
DE Human CADECM-33 protein SEQ ID NO:33.  
PN WO2004015396-A2.  
PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.3%; Score 121.5; DB 8; Length 259;  
Best Local Similarity 34.9%; Pred. No. 0.011;  
RESULT 584  
ID RAY13381 standard; protein; 360 AA.  
DE Amino acid sequence of protein PRO271.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 2; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 585  
ID ADC78533 standard; protein; 360 AA.  
DE Human PRO271 protein.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 3; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 586  
ID AAB80249 standard; protein; 360 AA.  
DE Human PRO271 protein.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 4; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 587  
ID AAU29037 standard; protein; 360 AA.  
DE Human PRO polypeptide sequence #14.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 4; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 588  
ID AAM38965 standard; protein; 360 AA.  
DE Human polypeptide SEQ ID NO 2110.  
PN WO200153312-A1.  
PD 26-JUL-2001.

PA (HYSE-) HYSEQ INC.  
Query Match 7.3%; Score 121.5; DB 4; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 589  
ID ABUS8413 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 590  
ID ABU71627 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 591  
ID ABU87961 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 592  
ID ABU84276 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 593  
ID ABR66150 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032728-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 594  
ID ABR65540 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 595  
ID ABU99480 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 596  
ID ABU82719 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 597  
ID ABU89840 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 598  
ID ABU71482 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.

Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 599  
ID ABR68089 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 600  
ID ABU96142 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 601  
ID ABU92573 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 602  
ID AB008650 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 603  
ID AB002702 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 604  
ID ABR74856 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 605  
ID ABR94618 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 606  
ID ABU85591 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 607  
ID ABU98751 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US200303153-A1.  
PD 16-JAN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 608  
ID ABU97966 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 609  
ID ABU91672 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 610  
ID ABU71928 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein PRO271.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 611  
ID ABU93365 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 612  
ID ABU86206 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 613  
ID ABU67419 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 614  
ID ABU80447 standard; protein; 360 AA.  
DE Human PRO protein #14.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 615  
ID ABO01811 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 616  
ID ABR99365 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 617  
ID ABR98755 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 618  
ID ABO16278 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003027267-A1.  
PD 06-FEB-2003.

Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 619  
ID ABO06162 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 620  
ID ABO18919 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 621  
ID ABR78240 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 622  
ID ABU84976 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 623  
ID ABO00115 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 624  
ID ABO11447 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 625  
ID ABO02092 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 626  
ID ABU54384 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein PRO271.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 627  
ID ABU88666 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 628  
ID ABU83361 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
.. 7.3%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 629  
ID ABO06162 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 630  
ID ABR59198 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 631  
ID ABO09260 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 632  
ID ABO19124 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 633  
ID ABO11142 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 634  
ID ABR66760 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 635  
ID ABO15973 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 636  
ID ABO13679 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 637  
ID ABO47399 standard; protein; 360 AA.  
DE Human secreted/transmembrane polypeptide PRO271.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 638  
ID ABU65582 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, SEQ ID 28.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match  
..Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;



RESULT 639  
ID ABO07430 standard; protein; 360 AA.  
DE Human secreted polypeptide #14.  
FN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 640  
ID ABO03617 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 641  
ID ABR67065 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 642  
ID ABO15668 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 643  
ID ABU55949 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, PRO271.  
FN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 644  
ID ABU65277 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 645  
ID ABU95222 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
FN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 646  
ID ABO07735 standard; protein; 360 AA.  
DE Human PRO271 protein.  
FN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 647  
ID ABO07735 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 648  
ID ABR69976 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 649  
ID ABU83056 standard; protein; 360 AA.

ID ABR69309 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 650  
ID ABO01450 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US200308353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 651  
ID ABU81252 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 652  
ID ABR60049 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 653  
ID ABR67784 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 654  
ID ABR65172 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 655  
ID ABR68394 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 656  
ID ABR71806 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 657  
ID ABU85286 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 658  
ID ABU89876 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 659  
ID ABU83056 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.  
PN US20030321105-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 660  
ID ABU94912 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US20030321123-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 661  
ID ABU90460 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US20030321108-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 662  
ID ABU83971 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US20030321111-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 663  
ID ABU93622 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US20030321119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 664  
ID ABR64867 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 665  
ID ABR68699 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 666  
ID ABO06515 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 667  
ID ABR99060 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 668  
ID ABU56944 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 669  
ID ABU64536 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2002160374-A1.

PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 670  
ID ABU5896 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 671  
ID ABU67382 standard; protein; 360 AA.  
DE Human secreted protein PRO271.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 672  
ID ABU82183 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 673  
ID ABU87194 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 674  
ID ABU83666 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 675  
ID ABO08040 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 676  
ID ABO14902 standard; protein; 360 AA.  
DE Human secreted / transmembrane polypeptide PRO271.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 677  
ID ABU81751 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 678  
ID ABU65915 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 679  
ID ABR59744 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032120-A1.

Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 690			
ID	ABR70281 standard; protein; 360 AA.		
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.		
PN	US2003032139-A1.		
PD	13-FEB-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 691			
ID	ABU98446 standard; protein; 360 AA.		
DE	Human PRO polypeptide #14.		
PN	US2003022301-A1.		
PD	30-JAN-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 692			
ID	ABR65845 standard; protein; 360 AA.		
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.		
PN	US2003036165-A1.		
PD	20-FEB-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 693			
ID	ABR64562 standard; protein; 360 AA.		
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.		
PN	US2003027362-A1.		
PD	06-FEB-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 694			
ID	ABU79487 standard; protein; 360 AA.		
DE	Human PRO polypeptide #14.		
PN	US2003032110-A1.		
PD	13-FEB-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 695			
ID	ABU92878 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein (PRO) #14.		
PN	US2003036142-A1.		
PD	20-FEB-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 696			
ID	ABU95837 standard; protein; 360 AA.		
DE	Human PRO polypeptide #14.		
PN	US2003036145-A1.		
PD	20-FEB-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 697			
ID	ABU91057 standard; protein; 360 AA.		
DE	Novel human secreted and transmembrane protein PRO271.		
PN	US2003036154-A1.		
PD	20-FEB-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 698			
ID	ABU90150 standard; protein; 360 AA.		
DE	Novel human secreted and transmembrane protein PRO271.		
PN	US2003036153-A1.		
PD	20-FEB-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 699			
ID	ABO09565 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein (PRO) #14.		
PN	US2003044931-A1.		
PD	06-WAR-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	
RESULT 700			
ID	ABO09565 standard; protein; 360 AA.		
DE	Human secreted/transmembrane protein (PRO) #14.		
PN	US2003044931-A1.		
PD	06-WAR-2003.		
Query Match	7.3%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;	

ID ABO10837 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 701  
ID ABR70891 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 702  
ID ABU87499 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 703  
ID ABU91367 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 704  
ID ABU84581 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 705  
ID ABR69671 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 706  
ID ABU80048 standard; protein; 360 AA.  
DE Human PRO protein #14.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 707  
ID ABU69659 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 708  
ID ABU93317 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 709  
ID ABO09870 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 710  
ID ABO08955 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.

PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 711  
ID ABU10523 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein #14.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 712  
ID ABU95532 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 713  
ID ABU96741 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 714  
ID ABR70586 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 715  
ID ABO04937 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 716  
ID ABO08345 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 717  
ID ABO14841 standard; protein; 360 AA.  
DE Human secreted / transmembrane polypeptide PRO271.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 718  
ID ABO05552 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 719  
ID ABR73941 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 720  
ID ABR95533 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 721  
ID ABR80830 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 722  
ID ABR81135 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 723  
ID ABR88433 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 724  
ID ABR88433 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 725  
ID ABM77254 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 726  
ID ABO28738 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 727  
ID ABO31483 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 728  
ID ABM07900 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 729  
ID ABO40380 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.

PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 730  
ID ABO35805 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 731  
ID ABO43944 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 732  
ID ADA77780 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 733  
ID ABM24739 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 734  
ID ADE29418 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 735  
ID ABO03007 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 736  
ID ABR90263 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 737  
ID ABM17177 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 738  
ID ABR94923 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 739  
ID ABR95228 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 740  
ID ABO21466 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 741  
ID ABR97730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 742  
ID ABR87518 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 743  
ID ABR77559 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 744  
ID ABR27789 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 745  
ID ABR06070 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 746  
ID ABR03576 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 747  
ID ABR35027 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 748  
ID ABR26264 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 749  
ID ABO48046 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 750  
ID ABR92788 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 751  
ID ABO24549 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 752  
ID ABR11560 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003084447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 753  
ID ABR02661 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 754  
ID ABR15957 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 755  
ID ABO27518 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003084451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 756  
ID ABR29009 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 757  
ID ABR06985 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 758  
ID ABM21079 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 759  
ID ABM09425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 760  
ID ABO411295 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 761  
ID ABO36110 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 762  
ID ABO43639 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 763  
ID ABM76339 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 764  
ID ABM76035 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 765  
ID ABM25654 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 766  
ID ABM25959 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 767  
ID ABR71196 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059880-A1.  
PD 27-MAR-2003.

Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 767  
ID ABO03312 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 768  
ID ABO02397 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 769  
ID ABR90568 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 770  
ID ABR73636 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 771  
ID ABO16888 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 772  
ID ABR94313 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 773  
ID ABR75820 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 774  
ID ADA18274 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 775  
ID ABO32793 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein PRO271.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 776  
ID ABR71196 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059880-A1.  
PD 27-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 777  
ID ABR93093 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 778  
ID ABR93398 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 779  
ID ABR87823 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 780  
ID ABO27823 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 781  
ID ABO29958 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 782  
ID ABO33167 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 783  
ID ABO4855 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 784  
ID ABO8815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 785  
ID ABO36415 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 786  
ID ABO39465 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 787  
ID ABO39465 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 788  
ID ABO10340 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 789  
ID ABO11865 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 790  
ID ABO52011 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 791  
ID ABO52316 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 792  
ID ABO23634 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 793  
ID ABR97120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 794  
ID ABR86908 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 795  
ID ABO36415 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;



RESULT 795  
ID ABM10950 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 796  
ID ABM28094 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 797  
ID ABO32093 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 798  
ID ABM15220 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 799  
ID ABM06375 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 800  
ID ABM04186 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 801  
ID ABM22299 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 802  
ID ABM07595 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 803  
ID ABO40685 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 804  
ID ABO40685 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
FN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

ID ABM35332 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 805  
ID ABM33095 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 806  
ID ABO52621 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 807  
ID ABO50181 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 808  
ID ABU99175 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 809  
ID ABO04227 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 810  
ID ABO05857 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 811  
ID ABO34853 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
FN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 812  
ID ABM18397 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 813  
ID ADA16249 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
FN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 814				
ID ABR97425 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003059885-A1.				
PD 27-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 815				
ID ABR80525 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003049740-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 816				
ID ABR01136 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003049770-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 817				
ID ABR88738 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003073169-A1.				
PD 17-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 818				
ID ABR13390 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003064457-A1.				
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 819				
ID ABR20774 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003068711-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 820				
ID ABO41905 standard; protein; 360 AA.				
DE Human secreted/transmembrane protein (PRO) #14.				
PN US2003049745-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 821				
ID ABO42515 standard; protein; 360 AA.				
DE Human secreted/transmembrane protein (PRO) #14.				
PN US2003049751-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 822				
ID ABR10035 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003067478-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 823				
ID ABR10035 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003067478-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 824				
ID ABR10035 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003067478-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 825				
ID ABR10035 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003067478-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;			

RESULT 823	ID ABO38550 standard; protein; 360 AA.				
DE	Human secreted/transmembrane protein (PRO) #14.				
PN	US2003068773-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 824	ID ABM32790 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003073185-A1.				
PD	17-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 825	ID ABM22604 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003087373-A1.				
PD	08-MAY-2003.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 826	ID ABM74815 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003096353-A1.				
PD	22-MAY-2003.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 827	ID ADA79572 standard; protein; 360 AA.				
DE	Human secreted/transmembrane protein (PRO) #14.				
PN	US2003073173-A1.				
PD	17-APR-2003.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 828	ID ABR96205 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003054458-A1.				
PD	20-MAR-2003.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 829	ID ABM02356 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003059886-A1.				
PD	27-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 830	ID ABR86298 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003049758-A1.				
PD	13-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 831	ID ABR86603 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003049772-A1.				
PD	13-MAR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			
RESULT 832	ID ABM16567 standard; protein; 360 AA.				
DE	Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN	US2003064448-A1.				
PD	03-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;	
Best Local Similarity	34.9%;	Pred. No. 0.017;			

PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 833  
ID ABM29619 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 834  
ID AB029043 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 835  
ID ABM23824 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 836  
ID ABM23214 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 837  
ID ABM21994 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 838  
ID AB037635 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 839  
ID ABM28399 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 840  
ID ABM28704 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 841  
ID ABM66348 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 842  
ID ABW75730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 843  
ID ABM34010 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 844  
ID ABM34315 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 845  
ID AB020246 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 846  
ID AB021161 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 847  
ID AB022076 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 848  
ID ABR96510 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 849  
ID ABR85688 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 850  
ID ABR96670 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 851  
ID ABM00221 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

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PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 852
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 853
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 854
ID ABM23519 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 855
ID ABM29314 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068679-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 856
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 857
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 858
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104557-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 859
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 860
ID ADA81299 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 861
ID ABO16583 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 862
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 863
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 864
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 865
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 866
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 867
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064367-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 868
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049783-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 869
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.017;
RESULT 870
ID ABM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
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Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 880				
ID ABO47436 standard; protein; 360 AA.				
DE Human secreted/transmembrane protein (PRO) #14.				
PN US2003049742-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 881				
ID ABO47741 standard; protein; 360 AA.				
DE Human secreted/transmembrane protein (PRO) #14.				
PN US2003049747-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 882				
ID ABO48351 standard; protein; 360 AA.				
DE Human secreted/transmembrane protein (PRO) #14.				
PN US2003049750-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 883				
ID ABO51401 standard; protein; 360 AA.				
DE Human PRO polypeptide #14.				
PN US2003049766-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 884				
ID ABO51706 standard; protein; 360 AA.				
DE Human PRO polypeptide #14.				
PN US2003049767-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 885				
ID ABO50486 standard; protein; 360 AA.				
DE Human secreted/transmembrane protein (PRO) #14.				
PN US2003049779-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 886				
ID ABR79610 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003040059-A1.				
PD 27-FEB-2003.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 887				
ID ABM16872 standard; protein; 360 AA.				
DE Human secreted polypeptide PRO271, SEQ ID NO:28.				
PN US2003040078-A1.				
PD 27-FEB-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 888				
ID ABO17904 standard; protein; 360 AA.				
DE Human secreted/transmembrane protein (PRO) #14.				
PN US2003044918-A1.				
PD 06-MAR-2003.				
Query Match	7.3%;	Score 121.5;	DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.017;		
RESULT 889				

ID ABO20856 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 890  
ID ABR96815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 891  
ID ABM12170 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 892  
ID ABM16262 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 893  
ID ABM24129 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 894  
ID ABM14610 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 895  
ID ABM04491 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 896  
ID ABM06680 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 897  
ID ABM09120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 898  
ID ABO39160 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068775-A1.  
PD 10-APR-2003.

PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 899  
ID ABM75425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 900  
ID ABM25349 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 901  
ID ABM19859 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 902  
ID ABO46765 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 903  
ID ABO47070 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 904  
ID ADA83097 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 905  
ID ABR71501 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 906  
ID ABR72111 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 907  
ID ABR98450 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.017;  
RESULT 908  
ID ABO6820 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 909  
ID ABR84773 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 910  
ID ABR73331 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 911  
ID ABR76425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 912  
ID ABR73026 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 913  
ID ABM18092 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 914  
ID ABO20551 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 915  
ID ABO25294 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 916  
ID ABO25599 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 917  
ID ABR94008 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;

RESULT 918  
ID ABR79915 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 919  
ID ABM11255 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 920  
ID ABO32862 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 921  
ID ABO30568 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 922  
ID ABO30873 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 923  
ID ABM27179 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 924  
ID ABM29924 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 925  
ID ABM05460 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 926  
ID ABM15525 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 927  
ID ABM08510 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 928  
ID ABO42210 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 929  
ID ABO37940 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 930  
ID ABO45850 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 931  
ID ABO66653 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 932  
ID ABO20140 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 933  
ID ABO19554 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 934  
ID ABO49266 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 935  
ID ABO49571 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 936  
ID ADA78392 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073181-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 937  
ID ABR88128 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 938  
ID ABM26874 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003088739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 939  
ID ABM03271 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 940  
ID ABO39770 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;  
RESULT 941  
ID ABO49876 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 942  
ID ABO50791 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 943  
ID ABO05247 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 944  
ID ABR74551 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 945  
ID ABR77030 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 946  
ID ADA78392 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073181-A1.



RESULT 946  
ID ADA16673 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 947  
ID ABM17787 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 948  
ID ABR95838 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 949  
ID ADA13102 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 950  
ID ABO21771 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 951  
ID ABO19941 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 952  
ID ABO24244 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 953  
ID ABR85993 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 954  
ID ABM10645 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 955  
ID ABM76644 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054465-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 956  
ID ABR89348 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 957  
ID ABM12475 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 958  
ID ABO5765 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 959  
ID ABO34890 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 960  
ID ABO2966 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 961  
ID ABM18944 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 962  
ID ABM19249 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 963  
ID ABO46460 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 964  
ID ABO48961 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

PN US2003059884-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 975  
 ID ABR87213 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003068687-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 976  
 ID ABM12780 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003073186-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 977  
 ID ABM30534 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003064443-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 978  
 ID ABM24434 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003064444-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 979  
 ID ABO29348 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003068597-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 980  
 ID ABO31178 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003068710-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 981  
 ID ABM14305 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003068686-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 982  
 ID ABM09730 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003073178-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 7; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 983  
 ID ABO38855 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003068774-A1

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 984  
ID ABM34620 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 985  
ID AB051096 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 986  
ID ADA42820 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 987  
ID AB003922 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 988  
ID AB010392 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 989  
ID ABR77635 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 990  
ID ABR78845 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 991  
ID ABO23939 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 992  
ID ABR93703 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 993  
ID ABM01746 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 994  
ID ABR78169 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 995  
ID ABR89958 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 996  
ID ABR27484 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 997  
ID ABR13085 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 998  
ID ABO31788 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 999  
ID ABR14000 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1000  
ID ABR08205 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1001  
ID ABO40075 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1002  
ID ABR74510 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096351-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1003  
ID ABR33705 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1004  
ID ABR20164 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1005  
ID ABO48656 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1006  
ID ABR72721 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1007  
ID ABO15363 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1008  
ID ABR85078 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1009  
ID ABO15058 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1010  
ID ABO17193 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1011  
ID ABR17482 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1012  
ID ABR85383 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1013  
ID ABO17592 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
FN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1014  
ID ABR76949 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1015  
ID ABO28128 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1016  
ID ABR22909 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1017  
ID ABR30229 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1018  
ID ABR21689 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1019  
ID ABR21384 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1020  
ID ABR14915 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1021  
ID ABO40990 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068694-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1022  
ID ABO36720 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1023  
ID ABO37330 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1024  
ID ABM75120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1025  
ID ABM33400 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1026  
ID ABO46155 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1027  
ID ADA82463 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1028  
ID ABM31754 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1029  
ID ABM31144 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1030  
ID ADB77739 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;

Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1031  
ID ADB74875 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1032  
ID ADB85771 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1033  
ID ABM32059 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1034  
ID ABM32364 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1035  
ID ABM31449 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1036  
ID ABM30839 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1037  
ID ADC28521 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1038  
ID ADC39721 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1039  
ID ADC40235 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 121.5; DB 7; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1040  
ID ADC19059 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1041  
ID ADC34359 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1042  
ID ADC29414 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1043  
ID ADC28945 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1044  
ID ADC40830 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1045  
ID ADC19487 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1046  
ID ADC33935 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1047  
ID ADC13005 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1048  
ID ADC12457 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1049  
ID ADD05501 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1050  
ID ADD05012 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1051  
ID ADD04018 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1052  
ID ADD03594 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1053  
ID ADE34846 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1054  
ID ADG02496 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1055  
ID ADG01203 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1056  
ID ADF95378 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1057  
ID ADG12193 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1058  
ID ADH08853 standard; protein; 360 AA.

DE Human PRO polypeptide #14.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1059  
ID ADH59329 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1060  
ID ADI38108 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1061  
ID ADJ26376 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1062  
ID ADJ32634 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1063  
ID ADM30168 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;  
RESULT 1064  
ID ADE79291 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1065  
ID ADE79715 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1066  
ID ADE73391 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1067  
ID ADE74165 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.

PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1068  
ID ADE73926 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1069  
ID ADE74777 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1070  
ID ADE99480 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1071  
ID ADE98599 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1072  
ID ADE99026 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1073  
ID ADG40496 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A. J.  
PA (GODO/) GODOWSKI P. J.  
PA (GURN/) GURNEY A. L.  
PA (MATH/) MATHER J. P.  
PA (WILL/) WILLIAMS P. M.  
PA (WOOD/) WOOD W. I.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1074  
ID ADF73890 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1075  
ID ADF95990 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match  
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;  
RESULT 1076

ID ADF73466 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1077  
ID ADG04261 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1078  
ID ADG00421 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1079  
ID ADG82677 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1080  
ID ADG92309 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1081  
ID ADG92736 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1082  
ID ADH25958 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1083  
ID ADH32927 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1084  
ID ADH20525 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1085  
ID ADH07380 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.  
PN US2004006211-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1086  
ID ADH59925 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003215904-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1087  
ID ADH08953 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1088  
ID ADI18695 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003152999-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1089  
ID ADI65415 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1090  
ID ADI37678 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1091  
ID ADH97474 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003190610-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1092  
ID ADI65842 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148371-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1093  
ID ADH07380 standard; protein; 360 AA.



Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1093  
ID ADH60585 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004023331-A1.  
PD 05-FEB-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P. J.  
PA (GURN/) GURNEY A. L.  
PA (MATH/) MATHER J. P.  
PA (WILL/) WILLIAMS P. M.  
PA (WOOD/) WOOD W. I.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1094  
ID ADJ99642 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003187238-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1095  
ID ADL08835 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1096  
ID ADJ54666 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1097  
ID ADM25176 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1098  
ID ADM29926 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1099  
ID ADJ64437 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1100  
ID ADM31333 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1101  
ID ADM36380 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1102  
ID ADM40185 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1103  
ID ADL91793 standard; protein; 360 AA.  
DE Human PRO271 protein SEQ ID NO:14.  
PN WO2004024076-A2.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1104  
ID ADO06248 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1105  
ID ADN37793 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1106  
ID ADR11100 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004137561-A1.  
PD 15-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.017;  
RESULT 1107  
ID ADR18009 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D. L.  
PA (FERR/) FERRARA N.  
PA (FILIV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M. E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P. J.  
PA (GRIM/) GRIMALDI C. J.  
PA (GURN/) GURNEY A. L.  
PA (HILL/) HILLAN K. J.  
PA (KLJA/) KLJAVIN I. J.  
PA (MATH/) MATHER J. P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N. F.  
PA (ROYM/) ROY M. A.  
PA (STEW/) STEWART T. A.  
PA (TUMA/) TUMAS D.

PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 7.3%; Score 121.5; DB 8; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 1108  
 ID ADS74648 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein #42.  
 PN US200418531-A1.  
 PD 23-SEP-2004.  
 PA (ASHK/) ASHKENAZI A.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 7.3%; Score 121.5; DB 8; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 1109  
 ID ADT03685 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein, #42.  
 PN US2003152922-A1.  
 PD 14-AUG-2003.  
 PA (GETH/) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 8; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 1110  
 ID ABA37923 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein, #42.  
 PN US2005112725-A1.  
 PD 26-MAY-2005.  
 PA (GETH/) GENENTECH INC.  
 Query Match 7.3%; Score 121.5; DB 9; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.017;  
 RESULT 1111  
 ID AEA20028 standard; protein; 422 AA.  
 DE Novel human polypeptide SEQ ID NO 722.  
 PN WO2005049806-A2.  
 PD 02-JUN-2005.  
 PA (NUVE-) NUVELO INC.  
 Query Match 7.3%; Score 121.5; DB 9; Length 422;  
 Best Local Similarity 34.9%; Pred. No. 0.022;  
 RESULT 1112  
 ID AAW59882 standard; protein; 528 AA.  
 DE Amino acid sequence of the cDNA clone BEF (HSXCK41).  
 PN WO9831800-A2.  
 PD 23-JUL-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AUCK-) AUCKLAND UNISERVICES LTD.  
 Query Match 7.3%; Score 121; DB 2; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.033;  
 RESULT 1113  
 ID AAB61241 standard; protein; 528 AA.  
 DE Human BEF protein.  
 PN WO200100638-A2.  
 PD 04-JAN-2001.

PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 7.3%; Score 121; DB 4; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.033;  
 RESULT 1114  
 ID ABO32677 standard; protein; 528 AA.  
 DE Secreted polypeptide-related protein #75.  
 PN US2003022279-A1.  
 PD 30-JAN-2003.  
 PA (FRAS/) FRASER C C.  
 PA (BARV/) BARNES T M.  
 PA (SHAR/) SHARP J D.  
 PA (KIRS/) KIRST S J.  
 PA (MYER/) MYERS P S.  
 PA (LEIB/) LEIBY K R.  
 PA (HOLT/) HOLTZMAN D A.  
 PA (MCCA/) MCCARTHY S A.  
 PA (WRIG/) WRIGHTON N.  
 PA (MACK/) MACKAY C R.  
 PA (GOOD/) GOODEARL A D J.  
 Query Match 7.3%; Score 121; DB 6; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.033;  
 RESULT 1115  
 ID ADB90786 standard; protein; 528 AA.  
 DE Human BEF protein.  
 PN US2003082586-A1.  
 PD 01-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 7.3%; Score 121; DB 7; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.033;  
 RESULT 1116  
 ID ADF71521 standard; protein; 528 AA.  
 DE Human BEF protein.  
 PN US2003175733-A1.  
 PD 18-SEP-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 7.3%; Score 121; DB 7; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.033;  
 RESULT 1117  
 ID ADQ10337 standard; protein; 528 AA.  
 DE Human polypeptide #171.  
 PN US2004121396-A1.  
 PD 24-JUN-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 7.3%; Score 121; DB 8; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.033;  
 RESULT 1118  
 ID AAR46627 standard; protein; 1257 AA.  
 DE Neurocan core protein.  
 PN WO9403601-A2.  
 PD 17-FEB-1994.  
 PA (UNYU) UNIV NEW YORK STATE.  
 Query Match 7.3%; Score 120.5; DB 2; Length 1257;  
 Best Local Similarity 23.6%; Pred. No. 0.12;  
 RESULT 1119  
 ID ADQ39513 standard; protein; 1642 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 7.2%; Score 118.5; DB 8; Length 1642;  
 Best Local Similarity 25.5%; Pred. No. 0.27;  
 RESULT 1120  
 ID ADQ39515 standard; protein; 1642 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 7.2%; Score 118.5; DB 8; Length 1642;  
 Best Local Similarity 25.5%; Pred. No. 0.27;  
 RESULT 1121  
 ID ADN04531 standard; protein; 2000 AA.  
 DE Antipsoriatic protein sequence #458.  
 PN WO2004028479-A2.

PD 08-APR-2004.  
PA (GETH ) GENENTECH INC. 7.2%; Score 118.5; DB 8; Length 2000;  
Query Match 25.5%; Pred. No. 0.35;  
RESULT 1122  
ID ADP23738 standard; protein; 2000 AA.  
DE PRO polypeptide SEQ ID NO:916.  
FN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC. 7.2%; Score 118.5; DB 8; Length 2000;  
Query Match 25.5%; Pred. No. 0.35;  
RESULT 1123  
ID ADQ48597 standard; protein; 3396 AA.  
DE Human Protein P13611, SEQ ID NO 14303.  
FN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG. 7.2%; Score 118.5; DB 7; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1124  
ID ADN95526 standard; protein; 3396 AA.  
DE Human BEC/LEC-related protein sequence SeqID449.  
FN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD. 7.2%; Score 118.5; DB 7; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1125  
ID ADJ75521 standard; protein; 3396 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:773.  
FN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC. 7.2%; Score 118.5; DB 8; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1126  
ID ADQ39509 standard; protein; 3396 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.  
FN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 7.2%; Score 118.5; DB 8; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1127  
ID ADQ39510 standard; protein; 3396 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.  
FN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 7.2%; Score 118.5; DB 8; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1128  
ID ADP99164 standard; protein; 3396 AA.  
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.  
FN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB ) BAYER PHARM CORP. 7.2%; Score 118.5; DB 8; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1129  
ID ADZ09841 standard; protein; 3396 AA.  
DE Human breast cancer marker CSPG2 protein.  
FN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB ) BAYER HEALTHCARE AG. 7.2%; Score 118.5; DB 9; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1130  
ID ADZ70548 standard; protein; 3396 AA.  
DE Human protein from lung cancer marker gene CSPG2.

FN WO2005032495-A2.  
PD 14-APR-2005.  
PA (FARB ) BAYER PHARM CORP. 7.2%; Score 118.5; DB 9; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1131  
ID AEA04473 standard; protein; 3396 AA.  
DE Human protein from gene overexpressed in cancer, CSPG2.  
FN WO2005044990-A2.  
PD 19-MAY-2005.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES. 7.2%; Score 118.5; DB 9; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1132  
ID AEB17604 standard; protein; 3396 AA.  
DE Human CSPG2 protein SeqID18.  
FN JP2005110602-A.  
PD 28-APR-2005.  
PA (SUMO ) SUMITOMO SEIYAKU KK. 7.2%; Score 118.5; DB 9; Length 3396;  
Query Match 25.5%; Pred. No. 0.73;  
RESULT 1133  
ID ADZ09886 standard; protein; 6792 AA.  
DE Human breast cancer marker CSPG2 protein.  
FN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB ) BAYER HEALTHCARE AG. 7.2%; Score 118.5; DB 9; Length 6792;  
Query Match 25.5%; Pred. No. 1.9;  
RESULT 1134  
ID ADP71273 standard; protein; 191 AA.  
DE Human LP2 protein B-B' domain SeqID8.  
FN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SESK ) SEIKAGAKU KOGYO CO LTD. 7.1%; Score 117; DB 8; Length 191;  
Query Match 26.5%; Pred. No. 0.019;  
RESULT 1135  
ID ADM87304 standard; protein; 340 AA.  
DE Human protein SEQ ID NO:397.  
FN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC. 7.1%; Score 117; DB 8; Length 340;  
Query Match 26.5%; Pred. No. 0.043;  
RESULT 1136  
ID ABU11635 standard; protein; 343 AA.  
DE Human MDT polypeptide SEQ ID 582.  
FN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC. 7.1%; Score 117; DB 6; Length 343;  
Query Match 26.5%; Pred. No. 0.043;  
RESULT 1137  
ID ADJ76266 standard; protein; 2397 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1518.  
FN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC. 7.0%; Score 116; DB 8; Length 2397;  
Query Match 28.4%; Pred. No. 0.78;  
RESULT 1138  
ID AAR85443 standard; protein; 908 AA.  
DE Rat brevicain core protein.  
FN WO9526201-A1.  
PD 05-OCT-1995.  
PA (LJOL-) LA JOLLA CANCER RES FOUND. 6.9%; Score 115; DB 2; Length 908;  
Query Match 22.2%; Pred. No. 0.25;  
RESULT 1139  
ID ADO31200 standard; protein; 1257 AA.

DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.  
PN WO2004041197-A2.  
PD 21-MAY-2004.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

Query Match 6.9%; Score 114.5; DB 8; Length 1257;  
Best Local Similarity 23.1%; Pred. No. 0.44;

RESULT 1140

ID ADD48595 standard; protein; 656 AA.

DE Rat Protein AF072892, SEQ ID NO 14301.

PN WO2003016475-A2.

PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

Query Match 6.9%; Score 114; DB 7; Length 656;  
Best Local Similarity 28.4%; Pred. No. 0.2;

RESULT 1141

ID ABR10268 standard; protein; 287 AA.

DE Human CDNA SEQ ID NO: 576.

PN WO200154474-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 6.8%; Score 112.5; DB 4; Length 287;  
Best Local Similarity 25.7%; Pred. No. 0.09;

RESULT 1142

ID ABP66855 standard; protein; 287 AA.

DE Human polypeptide SEQ ID NO 576.

PN US2002090672-A1.

PD 11-JUL-2002.

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

Query Match 6.8%; Score 112.5; DB 5; Length 287;  
Best Local Similarity 25.7%; Pred. No. 0.09;

RESULT 1143

ID ABU36285 standard; protein; 402 AA.

DE Protein encoded by Prokaryotic essential gene #21812.

PN WO200277183-A2.

PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 6.7%; Score 111.5; DB 6; Length 402;  
Best Local Similarity 22.5%; Pred. No. 0.18;

RESULT 1144

ID ADP71271 standard; protein; 200 AA.

DE Human aggrecan protein B-B' domain SeqID6.

PN JP2004154038-A.

PD 03-JUN-2004.

PA (SEKG) SEIKAGAKU KOGYO CO LTD.

Query Match 6.7%; Score 111; DB 8; Length 200;  
Best Local Similarity 37.4%; Pred. No. 0.076;

RESULT 1145

ID AAM52242 standard; protein; 655 AA.

DE Human versican isoform V3 SEQ ID NO 2.

PN WO200179284-A2.

PD 25-OCT-2001.

PA (WIGH/) WIGHT T N.

PA (MERR/) MERRILEES M.

Query Match 6.7%; Score 111; DB 5; Length 655;  
Best Local Similarity 29.4%; Pred. No. 0.39;

RESULT 1146

ID ADQ39511 standard; protein; 655 AA.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Query Match 6.7%; Score 111; DB 8; Length 655;  
Best Local Similarity 29.4%; Pred. No. 0.39;

RESULT 1147

ID AAR12609 standard; protein; 2409 AA.

DE Versican.

PN WO9108230-A.

PD 13-JUN-1991.

PA (LJOL-) LA JOLLA CANCER RES FOUND.

PA (LJOL-) LA JOLLA CANCER RES FOUND.

Query Match 6.7%; Score 111; DB 2; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2.3;

RESULT 1148

ID ASR47429 standard; protein; 2409 AA.

DE Breast cancer associated protein sequence SEQ ID NO:90.

PN WO2003004989-A2.

PD 16-JAN-2003.

PA (MILL-) MILLENIUM PHARM INC.

Query Match 6.7%; Score 111; DB 6; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2.3;

RESULT 1149

ID ADQ39514 standard; protein; 2409 AA.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Query Match 6.7%; Score 111; DB 8; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2.3;

RESULT 1150

ID ADQ39512 standard; protein; 2409 AA.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Query Match 6.7%; Score 111; DB 8; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2.3;

RESULT 1151

ID ADV70260 standard; protein; 2409 AA.

DE Tumor-associated antigenic target polypeptide TAT498.

PN WO2004112829-A2.

PD 29-DEC-2004.

PA (GETH) GENENTECH INC.

Query Match 6.7%; Score 111; DB 9; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2.3;

RESULT 1152

ID AAB12304 standard; protein; 341 AA.

DE Human secreted protein encoded by gene 4 clone HFXHC41.

PN WO200029422-A1.

PD 25-MAY-2000.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 6.6%; Score 110; DB 3; Length 341;  
Best Local Similarity 28.5%; Pred. No. 0.2;

RESULT 1153

ID AAY93913 standard; protein; 353 AA.

DE A human hyaluronan-binding protein, designated BM-HABP.

PN WO200039166-A1.

PD 06-JUL-2000.

PA (AMNA-) AMERICAN NAT RED CROSS.

Query Match 6.6%; Score 109; DB 3; Length 353;  
Best Local Similarity 24.3%; Pred. No. 0.26;

RESULT 1154

ID ABP97200 standard; protein; 1321 AA.

DE Tumour-associated antigenic target protein TAT185 SEQ ID NO:82.

PN WO2003024392-A2.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.6%; Score 109; DB 6; Length 1321;  
Best Local Similarity 21.4%; Pred. No. 1.6;

RESULT 1155

ID ADJ69615 standard; protein; 1321 AA.

DE Human heat mitochondrial protein as a therapeutic target SeqID1421.

PN WO2003087768-A2.

PD 23-OCT-2003.

PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

Query Match 6.6%; Score 109; DB 7; Length 1321;  
Best Local Similarity 21.4%; Pred. No. 1.6;

RESULT 1156

ID ADN38944 standard; protein; 1321 AA.

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.

PN WO2003042661-A2.

PD 22-MAY-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.5%; Score 109; DB 7; Length 1321;  
Best Local Similarity 21.4%; Pred. No. 1.6;  
RESULT 1157  
ID AD0311196 standard; protein; 1321 AA.  
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.  
PN WO2004041197-A2.  
PD 21-MAY-2004.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
Query Match 6.6%; Score 109; DB 8; Length 1321;  
Best Local Similarity 21.4%; Pred. No. 1.6;  
RESULT 1158  
ID ABJ56909 standard; protein; 322 AA.  
DE 151P3D4 v-2 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 322;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1159  
ID ABJ56908 standard; protein; 322 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 322;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1160  
ID ABJ56918 standard; protein; 353 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 353;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1161  
ID AAJ57081 standard; protein; 354 AA.  
DE Human proteoglycan link protein precursor amino acid sequence.  
PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 6.5%; Score 108; DB 3; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1162  
ID AAJ57084 standard; protein; 354 AA.  
DE Human proteoglycan link protein precursor #2.  
PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 6.5%; Score 108; DB 3; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1163  
ID ABJ56902 standard; protein; 354 AA.  
DE 151P3D4 v-1 354aa protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1164  
ID ABJ56906 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1165  
ID ABJ56914 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1166  
ID ABJ56898 standard; protein; 354 AA.  
DE 151P3D4 v-8 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1167  
ID ABJ56895 standard; protein; 354 AA.  
DE 151P3D4 v-5 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1168  
ID ABJ56897 standard; protein; 354 AA.  
DE 151P3D4 v-7 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1169  
ID ABJ56901 standard; protein; 354 AA.  
DE 151P3D4 v-11 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1170  
ID ABJ56894 standard; protein; 354 AA.  
DE 151P3D4 v-4 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1171  
ID ABJ56905 standard; protein; 354 AA.  
DE Human cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1172  
ID ABJ56899 standard; protein; 354 AA.  
DE 151P3D4 v-9 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1173  
ID ABJ56912 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1174  
ID ABJ56893 standard; protein; 354 AA.  
DE 151P3D4 v-3 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;

Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1175  
ID ABJ56891 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1176  
ID ABJ56896 standard; protein; 354 AA.  
DE 151P3D4 v-6 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1177  
ID ABJ56900 standard; protein; 354 AA.  
DE 151P3D4 v-10 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1178  
ID ABJ56889 standard; protein; 354 AA.  
DE Transcript variant 121P1F1 v-1.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1179  
ID ABJ56904 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1180  
ID ADF07795 standard; protein; 354 AA.  
DE Human secreted protein, seq id 278.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 108; DB 8; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.32;  
RESULT 1181  
ID AAR77034 standard; protein; 355 AA.  
DE Rat brain-enriched hyaluronan binding protein.  
PN WO9527785-A1.  
PD 19-OCT-1995.  
PA (UYA) UNIV YALE.  
Query Match 6.5%; Score 108; DB 2; Length 355;  
Best Local Similarity 28.9%; Pred. No. 0.32;  
RESULT 1182  
ID ADH71348 standard; protein; 552 AA.  
DE Human protein of the invention NOV9s SEQ ID NO:244.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 108; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.59;  
RESULT 1183  
ID ABJ56890 standard; protein; 721 AA.  
DE Transcript variant 151P3D4 v-2.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 721;  
Best Local Similarity 28.6%; Pred. No. 0.85;

RESULT 1184  
ID ABJ56892 standard; protein; 721 AA.  
DE 151P3D4 v-2 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 721;  
Best Local Similarity 28.6%; Pred. No. 0.85;  
RESULT 1185  
ID ABJ56903 standard; protein; 721 AA.  
DE 151P3D4 v-1 721aa protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 108; DB 6; Length 721;  
Best Local Similarity 28.6%; Pred. No. 0.85;  
RESULT 1186  
ID ABG72500 standard; protein; 93 AA.  
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.  
PN WO200286093-A2.  
PD 31-OCT-2002.  
PA (WEIG/) WEIGEL P H.  
PD (WEIG/) WEIGEL J A.  
Query Match 6.5%; Score 107; DB 6; Length 93;  
Best Local Similarity 29.2%; Pred. No. 0.064;  
RESULT 1187  
ID AAB83358 standard; protein; 315 AA.  
DE NOV2 protein sequence.  
PN WO200138638-A2.  
PD 25-MAY-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 4; Length 315;  
Best Local Similarity 29.2%; Pred. No. 0.34;  
RESULT 1188  
ID ADH71316 standard; protein; 315 AA.  
DE Human protein of the invention NOV9c SEQ ID NO:212.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 315;  
Best Local Similarity 29.2%; Pred. No. 0.34;  
RESULT 1189  
ID AAY57083 standard; protein; 339 AA.  
DE Rat proteoglycan link protein precursor.  
PN WO956763-A1.  
PD 11-NOV-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 6.5%; Score 107; DB 3; Length 339;  
Best Local Similarity 28.6%; Pred. No. 0.38;  
RESULT 1190  
ID ABJ56915 standard; protein; 354 AA.  
DE Rat cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 107; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.4;  
RESULT 1191  
ID AAY57082 standard; protein; 355 AA.  
DE Chicken proteoglycan link protein precursor.  
PN WO956763-A1.  
PD 11-NOV-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 6.5%; Score 107; DB 3; Length 355;  
Best Local Similarity 34.9%; Pred. No. 0.4;  
RESULT 1192  
ID ABJ56907 standard; protein; 355 AA.  
DE Mouse cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.5%; Score 107; DB 6; Length 355;  
Best Local Similarity 28.6%; Pred. No. 0.4;

RESULT 1193  
ID ADH71336 standard; protein; 533 AA.  
DE Human protein of the invention NOV9m SEQ ID NO:232.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 533;  
Best Local Similarity 29.2%; Pred. No. 0.7;  
RESULT 1194  
ID ADH71334 standard; protein; 533 AA.  
DE Human protein of the invention NOV9l SEQ ID NO:230.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 533;  
Best Local Similarity 29.2%; Pred. No. 0.7;  
RESULT 1195  
ID ADH71340 standard; protein; 552 AA.  
DE Human protein of the invention NOV9o SEQ ID NO:236.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.73;  
RESULT 1196  
ID ADH71346 standard; protein; 552 AA.  
DE Human protein of the invention NOV9r SEQ ID NO:242.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.73;  
RESULT 1197  
ID ADH71354 standard; protein; 552 AA.  
DE Human protein of the invention NOV9v SEQ ID NO:250.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.73;  
RESULT 1198  
ID ADH71344 standard; protein; 552 AA.  
DE Human protein of the invention NOV9q SEQ ID NO:240.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.73;  
RESULT 1199  
ID ADH71342 standard; protein; 552 AA.  
DE Human protein of the invention NOV9p SEQ ID NO:238.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.73;  
RESULT 1200  
ID ADH71350 standard; protein; 552 AA.  
DE Human protein of the invention NOV9t SEQ ID NO:246.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.73;  
RESULT 1201  
ID ADH71314 standard; protein; 556 AA.  
DE Human protein of the invention NOV9b SEQ ID NO:210.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 556;  
Best Local Similarity 29.2%; Pred. No. 0.74;  
RESULT 1202

ID ABM83433 standard; protein; 774 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.  
FN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.5%; Score 107; DB 8; Length 774;  
Best Local Similarity 21.5%; Pred. No. 1.2;  
RESULT 1203  
ID ABM83432 standard; protein; 822 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.  
FN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.5%; Score 107; DB 8; Length 822;  
Best Local Similarity 21.5%; Pred. No. 1.3;  
RESULT 1204  
ID ADO31202 standard; protein; 1268 AA.  
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.  
FN WO2004041197-A2.  
PD 21-MAY-2004.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
Query Match 6.5%; Score 107; DB 8; Length 1268;  
Best Local Similarity 26.2%; Pred. No. 2.3;  
RESULT 1205  
ID ABB69806 standard; protein; 1795 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.5%; Score 107; DB 4; Length 1795;  
Best Local Similarity 24.1%; Pred. No. 3.7;  
RESULT 1206  
ID ADH71332 standard; protein; 2417 AA.  
DE Human protein of the invention NOV9k SEQ ID NO:228.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 8; Length 2417;  
Best Local Similarity 29.2%; Pred. No. 5.6;  
RESULT 1207  
ID ABJ10587 standard; protein; 2420 AA.  
DE Human novel protein NOV1b SEQ ID NO: 4.  
FN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 107; DB 5; Length 2420;  
Best Local Similarity 29.2%; Pred. No. 5.6;  
RESULT 1208  
ID ADO09838 standard; protein; 2420 AA.  
DE Human NOV1b.  
FN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHIMKETS R A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (WALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (MILL/) MILLER C E.  
PA (BOLD/) BOLDOG F L.  
PA (LILL/) LI L.  
PA (TAUP/) TAUPIER R J.  
PA (KEKU/) KEKUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERH/) ZERHUSEN B D.  
PA (LIUX/) LIU X.  
PA (COLM/) COLMAN S D.  
PA (TCHE/) TCHERNEV V T.  
PA (SIJJ/) SI J.  
PA (EDIN/) EDINGER S R.  
PA (STON/) STONE D J.

PA (SCIO/) SCIORE P.  
PA (MILL/) MILLET I.  
PA (ROTH/) ROTHENBERG M E.  
Query Match 6.5%; Score 107; DB 8; Length 2420;  
Best Local Similarity 29.2%; Pred. No. 5.6;  
RESULT 1209  
ID ADH71338 standard; protein; 552 AA.  
DE Human protein of the invention NOV9n SEQ ID NO:234.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.4%; Score 106; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.91;  
RESULT 1210  
ID AAY57080 standard; protein; 354 AA.  
DE Human link protein precursor amino acid sequence.  
PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 6.3%; Score 105; DB 3; Length 354;  
Best Local Similarity 33.7%; Pred. No. 0.62;  
RESULT 1211  
ID AB356913 standard; protein; 354 AA.  
DE Bovine cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.3%; Score 105; DB 6; Length 354;  
Best Local Similarity 33.7%; Pred. No. 0.62;  
RESULT 1212  
ID AAB42164 standard; protein; 330 AA.  
DE Human ORF1928 polypeptide sequence SEQ ID NO:3856.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.3%; Score 104.5; DB 3; Length 330;  
Best Local Similarity 18.7%; Pred. No. 0.62;  
RESULT 1213  
ID ABU07339 standard; protein; 139 AA.  
DE Human expressed protein tag (EPT) #2040.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.3%; Score 104; DB 6; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.21;  
RESULT 1214  
ID ABU07336 standard; protein; 139 AA.  
DE Human expressed protein tag (EPT) #2037.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 6.3%; Score 104; DB 6; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.21;  
RESULT 1215  
ID ADQ39387 standard; protein; 139 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.3%; Score 104; DB 8; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.21;  
RESULT 1216  
ID ADY16502 standard; protein; 139 AA.  
DE PRO polypeptide SEQ ID NO 2308.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 6.3%; Score 104; DB 9; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.21;  
RESULT 1217  
ID AEB29759 standard; protein; 139 AA.  
DE Human CD44 isoform RC.  
PN WO2005067667-A2.

PD 28-JUL-2005.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 6.3%; Score 104; DB 9; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.21;  
RESULT 1218  
ID ADP71269 standard; protein; 195 AA.  
DE Human LPI protein B-B' domain SeqID4.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG) SEIKAGAKU KOGYO CO LTD.  
Query Match 6.3%; Score 104; DB 8; Length 195;  
Best Local Similarity 33.7%; Pred. No. 0.34;  
RESULT 1219  
ID ADP71267 standard; protein; 200 AA.  
DE Human versican protein B-B' domain SeqID2.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG) SEIKAGAKU KOGYO CO LTD.  
Query Match 6.3%; Score 104; DB 8; Length 200;  
Best Local Similarity 32.5%; Pred. No. 0.35;  
RESULT 1220  
ID ADH71352 standard; protein; 552 AA.  
DE Human protein of the invention NOV9u SEQ ID NO:248.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.3%; Score 104; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 1.4;  
RESULT 1221  
ID ABB60536 standard; protein; 1712 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 8400.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.3%; Score 104; DB 4; Length 1712;  
Best Local Similarity 22.7%; Pred. No. 6.7;  
RESULT 1222  
ID ABB65987 standard; protein; 183 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.2%; Score 102.5; DB 4; Length 183;  
Best Local Similarity 29.7%; Pred. No. 0.43;  
RESULT 1223  
ID ADX72128 standard; protein; 309 AA.  
DE Plant full length insert polypeptide seqid 41494.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ) LIU J.  
PA (ZHOU) ZHOU Y.  
PA (KOVA) KOVALIC D K.  
PA (SCRE) SCREEN S E.  
PA (TABA) TABASKA J E.  
PA (CAOV) CAO Y.  
Query Match 6.2%; Score 102; DB 8; Length 309;  
Best Local Similarity 24.6%; Pred. No. 0.98;  
RESULT 1224  
ID ADN23553 standard; protein; 380 AA.  
DE Bacterial polypeptide #6206.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 6.1%; Score 101.5; DB 8; Length 380;  
Best Local Similarity 25.5%; Pred. No. 1.5;  
RESULT 1225  
ID AAB23034 standard; protein; 590 AA.  
DE Human SLIT protein-like splice variant, SECK 3352358-2.  
PN WO200053742-A2.



PD 14-SEP-2000.  
PA (CURA-) CURAGEN CORP. 6.1%; Score 101.5; DB 3; Length 590;  
Best Local Similarity 20.6%; Pred. No. 2.7;  
RESULT 1226  
ID ADA23289 standard; protein; 590 AA.  
DE Human SECX polypeptide, SEC6.  
PN US2003054514-A1.  
PD 20-MAR-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (LARO/) LAROCHELLE W J.  
Query Match 6.1%; Score 101.5; DB 6; Length 590;  
Best Local Similarity 20.6%; Pred. No. 2.7;  
RESULT 1227  
ID AUU76528 standard; protein; 402 AA.  
DE Human LP polypeptide #1.  
PN WO200216578-A2.  
PD 28-FEB-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 6.1%; Score 100.5; DB 5; Length 402;  
Best Local Similarity 30.9%; Pred. No. 2;  
RESULT 1228  
ID AAU09883 standard; protein; 402 AA.  
DE Novel human secreted protein #23.  
PN WO200179454-A1.  
PD 25-OCT-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 6.1%; Score 100.5; DB 5; Length 402;  
Best Local Similarity 30.9%; Pred. No. 2;  
RESULT 1229  
ID ADF59259 standard; protein; 402 AA.  
DE Human polypeptide sequence SEQ ID NO:1667.  
PN WO2003080795-A2.  
PD 02-OCT-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 100.5; DB 7; Length 402;  
Best Local Similarity 30.9%; Pred. No. 2;  
RESULT 1230  
ID ADF74155 standard; protein; 412 AA.  
DE Human novel brain/hippocampus protein #43.  
PN JP2003009886-A.  
PD 14-JAN-2003.  
PA (KAZU-) ZH KAZUSA DNA KENKUSHO.  
PA (PROT-) PROTEIN EXPRESS KK.  
Query Match 6.1%; Score 100.5; DB 7; Length 412;  
Best Local Similarity 30.9%; Pred. No. 2;  
RESULT 1231  
ID ABB68940 standard; protein; 1379 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33612.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.1%; Score 100.5; DB 4; Length 1379;  
Best Local Similarity 20.2%; Pred. No. 11;  
RESULT 1232  
ID AAR77035 standard; protein; 378 AA.  
DE Cat brain-enriched hyaluronan binding protein.  
PN WO9527785-A1.  
PD 19-OCT-1995.  
PA (UYVA) UNIV YALE.  
Query Match 6.0%; Score 100; DB 2; Length 378;  
Best Local Similarity 24.1%; Pred. No. 2;  
RESULT 1233  
ID ABP57346 standard; protein; 402 AA.  
DE Human secreted protein SEC-17 SEQ ID NO:17.  
PN WO2003004615-A2.  
PD 16-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
PA (LUYU/) LU Y.  
Query Match 6.0%; Score 99.5; DB 6; Length 402;  
Best Local Similarity 30.9%; Pred. No. 2.4;  
RESULT 1234

ID ABJ56917 standard; protein; 201 AA.  
DE Human cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.0%; Score 99; DB 6; Length 201;  
Best Local Similarity 28.0%; Pred. No. 1;  
RESULT 1235  
ID ABJ56916 standard; protein; 201 AA.  
DE 15IP3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.0%; Score 99; DB 6; Length 201;  
Best Local Similarity 28.0%; Pred. No. 1;  
RESULT 1236  
ID ADO29463 standard; protein; 410 AA.  
DE Mouse GPCR GPRC5B, SEQ ID NO:565.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 6.0%; Score 99; DB 8; Length 410;  
Best Local Similarity 22.0%; Pred. No. 2.8;  
RESULT 1237  
ID ABJ56919 standard; protein; 600 AA.  
DE 15IP3D4 v-2 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.0%; Score 99; DB 6; Length 600;  
Best Local Similarity 28.0%; Pred. No. 4.7;  
RESULT 1238  
ID ABB70377 standard; protein; 1428 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.0%; Score 99; DB 4; Length 1428;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 1239  
ID ABB69720 standard; protein; 1126 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 5.9%; Score 98.5; DB 4; Length 1126;  
Best Local Similarity 25.0%; Pred. No. 12;  
RESULT 1240  
ID AAY95559 standard; protein; 2870 AA.  
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).  
PN WO200040711-A2.  
PD 13-JUL-2000.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 5.9%; Score 98.5; DB 3; Length 2870;  
Best Local Similarity 23.1%; Pred. No. 45;  
RESULT 1241  
ID ADM07634 standard; protein; 2870 AA.  
DE Caenorhabditis elegans LOV -1 deletion mutant protein.  
PN US6723557-B1.  
PD 20-APR-2004.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 5.9%; Score 98.5; DB 8; Length 2870;  
Best Local Similarity 23.1%; Pred. No. 45;  
RESULT 1242  
ID ADW79951 standard; protein; 2870 AA.  
DE Nematode location of vulva (lov-1) mutant protein.  
PN US6849717-B1.  
PD 01-FEB-2005.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 5.9%; Score 98.5; DB 9; Length 2870;  
Best Local Similarity 23.1%; Pred. No. 45;  
RESULT 1243  
ID AAY95556 standard; protein; 3178 AA.

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DE Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN WO20040711-A2.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 3; Length 3178;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1244
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 8; Length 3178;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1245
ID ADW79940 standard; protein; 3178 AA.
DE Nematode location of vulva (lov-1) protein.
PN US6849717-B1.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 9; Length 3178;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1246
ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PA (PEKE ) PE CORP NY.
Query Match 5.9%; Score 98; DB 4; Length 2112;
Best Local Similarity 25.9%; Pred. No. 33;
RESULT 1247
ID AAB75555 standard; protein; 298 AA.
DE Gene 1 human secreted protein homologous amino acid sequence #109.
PN WO200077026-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.9%; Score 97.5; DB 4; Length 298;
Best Local Similarity 19.8%; Pred. No. 2.5;
RESULT 1248
ID ADE58456 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4331.
PN WO2003016475-A2.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1249
ID ADE58468 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4343.
PN WO2003016475-A2.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1250
ID ADE58460 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4335.
PN WO2003016475-A2.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1251
ID ADE58464 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4339.
PN WO2003016475-A2.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1252
ID ADE58472 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4347.
PN WO2003016475-A2.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1253
ID ADE58476 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4351.
PN WO2003016475-A2.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 1254
ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.
PN WO2004048529-A2.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 95.5; DB 8; Length 231;
Best Local Similarity 30.2%; Pred. No. 2.7;
RESULT 1255
ID ADO67145 standard; protein; 803 AA.
DE Novel human protein sequence #2118.
PN EP1440981-A2.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 94; DB 8; Length 803;
Best Local Similarity 21.9%; Pred. No. 21;
RESULT 1256
ID AAU18060 standard; protein; 258 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 205.
PN WO200155315-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.9;
RESULT 1257
ID ABB10532 standard; protein; 258 AA.
DE Human cDNA SEQ ID NO: 840.
PN WO200154474-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.9;
RESULT 1258
ID ABP67119 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 840.
PN US2002090672-A1.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.6%; Score 93.5; DB 5; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.9;
RESULT 1259
ID ADB31684 standard; protein; 258 AA.
DE Human novel protein SEQ ID NO 205.
PN US2003077606-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 7; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.9;
RESULT 1260
ID AAU17999 standard; protein; 261 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 144.

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PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.6%; Score 93.5; DB 4; Length 261;  
Best Local Similarity 24.6%; Pred. No. 5;  
RESULT 1261  
ID ABB10361 standard; protein; 261 AA.  
DE Human cDNA SEQ ID NO: 669.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.6%; Score 93.5; DB 4; Length 261;  
Best Local Similarity 24.6%; Pred. No. 5;  
RESULT 1262  
ID ABF66948 standard; protein; 261 AA.  
DE Human polypeptide SEQ ID NO 669.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 5.6%; Score 93.5; DB 5; Length 261;  
Best Local Similarity 24.6%; Pred. No. 5;  
RESULT 1263  
ID ADB31623 standard; protein; 261 AA.  
DE Human novel protein SEQ ID NO 144.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.6%; Score 93.5; DB 7; Length 261;  
Best Local Similarity 24.6%; Pred. No. 5;  
RESULT 1264  
ID ABG01510 standard; protein; 320 AA.  
DE Novel human diagnostic protein #1501.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.6%; Score 93.5; DB 4; Length 320;  
Best Local Similarity 23.2%; Pred. No. 6.6;  
RESULT 1265  
ID ADR36618 standard; protein; 339 AA.  
DE Plasmid pCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.6%; Score 93.5; DB 7; Length 339;  
Best Local Similarity 23.1%; Pred. No. 7.1;  
RESULT 1266  
ID ADE36592 standard; protein; 339 AA.  
DE Human NOV1a protein SEQ ID NO:2.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.6%; Score 93.5; DB 7; Length 339;  
Best Local Similarity 23.1%; Pred. No. 7.1;  
RESULT 1267  
ID ABR58582 standard; protein; 359 AA.  
DE Human cancer related protein SEQ ID NO:239.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 5.6%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1268  
ID ABP70439 standard; protein; 359 AA.  
DE Amino acid sequence of human TIM-1 allele 1.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.6%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1269  
ID ABP70441 standard; protein; 359 AA.

DE Amino acid sequence of human TIM-1 allele 4.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.6%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1270  
ID ABP70438 standard; protein; 359 AA.  
DE Amino acid sequence of human TIM-1 allele 1.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.6%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1271  
ID ABR48174 standard; protein; 359 AA.  
DE Human bladder cancer associated protein sequence SEQ ID NO:64.  
PN WO2003003906-A2.  
PD 16-JAN-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 5.6%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1272  
ID AAO26680 standard; protein; 359 AA.  
DE KIM-1 related protein, SEQ ID NO 8.  
PN WO200298920-A1.  
PD 12-DEC-2002.  
PA (BIOJ) BIOGEN INC.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 5.6%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1273  
ID ADE36594 standard; protein; 359 AA.  
DE Human NOV1b protein SEQ ID NO:4.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.6%; Score 93.5; DB 7; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1274  
ID ADN38984 standard; protein; 359 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 5.6%; Score 93.5; DB 7; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1275  
ID ADQ76690 standard; protein; 359 AA.  
DE Human kidney injury molecule-1 (KIM-1).  
PN WO2004060041-A2.  
PD 22-JUL-2004.  
PA (BIOG-) BIOGEN IDEC MA INC.  
Query Match 5.6%; Score 93.5; DB 8; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1276  
ID ABR99971 standard; protein; 359 AA.  
DE HAVCR1 protein, SEQ ID 25.  
PN WO2005001092-A2.  
PD 06-JAN-2005.  
PA (AMHP) WVEITH.  
Query Match 5.6%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1277  
ID ADY98071 standard; protein; 359 AA.  
DE Human TIM-1 allele 1-encoded protein.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 5.6%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1278

ID ADY98077 standard; protein; 359 AA.  
DE Human TIM-1 allele 4-encoded protein.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DNA FARMER CANCER INST INC.  
Query Match 5.6%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1279  
ID ADY98073 standard; protein; 359 AA.  
DE Human TIM-1 allele 2-encoded protein.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DNA FARMER CANCER INST INC.  
Query Match 5.6%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1280  
ID ADY79370 standard; protein; 359 AA.  
DE Human kidney injury molecule-1(b) complete protein.  
PN US2005112117-A1.  
PD 26-MAY-2005.  
PA (BAIL/) BAILLY V.  
PA (BONV/) BONVENTRE J.  
Query Match 5.6%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 7.7;  
RESULT 1281  
ID ABR63235 standard; protein; 2055 AA.  
DE Glucanucrase sequence from strain KG15.  
PN WO2003008618-A2.  
PD 30-JAN-2003.  
PA (NEDE ) NEDERLANDSE ORG TOEGEPAST.  
Query Match 5.6%; Score 93.5; DB 6; Length 2055;  
Best Local Similarity 23.3%; Pred. No. 84;  
RESULT 1284  
ID ADU82549 standard; protein; 311 AA.  
DE C. elegans SID-2 polypeptide, SEQ ID 3.  
PN WO2004093386-A2.  
PD 18-NOV-2004.  
PA (HARD ) HARVARD COLLEGE.  
Query Match 5.6%; Score 93; DB 8; Length 311;  
Best Local Similarity 18.4%; Pred. No. 7;  
RESULT 1285  
ID ADU82552 standard; protein; 311 AA.  
DE C. elegans SID-2 polypeptide, SEQ ID 6.  
PN WO2004093386-A2.  
PD 18-NOV-2004.  
PA (HARD ) HARVARD COLLEGE.  
Query Match 5.6%; Score 93; DB 8; Length 311;  
Best Local Similarity 18.4%; Pred. No. 7;  
RESULT 1286  
ID AAR88466 standard; protein; 629 AA.  
DE Drosophila scavenger receptor class CI.  
PN WO9600288-A2.  
PD 04-JAN-1996.  
PA (NASI ) MASSACHUSETTS INST TECHNOLOGY.  
Query Match 5.6%; Score 93; DB 2; Length 629;  
Best Local Similarity 23.4%; Pred. No. 7.5;  
RESULT 1287  
ID ABR33057 standard; protein; 629 AA.  
DE Fruit fly scavenger receptor type CI (dsr-CI).  
PN US6429289-B1.  
PD 06-AUG-2002.  
PA (NASI ) MASSACHUSETTS INST TECHNOLOGY.  
Query Match 5.6%; Score 93; DB 5; Length 629;  
Best Local Similarity 19.9%; Pred. No. 19;  
RESULT 1288  
ID AAR21524 standard; protein; 629 AA.  
DE Drosophila melanogaster scavenger receptor class CI (dsr-CI).  
PN US6350859-B1.  
PD 26-FEB-2002.  
PA (NASI ) MASSACHUSETTS INST TECHNOLOGY.  
Query Match 5.6%; Score 93; DB 5; Length 629;  
Best Local Similarity 19.9%; Pred. No. 19;  
RESULT 1289  
ID ABR73157 standard; protein; 40 AA.  
DE Deletion mutant of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEBLAD S.  
PA (KOGEL/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 5.6%; Score 92.5; DB 6; Length 40;  
Best Local Similarity 54.1%; Pred. No. 0.47;  
RESULT 1290  
ID AAM61380 standard; protein; 300 AA.  
DE Mouse junctional adhesion molecule protein.  
PN WO9824897-A1.  
PD 11-JUN-1998.  
PA (HOPF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 5.6%; Score 92.5; DB 2; Length 300;  
Best Local Similarity 23.4%; Pred. No. 7.5;  
RESULT 1291  
ID AAY23325 standard; protein; 300 AA.  
DE A33 related antigen JAM.  
PN WO9927098-A2.  
PD 03-JUN-1999.  
PA (GETH ) GENE-TECH INC.  
Query Match 5.6%; Score 92.5; DB 2; Length 300;  
Best Local Similarity 23.4%; Pred. No. 7.5;  
RESULT 1292  
ID ADH62537 standard; protein; 300 AA.  
DE Murine JAM protein used in the exemplification of the invention.  
PN US2003171568-A1.  
PD 11-SEP-2003.  
PA (ASHK/) ASHKENAZI A.  
PA (FONG/) FONG S.  
PA (GODD/) GODDARD A.  
PA (GURN/) GURNEY A L.  
PA (NAPI/) NAPIER M A.  
PA (TUNA/) TUNAS D.  
PA (WOOD/) WOOD W I.  
Query Match 5.6%; Score 92.5; DB 7; Length 300;  
Best Local Similarity 23.4%; Pred. No. 7.5;  
RESULT 1293  
ID ADK40853 standard; protein; 300 AA.  
DE Mouse junction adhesion molecule (JAM).  
PN US6699688-B1.  
PD 02-MAR-2004.  
PA (UYNY ) UNIV NEW YORK STATE RES FOUND.  
Query Match 5.6%; Score 92.5; DB 8; Length 300;  
Best Local Similarity 23.4%; Pred. No. 7.5;  
RESULT 1294  
ID ADN35293 standard; protein; 300 AA.  
DE Human JAM protein.  
PN WO2004031105-A2.  
PD 15-APR-2004.  
PA (GETH ) GENE-TECH INC.  
Query Match 5.6%; Score 92.5; DB 8; Length 300;  
Best Local Similarity 23.4%; Pred. No. 7.5;

RESULT 1295  
ID AD66693 standard; protein; 300 AA.  
DE Mouse junctional adhesion molecule (JAM).  
FN US2004235768-A1.  
PD 25-NOV-2004.  
PA (KORN/) KORNECKI E.  
PA (SOBO/) SOBOCKA M B.  
Query Match 5.6%; Score 92.5; DB 8; Length 300;  
Best Local Similarity 23.4%; Pred. No. 7.5;  
RESULT 1296  
ID ABP70440 standard; protein; 365 AA.  
DE Amino acid sequence of human TIM-1 allele 3.  
FN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.6%; Score 92.5; DB 6; Length 365;  
Best Local Similarity 22.6%; Pred. No. 9.8;  
RESULT 1297  
ID ADY98075 standard; protein; 365 AA.  
DE Human TIM-1 allele 3-encoded protein.  
FN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Query Match 5.6%; Score 92.5; DB 9; Length 365;  
Best Local Similarity 22.6%; Pred. No. 9.8;  
RESULT 1298  
ID ABB50001 standard; protein; 569 AA.  
DE Listeria monocytogenes protein #2705.  
FN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 5.6%; Score 92.5; DB 5; Length 569;  
Best Local Similarity 21.4%; Pred. No. 18;  
RESULT 1299  
ID ABU32518 standard; protein; 569 AA.  
DE Protein encoded by Prokaryotic essential gene #18045.  
FN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.6%; Score 92.5; DB 6; Length 569;  
Best Local Similarity 21.4%; Pred. No. 18;  
RESULT 1300  
ID AAU4853 standard; protein; 706 AA.  
DE Propionibacterium acnes immunogenic protein #9449.  
FN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.6%; Score 92.5; DB 4; Length 706;  
Best Local Similarity 25.4%; Pred. No. 24;  
RESULT 1301  
ID ABW45072 standard; protein; 706 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9748.  
FN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.6%; Score 92.5; DB 6; Length 706;  
Best Local Similarity 25.4%; Pred. No. 24;  
RESULT 1302  
ID ADN18863 standard; protein; 994 AA.  
DE Bacterial polypeptide #1516.  
FN US200323675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.6%; Score 92.5; DB 8; Length 994;  
Best Local Similarity 19.7%; Pred. No. 39;  
RESULT 1303  
ID ABR53566 standard; protein; 1636 AA.  
DE Protein sequence #SEQ ID 1997.

PN EPI258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 5.6%; Score 92.5; DB 6; Length 1636;  
Best Local Similarity 19.7%; Pred. No. 77;  
RESULT 1304  
ID AUK64364 standard; protein; 1636 AA.  
DE Disease creating protein complex-derived protein #1193.  
FN EPI338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 5.6%; Score 92.5; DB 7; Length 1636;  
Best Local Similarity 19.7%; Pred. No. 77;  
RESULT 1305  
ID ABP70442 standard; protein; 364 AA.  
DE Amino acid sequence of human TIM-1 allele 5.  
FN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.6%; Score 92; DB 6; Length 364;  
Best Local Similarity 21.6%; Pred. No. 11;  
RESULT 1306  
ID ADY98079 standard; protein; 364 AA.  
DE Human TIM-1 allele 5-encoded protein.  
FN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Query Match 5.6%; Score 92; DB 9; Length 364;  
Best Local Similarity 21.6%; Pred. No. 11;  
RESULT 1307  
ID AEG93047 standard; protein; 966 AA.  
DE S. cerevisiae BAX-associated protein fragment SEQ ID 52.  
FN WO200264766-A2.  
PD 22-AUG-2002.  
PA (JANC ) JANSSEN PHARM NV.  
Query Match 5.6%; Score 92; DB 5; Length 966;  
Best Local Similarity 20.3%; Pred. No. 41;  
RESULT 1308  
ID ADT87298 standard; protein; 966 AA.  
DE Yeast Stress-related protein from gene YBR112C.  
FN WO2004092398-A2.  
PD 28-OCT-2004.  
PA (BADI ) BASF PLANT SCI GMBH.  
Query Match 5.6%; Score 92; DB 8; Length 966;  
Best Local Similarity 20.3%; Pred. No. 41;  
RESULT 1309  
ID ADL72180 standard; protein; 2829 AA.  
DE X. laevis mutated adenomatous polyposis coli (APC) protein.  
FN WO2004018677-A1.  
PD 04-MAR-2004.  
PA (EISA ) EISAI CO LTD.  
Query Match 5.6%; Score 92; DB 8; Length 2829;  
Best Local Similarity 20.7%; Pred. No. 1.8e+02;  
RESULT 1310  
ID AAU18036 standard; protein; 166 AA.  
DE Human immunoglobulin polypeptide SEQ ID No 181.  
FN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.5%; Score 91.5; DB 4; Length 166;  
Best Local Similarity 31.9%; Pred. No. 4.1;  
RESULT 1311  
ID ABB10469 standard; protein; 166 AA.  
DE Human cDNA SEQ ID NO: 777.  
FN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.5%; Score 91.5; DB 4; Length 166;  
Best Local Similarity 31.9%; Pred. No. 4.1;  
RESULT 1312  
ID ABP67056 standard; protein; 166 AA.  
DE Human polypeptide SEQ ID NO 777.

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PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 5; Length 166;
RESULT 1313
ID ADB31660 standard; protein; 166 AA.
DE Human novel protein SEQ ID NO 181.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 7; Length 166;
RESULT 1314
ID ADR46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 8; Length 300;
RESULT 1315
ID AAM52302 standard; protein; 350 AA.
DE ActA protein fragment #2.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS ) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 4; Length 350;
RESULT 1316
ID AAM52301 standard; protein; 376 AA.
DE ActA protein fragment #1.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS ) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 4; Length 376;
RESULT 1317
ID AAM52300 standard; protein; 610 AA.
DE ActA protein.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS ) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 4; Length 610;
RESULT 1318
ID AAG79171 standard; protein; 639 AA.
DE Amino acid sequence of an ActA fragment.
PN WO200174858-A2.
PD 11-OCT-2001.
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 4; Length 639;
RESULT 1319
ID AAU09142 standard; protein; 639 AA.
DE Lysteria monocytogenes ActA.
PN WO200174853-A2.
PD 11-OCT-2001.
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 4; Length 639;
RESULT 1320
ID ABB47677 standard; protein; 639 AA.
DE Listeria monocytogenes protein #381.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INST ) INST PASTEUR.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 5; Length 639;
RESULT 1321
ID ADM48341 standard; protein; 681 AA.
DE Marburg virus glycoprotein, GP.
PN US2003215794-A1.
PD 20-NOV-2003.
PA (KAWA/) KAWAOKA Y.
PA (JASE/) JASENOSKY L D.
PA (NEUM/) NEUMANN G.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 8; Length 681;
RESULT 1322
ID ADN20575 standard; protein; 1103 AA.
DE Bacterial polypeptide #3228.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 5.5%; Score 91.5; DB 8; Length 1103;
RESULT 1323
ID ABP60839 standard; protein; 246 AA.
DE Caenorhabditis elegans thioredoxin-like protein SEQ ID NO:188.
PN WO200250289-A1.
PD 27-JUN-2002.
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 5.5%; Score 91; DB 5; Length 246;
RESULT 1324
ID AEA08149 standard; protein; 4262 AA.
DE Human mucin 17 (MUC17SEC) protein - SEQ ID 4.
PN US2005100925-A1.
PD 12-MAY-2005.
PA (BATR/) BATRA S.
PA (MONI/) MONIAUX N.
Query Match
Best Local Similarity 5.5%; Score 91; DB 9; Length 4262;
RESULT 1325
ID AEA08148 standard; protein; 4493 AA.
DE Human mucin 17 protein - SEQ ID 3.
PN US2005100925-A1.
PD 12-MAY-2005.
PA (BATR/) BATRA S.
PA (MONI/) MONIAUX N.
Query Match
Best Local Similarity 5.5%; Score 91; DB 9; Length 4493;
RESULT 1326
ID ADY11098 standard; protein; 463 AA.
DE Plant full length insert polypeptide seqid 66913.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 5.5%; Score 90.5; DB 8; Length 463;
RESULT 1327
ID ADG73740 standard; protein; 505 AA.
DE Aspergillus niger Brsa-109.
PN US2003215950-A1.
PD 20-NOV-2003.
PA (LASU/) LASURE L L.
PA (DAIZ/) DAI Z.
Query Match
Best Local Similarity 5.5%; Score 90.5; DB 8; Length 505;
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Best Local Similarity 27.0%; Pred. No. 24;  
RESULT 1328  
ID AB860186 standard; protein; 1714 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7350.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 5.5%; Score 90.5; DB 4; Length 1714;  
Best Local Similarity 26.7%; Pred. No. 1.3e+02;  
RESULT 1329  
ID AB869419 standard; protein; 1976 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35049.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 5.5%; Score 90.5; DB 4; Length 1976;  
Best Local Similarity 38.5%; Pred. No. 1.5e+02;  
RESULT 1330  
ID ABP70443 standard; protein; 364 AA.  
DE Amino acid sequence of human TIM-1 allele 6.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.4%; Score 90; DB 6; Length 364;  
Best Local Similarity 21.6%; Pred. No. 17;  
RESULT 1331  
ID ADY98081 standard; protein; 364 AA.  
DE Human TIM-1 allele 5-encoded protein.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PA (DAND) DANA FARBEN CANCER INST INC.  
Query Match 5.4%; Score 90; DB 9; Length 364;  
Best Local Similarity 21.6%; Pred. No. 17;  
RESULT 1332  
ID AB859507 standard; protein; 629 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 5313.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 5.4%; Score 90; DB 4; Length 629;  
Best Local Similarity 20.7%; Pred. No. 36;  
RESULT 1333  
ID ADP47260 standard; protein; 957 AA.  
DE Human Protein AAC02272, SEQ ID NO 12954.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 5.4%; Score 90; DB 7; Length 957;  
Best Local Similarity 18.3%; Pred. No. 63;  
RESULT 1334  
ID ADE58049 standard; protein; 957 AA.  
DE Human Protein AAC02272, SEQ ID NO 12958.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 5.4%; Score 90; DB 7; Length 957;  
Best Local Similarity 18.3%; Pred. No. 63;  
RESULT 1335  
ID ADP47264 standard; protein; 957 AA.  
DE Human Protein AAC02272, SEQ ID NO 12958.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 5.4%; Score 90; DB 7; Length 957;  
Best Local Similarity 18.3%; Pred. No. 63;  
RESULT 1336  
ID ADE58045 standard; protein; 957 AA.  
DE Human Protein AAC02272, SEQ ID NO 3913.  
PN WO2003016475-A2.

PD 27-FEB-2003.  
PA (GEO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 5.4%; Score 90; DB 7; Length 957;  
Best Local Similarity 18.3%; Pred. No. 63;  
RESULT 1337  
ID AQ29696 standard; protein; 1217 AA.  
DE Human colorectal cancer-associated protein #51.  
PN EPI439393-A2.  
PD 21-JUL-2004.  
PA (FARB) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 5.4%; Score 90; DB 8; Length 1217;  
Best Local Similarity 18.3%; Pred. No. 88;  
RESULT 1338  
ID ABG66756 standard; protein; 1296 AA.  
DE Human novel polypeptide #91.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.4%; Score 90; DB 5; Length 1296;  
Best Local Similarity 18.3%; Pred. No. 96;  
RESULT 1339  
ID ABG66702 standard; protein; 1296 AA.  
DE Human novel polypeptide #37.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.4%; Score 90; DB 5; Length 1296;  
Best Local Similarity 18.3%; Pred. No. 96;  
RESULT 1340  
ID ABP70432 standard; protein; 305 AA.  
DE Amino acid sequence of murine TIM-2 BALB/c allele.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.4%; Score 89.5; DB 6; Length 305;  
Best Local Similarity 24.3%; Pred. No. 15;  
RESULT 1341  
ID ABP70433 standard; protein; 305 AA.  
DE Amino acid sequence of murine TIM-2 ES-HBA and DBA/2J allele.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.4%; Score 89.5; DB 6; Length 305;  
Best Local Similarity 24.3%; Pred. No. 15;  
RESULT 1342  
ID ADY98061 standard; protein; 305 AA.  
DE Mouse TIM-2 variant.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PA (DAND) DANA FARBEN CANCER INST INC.  
Query Match 5.4%; Score 89.5; DB 9; Length 305;  
Best Local Similarity 24.3%; Pred. No. 15;  
RESULT 1343  
ID ADY98059 standard; protein; 305 AA.  
DE Mouse TIM-2.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PA (DAND) DANA FARBEN CANCER INST INC.  
Query Match 5.4%; Score 89.5; DB 9; Length 305;  
Best Local Similarity 24.3%; Pred. No. 15;  
RESULT 1344  
ID AAF69555 standard; protein; 410 AA.  
DE Human lysosomal membrane sialoglycoprotein lamp-2.  
PN WO9429342-A1.  
PD 22-DEC-1994.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 5.4%; Score 89.5; DB 2; Length 410;  
Best Local Similarity 21.0%; Pred. No. 22;

RESULT 1345  
ID AAR5213 standard; protein; 480 AA.  
DE Blowfly larvae PM95 antigen.  
PN AU9517609-A.  
PD 02-NOV-1995.  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
Query Match 5.4%; Score 89.5; DB 2; Length 480;  
Best Local Similarity 22.1%; Pred. No. 27;  
RESULT 1346  
ID ABO84994 standard; protein; 917 AA.  
DE Murine cancer-associated protein (CAP) MP07-101.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 5.4%; Score 89.5; DB 8; Length 917;  
Best Local Similarity 21.4%; Pred. No. 67;  
RESULT 1347  
ID ABB65879 standard; protein; 307 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.4%; Score 89; DB 4; Length 307;  
Best Local Similarity 31.6%; Pred. No. 17;  
RESULT 1348  
ID ABP69313 standard; protein; 343 AA.  
DE Human polypeptide SEQ ID NO 1360.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.4%; Score 89; DB 5; Length 343;  
Best Local Similarity 27.7%; Pred. No. 19;  
RESULT 1349  
ID AAR69554 standard; protein; 416 AA.  
DE Human lysosomal membrane sialoglycoprotein lamp-1.  
PN WO9423342-A1.  
PD 22-DEC-1994.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
PA (UNMI ) UNIV MICHIGAN.  
Query Match 5.4%; Score 89; DB 2; Length 416;  
Best Local Similarity 23.6%; Pred. No. 25;  
RESULT 1350  
ID AAY5250 standard; protein; 416 AA.  
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).  
PN WO9958658-A2.  
PD 18-NOV-1999.  
PA (EPIM-) EPIMUNE INC.  
Query Match 5.4%; Score 89; DB 3; Length 416;  
Best Local Similarity 23.6%; Pred. No. 25;  
RESULT 1351  
ID ADP6283 standard; protein; 416 AA.  
DE Human lysosomal-associated membrane protein 1.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 5.4%; Score 89; DB 7; Length 416;  
Best Local Similarity 23.6%; Pred. No. 25;  
RESULT 1352  
ID ADN03755 standard; protein; 416 AA.  
DE Antiproteolytic protein sequence #74.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 5.4%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 25;  
RESULT 1353  
ID ADP49321 standard; protein; 416 AA.  
DE Human lysosomal associated membrane protein LAMP #1.  
PN WO2004048537-A2.  
PD 10-JUN-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.4%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 25;

RESULT 1354  
ID ADP23231 standard; protein; 416 AA.  
DE PRO polypeptide SEQ ID NO:325.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 5.4%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 25;  
RESULT 1355  
ID ADU60107 standard; protein; 416 AA.  
DE Housekeeping gene protein, SEQ ID 68.  
PN US2004229233-A1.  
PD 18-NOV-2004.  
PA (NIGA ) NGK INSULATORS LTD.  
Query Match 5.4%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 25;  
RESULT 1356  
ID ADM85920 standard; protein; 416 AA.  
DE Human lysosomal-associated membrane protein-1.  
PN WO2005012912-A2.  
PD 10-FEB-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 5.4%; Score 89; DB 9; Length 416;  
Best Local Similarity 23.6%; Pred. No. 25;  
RESULT 1357  
ID ADR86408 standard; protein; 832 AA.  
DE Aspergillus fumigatus essential gene protein #458.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Query Match 5.4%; Score 89; DB 8; Length 832;  
Best Local Similarity 19.8%; Pred. No. 65;  
RESULT 1358  
ID ABB70039 standard; protein; 846 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 36909.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.4%; Score 89; DB 4; Length 846;  
Best Local Similarity 22.5%; Pred. No. 66;  
RESULT 1359  
ID ABB67102 standard; protein; 882 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28098.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.4%; Score 89; DB 4; Length 882;  
Best Local Similarity 22.5%; Pred. No. 70;  
RESULT 1360  
ID ADO37103 standard; protein; 951 AA.  
DE Cell proliferation-related polypeptide #118.  
PN WO2004061122-A2.  
PD 22-JUL-2004.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.4%; Score 89; DB 8; Length 951;  
Best Local Similarity 22.1%; Pred. No. 78;  
RESULT 1361  
ID ADM19804 standard; protein; 1076 AA.  
DE Protein encoded by novel human channel/transporter gene #122.  
PN WO200154472-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.4%; Score 89; DB 4; Length 1076;  
Best Local Similarity 21.1%; Pred. No. 92;  
RESULT 1362  
ID ADX97567 standard; protein; 2624 AA.  
DE Pancreatic cancer associated human protein, SEQ ID 115.  
PN EP1471075-A2.  
PD 27-OCT-2004.  
PA (HINZ/) HINZMANN B.  
PA (ROSE/) ROSENTHAL A.  
PA (PILA/) PILARSKY C.



PA (DAHL/) DAHL E.  
PA (SPEC/) SPECHT T.  
PA (LICH/) LICHTNER R.  
Query Match  
Best Local Similarity 5.4%; Score 89; DB 8; Length 2624;  
Result 1363  
ID AAG39194 standard; protein; 193 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48458.  
PN EP103405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 3; Length 193;  
Result 1364  
ID AAG39193 standard; protein; 199 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48457.  
PN EP103405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 3; Length 199;  
Result 1365  
ID ABG15314 standard; protein; 358 AA.  
DE Novel human diagnostic protein #15305.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 4; Length 358;  
Result 1366  
ID AAR11605 standard; protein; 392 AA.  
DE Human 75kD TNF-binding protein.  
PN EP417563-A.  
PD 20-MAR-1991.  
PA (HOFF) HOFFMANN-LA ROCHE AG.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 2; Length 392;  
Result 1367  
ID AAY30935 standard; protein; 392 AA.  
DE Human tumour necrosis factor binding protein fragment.  
PN EP939121-A2.  
PD 01-SEP-1999.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 2; Length 392;  
Result 1368  
ID AAB86818 standard; protein; 392 AA.  
DE Human TNFBP-associated protein #2.  
PN EP1132471-A2.  
PD 12-SEP-2001.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 4; Length 392;  
Result 1369  
ID ABO68455 standard; protein; 451 AA.  
DE Pseudomonas aeruginosa polypeptide #630.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 7; Length 451;  
Result 1370  
ID ABB63417 standard; protein; 481 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 17043.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE) PE CORP NV.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 4; Length 481;  
Result 1371  
ID AAG64210 standard; protein; 596 AA.  
DE Murine HSP47 interacting protein, M4.  
PN JP2001145493-A.  
PD 29-MAY-2001.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 4; Length 596;  
Result 1372  
ID AAY37234 standard; protein; 708 AA.  
DE Chlamydia trachomatis cellular envelope protein.  
PN WO928475-A2.  
PD 10-JUN-1999.  
PA (GBST) GENSET.  
Query Match  
Best Local Similarity 5.3%; Score 88.5; DB 2; Length 708;  
Result 1373  
ID AAR63068 standard; protein; 905 AA.  
DE Human EAA3b excitatory amino acid receptor.  
PN CA2110933-A.  
PD 12-JUN-1994.  
PA (KAMB/) KAMBOJ R.  
Query Match  
Best Local Similarity 5.3%; Score 88; DB 2; Length 905;  
Result 1374  
ID ADB86597 standard; protein; 995 AA.  
DE Frog tail resorption protein.  
PN US2003129685-A1.  
PD 10-JUL-2003.  
PA (NLJ/) NI J.  
PA (YOUN) YOUNG P E.  
PA (KENN) KENNY J J.  
PA (OLSE) OLSEN H S.  
PA (MOOR) MOORE P A.  
PA (WBIY) WEI Y.  
PA (GREE) GREENE J M.  
PA (RUBE) RUBEN S M.  
Query Match  
Best Local Similarity 5.3%; Score 88; DB 8; Length 995;  
Result 1375  
ID ADN23131 standard; protein; 3507 AA.  
DE Bacterial polypeptide #5784.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match  
Best Local Similarity 5.3%; Score 88; DB 8; Length 3507;  
Result 1376  
ID ABR43908 standard; protein; 4315 AA.  
DE MUC5B partial gene protein.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 5.3%; Score 88; DB 5; Length 4315;  
Result 1377  
ID ADL23265 standard; protein; 5703 AA.  
DE Human MUC5B.  
PN WO2004019041-A1.  
PD 04-MAR-2004.  
PA (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.  
PA (PACK) PACKER N H.  
PA (KARL) KARLSSON N.  
PA (SCHU) SCHULZ B L.  
Query Match  
Best Local Similarity 5.3%; Score 88; DB 8; Length 5703;  
Result 1378  
ID AEB56507 standard; protein; 5858 AA.  
DE Radiochemotherapy response detection associated protein SEQ ID NO 82.  
PN WO2005073411-A1.  
PD 11-AUG-2005.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match  
Best Local Similarity 5.3%; Score 88; DB 9; Length 5858;  
Result 1379

ID AAG13468 standard; protein; 310 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 12974.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 5.3%; Score 87.5; DB 3; Length 310;  
 Best Local Similarity 23.2%; Pred. No. 23;  
 RESULT 1380  
 ID AAG13467 standard; protein; 331 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 12973.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 5.3%; Score 87.5; DB 3; Length 331;  
 Best Local Similarity 23.2%; Pred. No. 25;  
 RESULT 1381  
 ID AAY52525 standard; protein; 536 AA.  
 DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.  
 PN WO954349-A2.  
 PD 28-OCT-1999.  
 PA (HESK-) HESKA CORP.  
 Query Match 5.3%; Score 87.5; DB 3; Length 536;  
 Best Local Similarity 23.9%; Pred. No. 49;  
 RESULT 1382  
 ID AAU96329 standard; protein; 536 AA.  
 DE Der HMW-map polypeptide #16.  
 PN WO200222807-A2.  
 PD 21-MAR-2002.  
 PA (HESK-) HESKA CORP.  
 Query Match 5.3%; Score 87.5; DB 5; Length 536;  
 Best Local Similarity 23.9%; Pred. No. 49;  
 RESULT 1383  
 ID AAY52523 standard; protein; 555 AA.  
 DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.  
 PN WO954349-A2.  
 PD 28-OCT-1999.  
 PA (HESK-) HESKA CORP.  
 Query Match 5.3%; Score 87.5; DB 3; Length 555;  
 Best Local Similarity 23.9%; Pred. No. 52;  
 RESULT 1384  
 ID AAU96327 standard; protein; 555 AA.  
 DE Der HMW-map polypeptide #14.  
 PN WO200222807-A2.  
 PD 21-MAR-2002.  
 PA (HESK-) HESKA CORP.  
 Query Match 5.3%; Score 87.5; DB 5; Length 555;  
 Best Local Similarity 23.9%; Pred. No. 52;  
 RESULT 1385  
 ID AAU96328 standard; protein; 555 AA.  
 DE Der HMW-map polypeptide #15.  
 PN WO200222807-A2.  
 PD 21-MAR-2002.  
 PA (HESK-) HESKA CORP.  
 Query Match 5.3%; Score 87.5; DB 5; Length 555;  
 Best Local Similarity 23.9%; Pred. No. 52;  
 RESULT 1386  
 ID ADB64946 standard; protein; 717 AA.  
 DE Human protein encoded by clone PROST20036350.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 5.3%; Score 87.5; DB 7; Length 717;  
 Best Local Similarity 17.8%; Pred. No. 73;  
 RESULT 1387  
 ID ADH71768 standard; protein; 904 AA.  
 DE Human protein of the invention NOV28n SEQ ID NO:664.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 5.3%; Score 87.5; DB 8; Length 904;  
 Best Local Similarity 23.8%; Pred. No. 1e+02;  
 RESULT 1388  
 ID AAU16313 standard; protein; 906 AA.  
 DE Yeast alpha factor-G-alpha protein fusion.

PN WO9711159-A1.  
 PD 27-MAR-1997.  
 PA (HEAR-) HEARTLAND BIOTECHNOLOGIES LLC.  
 Query Match 5.3%; Score 87.5; DB 2; Length 906;  
 Best Local Similarity 19.7%; Pred. No. 1e+02;  
 RESULT 1389  
 ID ADZ03664 standard; protein; 981 AA.  
 DE PRG4-Lub.1 protein.  
 PN WO2005016130-A2.  
 PD 24-FEB-2005.  
 PA (AMHP) WYETH.  
 Query Match 5.3%; Score 87.5; DB 9; Length 981;  
 Best Local Similarity 20.2%; Pred. No. 1.1e+02;  
 RESULT 1390  
 ID ADZ03672 standard; protein; 1038 AA.  
 DE PRG4-Lub.3 protein.  
 PN WO2005016130-A2.  
 PD 24-FEB-2005.  
 PA (AMHP) WYETH.  
 Query Match 5.3%; Score 87.5; DB 9; Length 1038;  
 Best Local Similarity 22.3%; Pred. No. 1.2e+02;  
 RESULT 1391  
 ID ADZ03676 standard; protein; 1069 AA.  
 DE PRG4-Lub.4 protein.  
 PN WO2005016130-A2.  
 PD 24-FEB-2005.  
 PA (AMHP) WYETH.  
 Query Match 5.3%; Score 87.5; DB 9; Length 1069;  
 Best Local Similarity 22.3%; Pred. No. 1.3e+02;  
 RESULT 1392  
 ID AAW54844 standard; protein; 1085 AA.  
 DE Bovine parathyroid calcium receptor 1 protein 5Kb fragment.  
 PN US5763589-A.  
 PD 03-JUN-1998.  
 PA (NPSP-) NPS PHARM INC.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 5.3%; Score 87.5; DB 2; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
 RESULT 1393  
 ID AAY41778 standard; protein; 1085 AA.  
 DE Bovine parathyroid calcium receptor 1 protein sequence.  
 PN US5962314-A.  
 PD 05-OCT-1999.  
 PA (NPSP-) NPS PHARM INC.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 5.3%; Score 87.5; DB 2; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
 RESULT 1394  
 ID AAW89563 standard; protein; 1085 AA.  
 DE Bovine parathyroid calcium receptor BoPCar 1.  
 PN US5858684-A.  
 PD 12-JAN-1999.  
 PA (NPSP-) NPS PHARM INC.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 5.3%; Score 87.5; DB 2; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
 RESULT 1395  
 ID AAY51825 standard; protein; 1085 AA.  
 DE Bovine calcium receptor BoPCar1 protein.  
 PN US6031003-A.  
 PD 29-FEB-2000.  
 PA (NPSP-) NPS PHARM INC.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 5.3%; Score 87.5; DB 3; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
 RESULT 1396  
 ID AAB47820 standard; protein; 1085 AA.  
 DE BoPCar1.  
 PN US6313146-B1.  
 PD 06-NOV-2001.  
 PA (NPSP-) NPS PHARM INC.  
 Query Match 5.3%; Score 87.5; DB 5; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.3e+02;

RESULT 1397  
ID AD93194 standard; protein; 1085 AA.  
DE Bovine extracellular Ca-sensing receptor.  
PN WO200296946-A1.  
PD 05-DEC-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 5.3%; Score 87.5; DB 7; Length 1085;  
Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
RESULT 1398  
ID ADI40961 standard; protein; 1085 AA.  
DE Bovine GPCR CASR.  
PN US2004018976-A1.  
PD 29-JAN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
Query Match 5.3%; Score 87.5; DB 8; Length 1085;  
Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
RESULT 1399  
ID ADI4015 standard; protein; 1085 AA.  
DE Bovine GPCR CASR #2.  
PN US2004018976-A1.  
PD 29-JAN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
Query Match 5.3%; Score 87.5; DB 8; Length 1085;  
Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
RESULT 1400  
ID ADZ03680 standard; protein; 1100 AA.  
DE PRG4-Lub:5 protein.  
PN WO2005016130-A2.  
PD 24-FEB-2005.  
PA (AMHP ) WYETH.  
Query Match 5.3%; Score 87.5; DB 9; Length 1100;  
Best Local Similarity 22.3%; Pred. No. 1.3e+02;  
RESULT 1401  
ID ADS24007 standard; protein; 1322 AA.  
DE Bacterial polypeptide #13040.  
PN US200323675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.3%; Score 87.5; DB 8; Length 1322;  
Best Local Similarity 22.9%; Pred. No. 1.7e+02;  
RESULT 1402  
ID ADD4997 standard; protein; 235 AA.  
DE Rat Protein CAA82313, SEQ ID NO 10428.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEOH ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 5.3%; Score 87; DB 7; Length 235;  
Best Local Similarity 27.8%; Pred. No. 18;  
RESULT 1403  
ID AAY29082 standard; protein; 288 AA.  
DE T. gondii immunogenic protein.  
PN WO932633-A1.  
PD 01-JUL-1999.  
PA (HESK-) HESKA CORP.  
Query Match 5.3%; Score 87; DB 2; Length 288;  
Best Local Similarity 29.7%; Pred. No. 23;  
RESULT 1404  
ID AAY29081 standard; protein; 288 AA.  
DE T. gondii immunogenic protein.  
PN WO932633-A1.  
PD 01-JUL-1999.  
PA (HESK-) HESKA CORP.  
Query Match 5.3%; Score 87; DB 2; Length 288;  
Best Local Similarity 29.7%; Pred. No. 23;  
RESULT 1397  
ID AD93194 standard; protein; 1085 AA.  
DE Bovine extracellular Ca-sensing receptor.  
PN WO200296946-A1.  
PD 05-DEC-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 5.3%; Score 87.5; DB 7; Length 1085;  
Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
RESULT 1398  
ID ADI40961 standard; protein; 1085 AA.  
DE Bovine GPCR CASR.  
PN US2004018976-A1.  
PD 29-JAN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
Query Match 5.3%; Score 87.5; DB 8; Length 1085;  
Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
RESULT 1399  
ID ADI4015 standard; protein; 1085 AA.  
DE Bovine GPCR CASR #2.  
PN US2004018976-A1.  
PD 29-JAN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
Query Match 5.3%; Score 87.5; DB 8; Length 1085;  
Best Local Similarity 22.7%; Pred. No. 1.3e+02;  
RESULT 1400  
ID ADZ03680 standard; protein; 1100 AA.  
DE PRG4-Lub:5 protein.  
PN WO2005016130-A2.  
PD 24-FEB-2005.  
PA (AMHP ) WYETH.  
Query Match 5.3%; Score 87.5; DB 9; Length 1100;  
Best Local Similarity 22.3%; Pred. No. 1.3e+02;  
RESULT 1401  
ID ADS24007 standard; protein; 1322 AA.  
DE Bacterial polypeptide #13040.  
PN US200323675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.3%; Score 87.5; DB 8; Length 1322;  
Best Local Similarity 22.9%; Pred. No. 1.7e+02;  
RESULT 1402  
ID ADD4997 standard; protein; 235 AA.  
DE Rat Protein CAA82313, SEQ ID NO 10428.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEOH ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 5.3%; Score 87; DB 7; Length 235;  
Best Local Similarity 27.8%; Pred. No. 18;  
RESULT 1403  
ID AAY29082 standard; protein; 288 AA.  
DE T. gondii immunogenic protein.  
PN WO932633-A1.  
PD 01-JUL-1999.  
PA (HESK-) HESKA CORP.  
Query Match 5.3%; Score 87; DB 2; Length 288;  
Best Local Similarity 29.7%; Pred. No. 23;  
RESULT 1404  
ID AAY29081 standard; protein; 288 AA.  
DE T. gondii immunogenic protein.  
PN WO932633-A1.  
PD 01-JUL-1999.  
PA (HESK-) HESKA CORP.  
Query Match 5.3%; Score 87; DB 2; Length 288;  
Best Local Similarity 29.7%; Pred. No. 23;  
RESULT 1405  
ID AAU25553 standard; protein; 288 AA.  
DE T. gondii immunogenic protein PTg1397.  
PN US2001014447-A1.  
PD 16-AUG-2001.  
PA (MILH/) MILHAUSEN M J.  
Query Match 5.3%; Score 87; DB 4; Length 288;  
Best Local Similarity 29.7%; Pred. No. 23;  
RESULT 1406  
ID AAU25552 standard; protein; 288 AA.  
DE T. gondii immunogenic protein PTg288.  
PN US2001014447-A1.  
PD 16-AUG-2001.  
PA (MILH/) MILHAUSEN M J.  
Query Match 5.3%; Score 87; DB 4; Length 288;  
Best Local Similarity 29.7%; Pred. No. 23;  
RESULT 1407  
ID ADG17391 standard; protein; 288 AA.  
DE T. gondii protein #79.  
PN US2003194393-A1.  
PD 16-OCT-2003.  
PA (MILH/) MILHAUSEN M J.  
Query Match 5.3%; Score 87; DB 7; Length 288;  
Best Local Similarity 29.7%; Pred. No. 23;  
RESULT 1408  
ID ADG17394 standard; protein; 288 AA.  
DE T. gondii protein #82.  
PN US2003194393-A1.  
PD 16-OCT-2003.  
PA (MILH/) MILHAUSEN M J.  
Query Match 5.3%; Score 87; DB 7; Length 288;  
Best Local Similarity 29.7%; Pred. No. 23;  
RESULT 1409  
ID ADJ76313 standard; protein; 363 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1565.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 5.3%; Score 87; DB 8; Length 363;  
Best Local Similarity 25.3%; Pred. No. 32;  
RESULT 1410  
ID ADY37611 standard; protein; 363 AA.  
DE Lung cancer related protein, SEQ ID 87.  
PN US2005048589-A1.  
PD 03-MAR-2005.  
PA (JEND/) JENDOUBI M.  
Query Match 5.3%; Score 87; DB 9; Length 363;  
Best Local Similarity 25.3%; Pred. No. 32;  
RESULT 1411  
ID AAR01940 standard; protein; 417 AA.  
DE Tumour necrosis factor.  
PN JP01285191-A.  
PD 16-NOV-1989.  
PA (GREC ) GREEN CROSS CORP.  
Query Match 5.3%; Score 87; DB 2; Length 417;  
Best Local Similarity 23.6%; Pred. No. 39;  
RESULT 1412  
ID ADX91714 standard; protein; 611 AA.  
DE Plant full length insert polypeptide seqid 54378.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIJO/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 5.3%; Score 87; DB 8; Length 611;  
Best Local Similarity 21.8%; Pred. No. 66;  
RESULT 1413  
ID AAG83274 standard; protein; 631 AA.  
DE Chlamydia trachomatis PmpH(N-term) fusion protein.  
PN WO200140474-A2.

PD 07-JUN-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.3%; Score 87; DB 4; Length 631;  
Best Local Similarity 28.1%; Pred. No. 69;  
RESULT 1414  
ID AB994245 standard; protein; 631 AA.  
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.  
PN WO200208267-A2.  
PD 31-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 5.3%; Score 87; DB 5; Length 631;  
Best Local Similarity 28.1%; Pred. No. 69;  
RESULT 1415  
ID ADD42755 standard; protein; 664 AA.  
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.  
PN WO2003041560-A2.  
PD 22-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.3%; Score 87; DB 7; Length 664;  
Best Local Similarity 28.1%; Pred. No. 74;  
RESULT 1416  
ID AAR63070 standard; protein; 849 AA.  
DE Human EAA3d excitatory amino acid receptor.  
PN CA2110933-A.  
PD 12-JUN-1994.  
PA (KAMB/) KAMBOJ R.  
Query Match 5.3%; Score 87; DB 2; Length 849;  
Best Local Similarity 22.4%; Pred. No. 1e+02;  
RESULT 1417  
ID AAR60563 standard; protein; 862 AA.  
DE Yeast 2.6 KB agglutination gene FLO1s.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SAPB) SAPPORO BREWERIES.  
PA (PANI-) PANINOLABORATORIO BRYGGERILABORATORIUM.  
Query Match 5.3%; Score 87; DB 2; Length 862;  
Best Local Similarity 19.1%; Pred. No. 1.1e+02;  
RESULT 1418  
ID AAR58754 standard; protein; 894 AA.  
DE S. cerevisiae FLO1.  
PN WO9418330-A1.  
PD 18-AUG-1994.  
PA (UNIL) UNILEVER PLC.  
PA (UNIL) UNILEVER NV.  
Query Match 5.3%; Score 87; DB 2; Length 894;  
Best Local Similarity 19.1%; Pred. No. 1.1e+02;  
RESULT 1419  
ID AAR47578 standard; protein; 894 AA.  
DE Flocculation protein of *Saccharomyces cerevisiae*.  
PN WO9401567-A1.  
PD 20-JAN-1994.  
PA (UNIL) UNILEVER PLC.  
PA (UNIL) UNILEVER NV.  
Query Match 5.3%; Score 87; DB 2; Length 894;  
Best Local Similarity 19.1%; Pred. No. 1.1e+02;  
RESULT 1420  
ID AAR60112 standard; protein; 905 AA.  
DE Human EAA3a excitatory amino acid receptor.  
PN CA2110933-A.  
PD 12-JUN-1994.  
PA (KAMB/) KAMBOJ R.  
Query Match 5.3%; Score 87; DB 2; Length 905;  
Best Local Similarity 22.4%; Pred. No. 1.1e+02;  
RESULT 1421  
ID AAR75883 standard; protein; 905 AA.  
DE Human EAA3 receptor (Q-591).  
PN WO9517508-A2.  
PD 29-JUN-1995.  
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.  
Query Match 5.3%; Score 87; DB 2; Length 905;  
Best Local Similarity 22.4%; Pred. No. 1.1e+02;  
RESULT 1422  
ID AAB19496 standard; protein; 905 AA.

DE The Q591 form of the human EAA3 receptor.  
PN US6136544-A.  
PD 24-OCT-2000.  
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.  
Query Match 5.3%; Score 87; DB 4; Length 905;  
Best Local Similarity 22.4%; Pred. No. 1.1e+02;  
RESULT 1423  
ID ADX26248 standard; protein; 905 AA.  
DE Novel cell pain response detection method-related human protein SeqID594.  
PN WO2005014849-A2.  
PD 17-FEB-2005.  
PA (EURO-) EUROCELTIQUE SA.  
Query Match 5.3%; Score 87; DB 9; Length 905;  
Best Local Similarity 22.4%; Pred. No. 1.1e+02;  
RESULT 1424  
ID AAU38901 standard; protein; 1016 AA.  
DE C. trachomatis CT872 protein.  
PN WO200181379-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.3%; Score 87; DB 4; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.3e+02;  
RESULT 1425  
ID ABG91037 standard; protein; 1016 AA.  
DE Chlamydia trachomatis outer membrane protein H protein.  
PN WO200262380-A2.  
PD 15-AUG-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 5.3%; Score 87; DB 5; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.3e+02;  
RESULT 1426  
ID ADD42682 standard; protein; 1016 AA.  
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.  
PN WO2003041560-A2.  
PD 22-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.3%; Score 87; DB 7; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.3e+02;  
RESULT 1427  
ID ADD43800 standard; protein; 1016 AA.  
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 95.  
PN WO2003049762-A2.  
PD 19-JUN-2003.  
PA (CHIR-) CHIRON SPA.  
Query Match 5.3%; Score 87; DB 7; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.3e+02;  
RESULT 1428  
ID ADW29028 standard; protein; 1016 AA.  
DE C trachomatis polymorphic membrane protein (PmpH) Seq 22.  
PN WO2005002619-A2.  
PD 13-JAN-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 5.3%; Score 87; DB 9; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.3e+02;  
RESULT 1429  
ID AEA19092 standard; protein; 1016 AA.  
DE Chlamydia trachomatis protein - SEQ ID 95.  
PN US2005106162-A1.  
PD 19-MAY-2005.  
PA (GRAN/) GRANDI G.  
PA (RATT/) RATTI G.  
Query Match 5.3%; Score 87; DB 9; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.3e+02;  
RESULT 1430  
ID AAR60562 standard; protein; 1537 AA.  
DE Yeast 4.7 KB agglutination gene FLO1L.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SAPB) SAPPORO BREWERIES.  
PA (PANI-) PANINOLABORATORIO BRYGGERILABORATORIUM.  
Query Match 5.3%; Score 87; DB 2; Length 1537;  
Best Local Similarity 19.1%; Pred. No. 2.3e+02;  
RESULT 1431

ID ADP87475 standard; protein; 1537 AA.  
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.  
FN WO2004057033-A1.  
PD 08-JUL-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
Query Match 5.3%; Score 87; DB 8; Length 1537;  
Best Local Similarity 19.1%; Pred. No. 2.3e+02;  
RESULT 1432  
ID ADN18745 standard; protein; 1537 AA.  
DE Bacterial polypeptide #1398.  
FN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.3%; Score 87; DB 8; Length 1537;  
Best Local Similarity 19.1%; Pred. No. 2.3e+02;  
RESULT 1433  
ID ABB67362 standard; protein; 1575 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28878.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.3%; Score 87; DB 4; Length 1575;  
Best Local Similarity 20.5%; Pred. No. 2.4e+02;  
RESULT 1434  
ID AAU39177 standard; protein; 238 AA.  
DE Propionibacterium acnes immunogenic protein #73.  
FN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.2%; Score 86.5; DB 4; Length 238;  
Best Local Similarity 22.7%; Pred. No. 20;  
RESULT 1435  
ID ABM35696 standard; protein; 238 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #372.  
FN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.2%; Score 86.5; DB 6; Length 238;  
Best Local Similarity 22.7%; Pred. No. 20;  
RESULT 1436  
ID AAP91941 standard; peptide; 400 AA.  
DE Sequence of preprospasmolysin.  
FN DE3808456-A.  
PD 28-SEP-1989.  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
Query Match 5.2%; Score 86.5; DB 1; Length 400;  
Best Local Similarity 30.8%; Pred. No. 41;  
RESULT 1437  
ID ADN19290 standard; protein; 503 AA.  
DE Bacterial polypeptide #1943.  
FN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 86.5; DB 8; Length 503;  
Best Local Similarity 22.1%; Pred. No. 56;  
RESULT 1438  
ID ABU25742 standard; protein; 687 AA.  
DE Protein encoded by Prokaryotic essential gene #11269.  
FN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 86.5; DB 6; Length 687;  
Best Local Similarity 23.2%; Pred. No. 86;  
RESULT 1439  
ID ABG15647 standard; protein; 714 AA.

DE Novel human diagnostic protein #15638.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.2%; Score 86.5; DB 4; Length 714;  
Best Local Similarity 18.2%; Pred. No. 91;  
RESULT 1440  
ID ABG15147 standard; protein; 714 AA.  
DE Novel human diagnostic protein #15138.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.2%; Score 86.5; DB 4; Length 714;  
Best Local Similarity 18.2%; Pred. No. 91;  
RESULT 1441  
ID AAY54466 standard; protein; 788 AA.  
DE Amino acid sequence of intestinal insect mucin isoform IIM14.  
FN WO9967373-A2.  
PD 29-DEC-1999.  
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.  
Query Match 5.2%; Score 86.5; DB 3; Length 788;  
Best Local Similarity 27.2%; Pred. No. 1e+02;  
RESULT 1442  
ID AAY54467 standard; protein; 807 AA.  
DE Amini acid sequence of intestinal insect mucin isoform IIM22.  
FN WO9967373-A2.  
PD 29-DEC-1999.  
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.  
Query Match 5.2%; Score 86.5; DB 3; Length 807;  
Best Local Similarity 27.2%; Pred. No. 1.1e+02;  
RESULT 1443  
ID ADA14416 standard; protein; 1579 AA.  
DE Mouse spermatogenesis related protein sequence SEQ ID NO:158.  
FN WO2003068969-A1.  
PD 21-AUG-2003.  
PA (NTSC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 5.2%; Score 86.5; DB 6; Length 1579;  
Best Local Similarity 21.1%; Pred. No. 2.7e+02;  
RESULT 1444  
ID ADT07505 standard; protein; 2109 AA.  
DE Human colon-specific polypeptide (CSP) #22.  
FN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 5.2%; Score 86.5; DB 8; Length 2109;  
Best Local Similarity 26.1%; Pred. No. 4e+02;  
RESULT 1445  
ID ADT07506 standard; protein; 2254 AA.  
DE Human colon-specific polypeptide (CSP) #23.  
FN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 5.2%; Score 86.5; DB 8; Length 2254;  
Best Local Similarity 26.1%; Pred. No. 4.4e+02;  
RESULT 1446  
ID ADT07507 standard; protein; 2401 AA.  
DE Human colon-specific polypeptide (CSP) #24.  
FN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 5.2%; Score 86.5; DB 8; Length 2401;  
Best Local Similarity 26.1%; Pred. No. 4.8e+02;  
RESULT 1447  
ID AAY57453 standard; protein; 2781 AA.  
DE Human transcriptional regulatory factor SEQ ID NO:10.  
FN WO9957143-A1.  
PD 11-NOV-1999.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.2%; Score 86.5; DB 3; Length 2781;  
Best Local Similarity 20.8%; Pred. No. 5.9e+02;  
RESULT 1448  
ID ADF42724 standard; protein; 2781 AA.  
DE Human BPTF amino acid sequence SEQ ID NO:30.

PN WO2003102163-A2.  
PD 11-DEC-2003.  
PA (META-) METABOLEX INC.  
Query Match 5.2%; Score 86.5; DB 8; Length 2781;  
Best Local Similarity 20.8%; Pred. No. 5.9e+02;  
RESULT 1449  
ID ADO00984 standard; protein; 2781 AA.  
DE Human homologue of Fruit fly AD-related protein CG17135.  
PN US2004067535-A1.  
PD 08-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Query Match 5.2%; Score 86.5; DB 8; Length 2781;  
Best Local Similarity 20.8%; Pred. No. 5.9e+02;  
RESULT 1450  
ID ADO18653 standard; protein; 2781 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1472.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.2%; Score 86.5; DB 8; Length 2781;  
Best Local Similarity 20.8%; Pred. No. 5.9e+02;  
RESULT 1451  
ID AAY57452 standard; protein; 2907 AA.  
DE Human transcriptional regulatory factor SEQ ID NO:1.  
PN WO9957143-A1.  
PD 11-NOV-1999.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.2%; Score 86.5; DB 3; Length 2907;  
Best Local Similarity 20.8%; Pred. No. 6.2e+02;  
RESULT 1452  
ID AWM82857 standard; protein; 476 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3106.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 5.2%; Score 86; DB 8; Length 476;  
Best Local Similarity 32.1%; Pred. No. 58;  
RESULT 1453  
ID AWM83144 standard; protein; 476 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3393.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 5.2%; Score 86; DB 8; Length 476;  
Best Local Similarity 32.1%; Pred. No. 58;  
RESULT 1454  
ID AAB98978 standard; protein; 551 AA.  
DE Rabbit PCIP1.  
PN WO200134797-A1.  
PD 17-MAY-2001.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 5.2%; Score 86; DB 4; Length 551;  
Best Local Similarity 26.4%; Pred. No. 71;  
RESULT 1455  
ID ADD18594 standard; protein; 601 AA.  
DE Human disease related protein SeqID25.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 5.2%; Score 86; DB 7; Length 601;  
Best Local Similarity 22.0%; Pred. No. 80;  
RESULT 1456  
ID AAY05477 standard; protein; 750 AA.  
DE C. albicans Rbt1 protein sequence.  
PN WO9918115-A1.  
PD 15-APR-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 5.2%; Score 86; DB 2; Length 750;  
Best Local Similarity 23.4%; Pred. No. 1.1e+02;  
RESULT 1457  
ID ADX76173 standard; protein; 857 AA.  
DE Plant full length insert polypeptide seqid 45539.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 5.2%; Score 86; DB 8; Length 857;  
Best Local Similarity 22.1%; Pred. No. 1.3e+02;  
RESULT 1458  
ID AAB19499 standard; protein; 905 AA.  
DE Amino acid sequence of the R591 form of the human EAA3 receptor.  
PN US6136544-A.  
PD 24-OCT-2000.  
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.  
Query Match 5.2%; Score 86; DB 4; Length 905;  
Best Local Similarity 22.4%; Pred. No. 1.4e+02;  
RESULT 1459  
ID ADB79822 standard; protein; 1080 AA.  
DE Mouse putative deubiquitinating enzyme 8, SEQ ID 62.  
PN EP1279744-A2.  
PD 29-JAN-2003.  
PA (WARN) WARNER LAMBERT CO.  
Query Match 5.2%; Score 86; DB 7; Length 1080;  
Best Local Similarity 20.2%; Pred. No. 1.8e+02;  
RESULT 1460  
ID AEG28388 standard; protein; 1086 AA.  
DE Novel human diagnostic protein #28379.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.2%; Score 86; DB 4; Length 1086;  
Best Local Similarity 19.8%; Pred. No. 1.8e+02;  
RESULT 1461  
ID AEG05675 standard; protein; 1190 AA.  
DE Novel human diagnostic protein #5666.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.2%; Score 86; DB 4; Length 1190;  
Best Local Similarity 19.8%; Pred. No. 2e+02;  
RESULT 1462  
ID AAG23116 standard; protein; 193 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26303.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.2%; Score 85.5; DB 3; Length 193;  
Best Local Similarity 20.9%; Pred. No. 19;  
RESULT 1463  
ID AAG23115 standard; protein; 199 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26302.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.2%; Score 85.5; DB 3; Length 199;  
Best Local Similarity 20.9%; Pred. No. 20;  
RESULT 1464  
ID AAB09826 standard; protein; 346 AA.  
DE Endoglucanase protein sequence 6.  
PN WO200024879-A1.  
PD 04-MAY-2000.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.2%; Score 85.5; DB 3; Length 346;  
Best Local Similarity 22.4%; Pred. No. 42;  
RESULT 1465  
ID AAO15057 standard; protein; 346 AA.  
DE Phycomyces nitens endoglucanase-related protein.  
PN WO200242474-A1.  
PD 30-MAY-2002.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.2%; Score 85.5; DB 5; Length 346;  
Best Local Similarity 22.4%; Pred. No. 42;  
RESULT 1466  
ID ABB08065 standard; protein; 346 AA.

DE P. nitens CP99002 PCEI protein.  
PN WO200238754-A1.  
PD 16-MAY-2002.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.2%; Score 85.5; DB 5; Length 346;  
Best Local Similarity 22.4%; Pred. No. 42;  
RESULT 1467  
ID ADA37114 standard; protein; 346 AA.  
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.  
PN WO2003052105-A1.  
PD 26-JUN-2003.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.2%; Score 85.5; DB 6; Length 346;  
Best Local Similarity 22.4%; Pred. No. 42;  
RESULT 1468  
ID AAR57350 standard; protein; 354 AA.  
DE Human cartilage link protein.  
PN WO9415627-A1.  
PD 21-JUL-1994.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 5.2%; Score 85.5; DB 2; Length 354;  
Best Local Similarity 26.2%; Pred. No. 43;  
RESULT 1469  
ID ABB93134 standard; protein; 649 AA.  
DE Herbicidically active polypeptide SEQ ID NO 2345.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 5.2%; Score 85.5; DB 5; Length 649;  
Best Local Similarity 23.4%; Pred. No. 99;  
RESULT 1470  
ID ABB78250 standard; protein; 652 AA.  
DE Amino acid sequence of a human heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 5.2%; Score 85.5; DB 5; Length 652;  
Best Local Similarity 22.4%; Pred. No. 99;  
RESULT 1471  
ID ABUL5839 standard; protein; 686 AA.  
DE Protein encoded by Prokaryotic essential gene #1366.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 85.5; DB 6; Length 686;  
Best Local Similarity 24.2%; Pred. No. 1.1e+02;  
RESULT 1472  
ID ADN47243 standard; protein; 695 AA.  
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1121.  
PN WO2004022736-A1.  
PD 18-MAR-2004.  
PA (NTSC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 5.2%; Score 85.5; DB 8; Length 695;  
Best Local Similarity 20.6%; Pred. No. 1.1e+02;  
RESULT 1473  
ID ADD47689 standard; protein; 780 AA.  
DE Human Protein XP\_027074, SEQ ID NO 13385.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 5.2%; Score 85.5; DB 7; Length 780;  
Best Local Similarity 23.2%; Pred. No. 1.3e+02;  
RESULT 1474  
ID ADD47692 standard; protein; 780 AA.  
DE Human Protein XP\_027074, SEQ ID NO 13388.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 5.2%; Score 85.5; DB 7; Length 780;  
Best Local Similarity 23.2%; Pred. No. 1.3e+02;  
RESULT 1475

ID AAB07743 standard; protein; 781 AA.  
DE A snake venom protease (SVPH-4) polypeptide variant SVPH-4b.  
PN WO200403525-A2.  
PD 27-JUL-2000.  
PA (IMWV ) IMMUNEX CORP.  
Query Match 5.2%; Score 85.5; DB 3; Length 781;  
Best Local Similarity 17.9%; Pred. No. 1.3e+02;  
RESULT 1476  
ID ADE71292 standard; protein; 781 AA.  
DE Novel human protein #46.  
PN JP2002345493-A.  
PD 03-DEC-2002.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
Query Match 5.2%; Score 85.5; DB 7; Length 781;  
Best Local Similarity 23.2%; Pred. No. 1.3e+02;  
RESULT 1477  
ID ABB78248 standard; protein; 841 AA.  
DE Amino acid sequence of a zebrafish heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 5.2%; Score 85.5; DB 5; Length 841;  
Best Local Similarity 22.4%; Pred. No. 1.4e+02;  
RESULT 1478  
ID ABB71012 standard; protein; 843 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.2%; Score 85.5; DB 4; Length 843;  
Best Local Similarity 22.5%; Pred. No. 1.4e+02;  
RESULT 1479  
ID ABB78249 standard; protein; 977 AA.  
DE Amino acid sequence of a zebrafish heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 5.2%; Score 85.5; DB 5; Length 977;  
Best Local Similarity 22.4%; Pred. No. 1.7e+02;  
RESULT 1480  
ID ABU54710 standard; protein; 1784 AA.  
DE Human CA125 protein amino terminal sequence.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 5.2%; Score 85.5; DB 6; Length 1784;  
Best Local Similarity 27.2%; Pred. No. 4e+02;  
RESULT 1481  
ID ABU54858 standard; protein; 1794 AA.  
DE Human CA125 amino terminal domain.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 5.2%; Score 85.5; DB 6; Length 1794;  
Best Local Similarity 27.2%; Pred. No. 4e+02;  
RESULT 1482  
ID ABU54707 standard; protein; 1821 AA.  
DE Human CA125 amino terminal domain.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 5.2%; Score 85.5; DB 6; Length 1821;  
Best Local Similarity 27.2%; Pred. No. 4.1e+02;  
RESULT 1483  
ID ADB40509 standard; protein; 2055 AA.  
DE Human nuclear receptor coactivator ARAP3.  
PN DE10135787-A1.  
PD 13-FEB-2003.  
PA (JENP ) JENAPHARM GMBH & CO KG.  
Query Match 5.2%; Score 85.5; DB 8; Length 2055;  
Best Local Similarity 20.5%; Pred. No. 4.8e+02;  
RESULT 1484  
ID ABG95034 standard; protein; 2311 AA.

DE Human translocation (4; 11)(q21; q23) protein #1.  
PN WO200269900-A2.  
PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Query Match 5.2%; Score 85.5; DB 5; Length 2311;  
Best Local Similarity 24.3%; Pred. No. 5.7e+02;  
RESULT 1485  
ID AEB29721 standard; protein; 2448 AA.  
DE Human Mucin 5 (subtypes A and C).  
PN WO2005067667-A2.  
PD 28-JUL-2005.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 5.2%; Score 85.5; DB 9; Length 2448;  
Best Local Similarity 24.8%; Pred. No. 6.1e+02;  
RESULT 1486  
ID ABG31317 standard; protein; 2586 AA.  
DE Human 5-3 corrected OCP protein.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.2%; Score 85.5; DB 5; Length 2586;  
Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1487  
ID ABG32891 standard; protein; 2586 AA.  
DE Human osteoclast protein (OCP) #1.  
PN US2002086825-A1.  
PD 04-JUL-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 5.2%; Score 85.5; DB 5; Length 2586;  
Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1488  
ID ADL02231 standard; protein; 2586 AA.  
DE Human OCP protein #1.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.2%; Score 85.5; DB 8; Length 2586;  
Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1489  
ID ADL02234 standard; protein; 2586 AA.  
DE Human OCP protein #2.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.2%; Score 85.5; DB 8; Length 2586;  
Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1490  
ID AAB47935 standard; protein; 2587 AA.  
DE Human OCP.  
PN US2002022026-A1.  
PD 21-FEB-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 5.2%; Score 85.5; DB 5; Length 2587;  
Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1491  
ID ABG32896 standard; protein; 2587 AA.  
DE Human osteoclast protein (OCP) #2.  
PN US2002086825-A1.  
PD 04-JUL-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 5.2%; Score 85.5; DB 5; Length 2587;

Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1492  
ID ADL02236 standard; protein; 2587 AA.  
DE Human OCP protein #3.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.2%; Score 85.5; DB 8; Length 2587;  
Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1493  
ID ABG31323 standard; protein; 2589 AA.  
DE Human OCP protein.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.2%; Score 85.5; DB 5; Length 2589;  
Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1494  
ID ADL02244 standard; protein; 2589 AA.  
DE Human OCP protein #5.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.2%; Score 85.5; DB 8; Length 2589;  
Best Local Similarity 25.8%; Pred. No. 6.6e+02;  
RESULT 1495  
ID AAE34702 standard; protein; 5877 AA.  
DE Human mucin (MUC-16B).  
PN WO200292836-A2.  
PD 21-NOV-2002.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 5.2%; Score 85.5; DB 6; Length 5877;  
Best Local Similarity 27.2%; Pred. No. 2e+03;  
RESULT 1496  
ID ABU54721 standard; protein; 11721 AA.  
DE Human CAL25 full length protein sequence.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 5.2%; Score 85.5; DB 6; Length 11721;  
Best Local Similarity 27.2%; Pred. No. 5.2e+03;  
RESULT 1497  
ID ADP84155 standard; protein; 22157 AA.  
DE Human CAL25 protein sequence SeqID 5.  
PN WO2004045553-A2.  
PD 03-JUN-2004.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 5.2%; Score 85.5; DB 8; Length 22157;  
Best Local Similarity 27.2%; Pred. No. 1.3e+04;  
RESULT 1498  
ID AAB39253 standard; protein; 280 AA.  
DE Gene 15 human secreted protein homologous amino acid sequence #133.  
PN WO200056754-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.1%; Score 85; DB 3; Length 280;  
Best Local Similarity 23.2%; Pred. No. 35;  
RESULT 1499  
ID ABM91067 standard; protein; 318 AA.  
DE M. xanthus protein sequence, seq id 10266.  
PN US6833447-B1.  
PD 21-DEC-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match 5.1%; Score 85; DB 9; Length 318;  
Best Local Similarity 23.7%; Pred. No. 41;  
RESULT 1500  
ID ABB71546 standard; protein; 326 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 41430.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 5.1%; Score 85; DB 4; Length 326;  
Best Local Similarity 22.8%; Pred. No. 43;



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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:08:18 ; Search time 69.4882 Seconds  
(without alignments)  
3269.333 Million cell updates/sec

Title: US-10-063-510-6

Perfect score: 1657

Sequence: 1 MARCFSLVLLLTSTWTRLL.....NPRESKSPKNTVRCLEAEV 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1657	100.0	322	2	Q9UNP4_HUMAN
2	1643	99.2	322	2	Q8TC18_HUMAN
3	1638	98.9	322	2	Q9YSY7_HUMAN
4	1174	70.9	322	2	Q6UC88_BOVIN
5	1103	66.6	318	2	Q8BHC0_MOUSE
6	1095	66.1	318	2	Q99NE4_MOUSE
7	726.5	43.8	201	2	Q7YS22_PIG
8	245	14.8	392	2	Q58B15_XENLA
9	241	14.5	441	2	Q6GM56_XENLA
10	233.5	14.1	362	1	CD44_CRIGR
11	229.5	13.9	437	2	Q6P8A2_XENTR
12	227	13.7	364	2	Q70509_RAT
13	222.5	13.4	362	1	CD44_PAPHA
14	222	13.4	503	1	CD44_RAT
15	219.5	13.2	780	2	Q08779_RAT
16	219	13.2	265	2	Q98R55_ANAPL
17	217.5	13.1	398	2	Q90ZL8_ANAPL
18	212.5	12.8	431	1	CD44_MESAU
19	210	12.7	778	1	CD44_MOUSE
20	208.5	12.6	366	1	CD44_BOVIN
21	206.5	12.5	366	1	Q90ZL6_ANAPL
22	204	12.3	361	2	Q86T72_HUMAN
23	203.5	12.3	364	2	Q97569_CERSI
24	203.5	12.3	396	2	Q9W6S4_CHICK
25	203	12.3	742	2	Q9UJ36_HUMAN
26	202.5	12.2	351	1	CD44_CANFA
27	202	12.2	361	2	Q8N6S4_HUMAN
28	202	12.2	742	1	CD44_HUMAN
29	201	12.1	580	2	Q80X37_MOUSE
30	199.5	12.0	493	2	Q86227_HUMAN
31	199.5	12.0	493	2	Q5R9V4_PONPY
					Q9unf4 homo sapien
					Q8tc18 homo sapien
					Q9ysy7 homo sapien
					Q6uc88 bos taurus
					Q8bhc0 mus musculus
					Q99ne4 mus musculus
					Q7ys22 sus scrofa
					Q58e15 xenopus lae
					Q6gm56 xenopus lae
					P20944 cricetus
					Q6p8a2 xenopus tro
					Q70509 rattus norv
					P14745 papio hamad
					P26051 rattus norv
					Q08779 rattus norv
					Q98r55 anas platyr
					Q90zl8 anas platyr
					Q60522 m cd44 anti
					P15379 mus musculus
					Q29423 bos taurus
					Q86t72 homo sapien
					Q97569 ceratotheri
					Q9w6s4 gallus gall
					Q9ui36 homo sapien
					Q28284 canis fami
					Q8n6s4 homo sapien
					P16070 h cd44 anti
					Q80x37 mus musculus
					Q86227 homo sapien
					Q5r9v4 pongo pygma

Q9h5a4	homo sapien	338	12.0	32	199	Q9H5A4_HUMAN
Q9h5a5	homo sapien	719	11.9	33	197	Q9H5A5_HUMAN
Q92493	homo sapien	294	11.8	34	196	Q92493_HUMAN
Q9h5a7	homo sapien	676	11.6	35	191.5	Q9H5A7_HUMAN
Q9h5a3	homo sapien	271	11.5	36	191	Q9H5A3_HUMAN
Q9h5a6	homo sapien	470	11.5	37	191	Q9H5A6_HUMAN
Q05078	equus caball	359	11.2	38	186	CD44_HORSE
Q48195	tetraodon n	153	10.5	39	173.5	Q48195_TETNG
Q29011	sus scrofa	537	9.1	40	150	PGCA_PIG
P79787	gallus gall	2109	9.0	41	149.5	P79787_CHICK
F07898	gallus gall	2109	9.0	42	148.5	PGCA_CHICK
Q48988	tetraodon n	243	8.9	43	147.5	Q48988_TETNG
Q9bgh3	sus scrofa	494	8.8	44	145.5	Q9BGH3_PIG
Q90953	gallus gall	3562	8.8	45	145.5	CSPG2_CHICK
P98066	homo sapien	277	8.8	46	145	TSG6_HUMAN
Q53i17	homo sapien	277	8.8	47	145	Q53I17_HUMAN
Q08859	mus musculus	275	8.7	48	144	TSG6_MOUSE
Q5w1c4	bos taurus	280	8.7	49	144	Q5W1C4_BOVIN
Q6x168	bos taurus	2149	8.6	50	143	Q6X168_BOVIN
Q6x166	bos taurus	2327	8.6	51	143	Q6X166_BOVIN
P13608	bos taurus	2364	8.6	52	143	PGCA_BOVIN
Q6x167	bos taurus	2365	8.6	53	143	Q6X167_BOVIN
Q8r4y4	mus musculus	2571	8.5	54	140.5	STAB1_MOUSE
Q28343	canis fami	2333	8.4	55	139.5	PGCA_CANFA
P98065	oryctolagus	276	8.3	56	137	TSG6_RABIT
Q8r4u0	mus musculus	2559	8.2	57	136	STAB2_MOUSE
Q62913	rattus norv	514	8.0	58	133	Q62913_RAT
Q8c8m6	rattus norv	1431	8.0	59	133	STAB2_RAT
Q8wwq8	h stabilin	2551	8.0	60	133	STAB2_HUMAN
Q6p1d9	homo sapien	721	8.0	61	132.5	Q6P1D9_HUMAN
Q481v9	tetraodon n	1046	8.0	62	132	Q481V9_TETNG
P07897	rattus norv	2124	7.9	63	131.5	PGCA_RAT
Q48878	tetraodon n	314	7.9	64	131	Q48E78_TETNG
Q61282	mus musculus	2132	7.9	65	131	PGCA_MOUSE
Q61361	mus musculus	883	7.9	66	130.5	PGCB_MOUSE
P55068	rattus norv	883	7.9	67	130.5	PGCB_RAT
Q80wt7	mus musculus	883	7.9	68	130.5	Q80WT7_MOUSE
Q90wm2	xenopus lae	1152	7.9	69	130.5	Q90WM2_XENLA
P16112	homo sapien	2415	7.9	70	130.5	PGCA_HUMAN
Q9ny15	homo sapien	2570	7.9	71	130.5	STAB1_HUMAN
Q28062	bos taurus	912	7.8	72	128.5	PGCB_BOVIN
Q4rv64	tetraodon n	77	7.7	73	128	Q4RV64_TETNG
Q5t315	homo sapien	671	7.7	74	127.5	Q5T315_HUMAN
Q59f90	homo sapien	850	7.7	75	127.5	Q59F90_HUMAN
Q968w7	homo sapien	911	7.7	76	127.5	PGCB_HUMAN
Q58x10	homo sapien	911	7.7	77	127.5	Q58X10_HUMAN
Q5i051	xenopus lae	266	7.7	78	127	Q5I051_XENLA
Q62059	mus musculus	3358	7.6	79	126	CSPG2_MOUSE
Q5rg03	brachydanio	536	7.6	80	125.5	Q5RG03_BRARE
Q4t6a4	tetraodon n	1515	7.5	81	124.5	Q4T6A4_TETNG
Q4rup1	tetraodon n	2586	7.5	82	124	Q4RUP1_TETNG
Q48472	tetraodon n	386	7.5	83	123.5	Q48472_TETNG
Q4t8g9	tetraodon n	2760	7.4	84	123.5	Q4T8G9_TETNG
Q5b160	xenopus tro	383	7.4	85	122	Q5BJ60_XENTR
Q28670	oryctolagus	394	7.4	86	122	PGCA_RABIT
Q96886	homo sapien	360	7.3	87	121.5	HPLN3_HUMAN
Q48e77	tetraodon n	1091	7.3	88	121.5	Q48E77_TETNG
Q81wx2	homo sapien	516	7.3	89	121	Q81WX2_HUMAN
Q75213	brachydanio	1570	7.3	90	120.5	Q75213_BRARE
Q48h19	tetraodon n	313	7.2	91	120	Q48H19_TETNG
Q702x3	human herpe	411	7.2	92	119.5	Q702X4_HV1
Q72x17	xenopus lae	359	7.2	93	119	Q72X17_XENLA
Q55dv2	dictyosteli	1452	7.2	94	119	Q55DV2_DICTDI
P13611	homo sapien	3396	7.2	95	118.5	CSPG2_HUMAN
Q95fg9	homo sapien	3410	7.2	96	118.5	Q95FG9_HUMAN
Q9esm3	mus musculus	341	7.1	97	118	HPLN2_MOUSE
Q702x3	human herpe	397	7.1	98	117.5	Q702X3_HV1
Q9grv7	homo sapien	340	7.1	99	117	HPLN2_HUMAN
Q5t3j0	homo sapien	340	7.1	100	117	Q5T3J0_HUMAN
Q41qu7	gibberella	537	7.1	101	117	Q41QU7_GIBZE
Q8bs97	mus musculus	368	7.0	102	116	Q8BS97_MOUSE
Q4va91	mus musculus	368	7.0	103	116	Q4VA91_MOUSE
Q9erb4	rattus norv	2738	7.0	104	116	CSPG2_RAT

105	115.5	7.0	744	2	Q4RLD6_TETNG	Q4rlD6 tetraodon n	178	102.5	6.2	595	2	Q5UPW9_MIMIV	Q5upw9 mimivirus.
106	115	6.9	370	2	Q7M2W7_PIG	Q7m2w7 sus scrofa	179	102.5	6.2	699	2	Q8QVE9_9REOV	Q8qve9 eyach virus
107	115	6.9	394	2	Q5DC16_XENLA	Q5dc16 xenopus lae	180	102	6.2	391	2	Q753G3_ASHGO	Q753g3 ashbya goss
108	115	6.9	3381	1	CSFG2_BOVIN	P81282 bos taurus	181	102	6.2	404	2	Q702X0_HHV1	Q702x0 human herpe
109	114.5	6.9	1039	2	Q4S473_TETNG	Q4s473 tetraodon n	182	102	6.2	404	2	Q702Y3_HHV1	Q702y3 human herpe
110	114.5	6.9	1257	1	CSFG3_RAT	P55067 rattus norv	183	102	6.2	1879	2	Q4VZL0_CUCSA	Q4vzl0 cucumis sat
111	114	6.9	610	2	Q9N3C0_CAEBL	Q9n3c0 caenorhabdi	184	101.5	6.1	380	2	O02343_CAEBL	O02343 caenorhabdi
112	113.5	6.8	289	2	Q60T22_CAEBR	Q60t22 caenorhabdi	185	101.5	6.1	768	2	O60279_HUMAN	O60279 homo sapien
113	113.5	6.8	1290	2	Q9W6E1_CHICK	Q9w6e1 gallus gall	186	101.5	6.1	1853	2	Q7KT96_DROME	Q7kt96 drosophila
114	113	6.8	341	1	HPLN2_RAT	Q9esm2 rattus norv	187	101.5	6.1	1893	2	Q9NKC9_DROME	Q9nkc9 drosophila
115	113	6.8	459	2	Q54G90_DICDI	Q54g90 dictyosteli	188	101.5	6.1	4370	2	Q4Q1Q2_LEIMA	Q4q1q2 leishmania
116	113	6.8	892	1	LDLR2_XENLA	Q99088 xenopus lae	189	101	6.1	700	2	Q8TG00_ASPFU	Q8tg00 aspergillus
117	112.5	6.8	417	1	PCCB_FELCA	P41725 felis silve	190	101	6.1	700	2	Q4WS89_ASPFU	Q4ws89 aspergillus
118	112	6.8	210	2	Q8C9J7_MOUSE	Q8c9u7 mus musculu	191	101	6.1	708	2	Q18175_CAEBL	Q18175 caenorhabdi
119	112	6.8	390	1	VGLI1_HHV11	P06487 human herpe	192	101	6.1	1777	2	Q54FB8_DICDI	Q54fb8 dictyosteli
120	112	6.8	390	2	Q702X7_HHV1	Q702x7 human herpe	193	101	6.1	2535	2	Q755B8_ASHGO	Q755b8 ashbya goss
121	111.5	6.7	402	1	ODP2_MYCPN	P75392 mycoplasma	194	100.5	6.1	353	2	Q4IH62_GIBZE	Q4ih62 gibberella
122	111	6.7	354	2	Q86W61_HUMAN	Q86w61 homo sapien	195	100.5	6.1	402	1	HPLN4_HUMAN	H86uw6 homo sapien
123	111	6.7	359	2	Q5R1X6_RAT	Q5rlx6 rattus norv	196	100.5	6.1	411	2	Q702X5_HHV1	Q702x5 human herpe
124	110	6.6	363	2	Q6NV41_BRARE	Q6nv41 brachydanio	197	100.5	6.1	841	2	Q4Q5Z4_LEIMA	Q4q5z4 leishmania
125	109	6.6	816	2	Q70474_RAT	Q70474 rattus norv	198	100.5	6.1	1121	2	Q59YM6_CANAL	Q59ym6 candida alb
126	109	6.6	1321	1	CSFG3_HUMAN	Q41594 homo sapien	199	100.5	6.1	1121	2	Q7Z884_CANAL	Q7z884 candida alb
127	109	6.6	1335	2	Q4LE67_HUMAN	Q4le67 homo sapien	200	100	6.0	319	2	Q4S1V7_TETNG	Q4s1v7 tetraodon n
128	108.5	6.5	397	2	Q702X6_HHV1	Q702x6 human herpe	201	100	6.0	403	2	Q702W8_HHV1	Q702w8 human herpe
129	108.5	6.5	1441	2	Q4S3C4_TETNG	Q4s3c4 tetraodon n	202	100	6.0	404	2	Q702W6_HHV1	Q702w6 human herpe
130	108	6.5	354	1	HPLN1_HUMAN	P10915 homo sapien	203	100	6.0	404	2	Q702Y0_HHV1	Q702y0 human herpe
131	108	6.5	359	1	HPLN1_MOUSE	Q80wm5 mus musculu	204	100	6.0	441	2	Q5BA48_EMENI	Q5ba48 aspergillus
132	108	6.5	624	2	Q19780_CAEBL	Q19780 caenorhabdi	205	100	6.0	486	2	Q8FRY2_COREF	Q8fry2 corynebacte
133	107.5	6.5	739	2	O02360_CAEBL	O02360 caenorhabdi	206	100	6.0	738	2	Q5WN81_CAEBR	Q5wn81 caenorhabdi
134	107	6.5	354	1	HPLN1_RAT	P03994 rattus norv	207	100	6.0	1317	1	YQJ3_CAEBL	Y09550 caenorhabdi
135	107	6.5	355	1	HPLN1_CHICK	Q70354 gallus gall	208	99.5	6.0	335	2	Q60H44_BRARE	Q60h44 brachydanio
136	107	6.5	356	1	HPLN1_MOUSE	Q9qps5 mus musculu	209	99.5	6.0	478	2	Q7YX15_CAEBL	Q7yx15 caenorhabdi
137	107	6.5	527	2	Q54VQ0_DICDI	Q54vq0 dictyosteli	210	99.5	6.0	577	2	Q52GY0_CAEBL	Q52gy0 caenorhabdi
138	107	6.5	543	2	Q4YVC9_PLABE	Q4yvc9 plasmodium	211	99.5	6.0	1092	1	NCA12_XENLA	P36335 xenopus lae
139	107	6.5	862	2	Q9UF98_HUMAN	Q9uf98 homo sapien	212	99.5	6.0	1117	2	Q54SZ6_DICDI	Q54sz6 dictyosteli
140	107	6.5	956	2	Q60MG7_CAEBR	Q60mg7 caenorhabdi	213	99.5	6.0	1165	2	Q60NC3_CAEBR	Q60nc3 caenorhabdi
141	107	6.5	1268	1	CSFG3_MOUSE	P55066 mus musculu	214	99.5	6.0	2297	2	O5P243_BRARE	O5p243 brachydanio
142	107	6.5	1321	1	CSFG3_PANTR	Q5i841 pan troglod	215	99	6.0	178	2	Q8FQJ3_COREF	Q8fqj3 corynebacte
143	107	6.5	1795	2	Q76894_DROME	Q76894 drosophila	216	99	6.0	388	2	Q4H2F0_HPV27	Q4h2f0 human papil
144	106.5	6.4	1390	2	Q54GX9_DICDI	Q54gx9 dictyosteli	217	99	6.0	410	1	GPC5B_MOUSE	Q92320 mus musculu
145	106	6.4	1059	2	Q5ISN4_MACFA	Q5isn4 macaca fasc	218	99	6.0	545	2	Q5A7A3_CANAL	Q5a7a3 candida alb
146	106	6.4	1153	2	Q4IAN9_GIBZE	Q4ian9 gibberella	219	99	6.0	604	2	Q6E9B8_LISMO	Q6e9b8 listeria mo
147	105.5	6.4	374	2	Q9Z209_CRIGR	Q9z209 cricetus	220	99	6.0	620	2	O5A7H9_CANAL	O5a7h9 candida alb
148	105.5	6.4	573	2	Q8CJD9_RAT	Q8cjd9 rattus norv	221	99	6.0	856	2	Q20253_CAEBL	Q20253 caenorhabdi
149	105.5	6.4	830	2	Q5CA10_YARLI	Q5cay0 yarrowia li	222	99	6.0	1100	2	Q8CCT8_MOUSE	Q8ccct8 mus musculu
150	105	6.3	354	1	HPLN1_BOVIN	P55252 bos taurus	223	99	6.0	5376	1	ZAN_MOUSE	Q9n528 caenorhabdi
151	105	6.3	438	2	Q4X548_PLACH	Q4x548 plasmodium	224	98.5	5.9	204	2	Q9NSZ8_CAEBL	Q9nsz8 caenorhabdi
152	105	6.3	463	2	Q7RNE3_PLAYO	Q7rne3 plasmodium	225	98.5	5.9	346	2	Q7S973_NEUCR	Q7s973 neurospora
153	105	6.3	480	2	O5CGV9_CRYHO	O5cgv9 cryptospori	226	98.5	5.9	397	2	Q702W7_HHV1	Q702w7 human herpe
154	105	6.3	612	2	Q6CD44_YARLI	Q6cd44 yarrowia li	227	98.5	5.9	397	2	Q702X1_HHV1	Q702x1 human herpe
155	104.5	6.3	862	1	CSFG2_MACNE	Q28858 macaca neme	228	98.5	5.9	425	2	Q702W3_HHV1	Q702w3 human herpe
156	104	6.3	139	2	O95370_HUMAN	Q95370 homo sapien	229	98.5	5.9	578	2	O63ZX6_MOUSE	O63zx6 mus musculu
157	104	6.3	354	1	HPLN1_HORSE	Q28381 equus cabal	230	98.5	5.9	889	2	Q4RUP0_TETNG	Q4rup0 tetraodon n
158	104	6.3	354	1	HPLN1_PIG	P10859 sus scrofa	231	98.5	5.9	1126	2	Q9VGK5_DROME	Q9vgk5 drosophila
159	104	6.3	627	2	Q8MPJ3_DICDI	Q8mpj9 dictyosteli	232	98.5	5.9	1203	2	O6ZQ56_MOUSE	O6zq56 mus musculu
160	104	6.3	681	2	Q555I9_DICDI	Q555i9 dictyosteli	233	98.5	5.9	3178	1	Y8S93_CAEBL	Y09624 caenorhabdi
161	104	6.3	1716	2	Q9I7Q8_DROME	Q9i7q8 drosophila	234	98	5.9	384	2	Q9DW41_RCMVM	Q9dw41 rat cytomeg
162	104	6.3	1912	2	Q9VS99_DROME	Q9vs99 drosophila	235	98	5.9	390	2	Q702W4_HHV1	Q702w4 human herpe
163	103.5	6.2	288	2	Q6QPC9_ADEN	Q6qpc9 simian aden	236	98	5.9	505	2	Q4FYQ6_LEIMA	Q4fyq6 leishmania
164	103.5	6.2	616	2	O5EBE4_BRARE	O5ebe4 brachydanio	237	98	5.9	604	2	O8GMR7_LISMO	O8gm7 listeria mo
165	103.5	6.2	952	2	O86A80_DICDI	Q86a80 dictyosteli	238	98	5.9	604	2	Q6E9T6_LISMO	Q6e9t6 listeria mo
166	103.5	6.2	1197	2	Q5IS86_PPRIM	Q5is86 saimiri bol	239	98	5.9	604	2	O8GMR1_LISMO	O8gm1 listeria mo
167	103.5	6.2	1254	2	Q94185_CAEBL	Q94185 caenorhabdi	240	98	5.9	771	2	Q22783_CAEBL	Q22783 caenorhabdi
168	103.5	6.2	1592	2	Q5AWR8_EMENI	Q5awr8 aspergillus	241	98	5.9	1015	2	Q54V57_DICDI	Q54v57 dictyosteli
169	103	6.2	80	2	O86U21_HUMAN	Q86u21 homo sapien	242	98	5.9	2112	2	Q9VEL9_DROME	Q9vel9 drosophila
170	103	6.2	231	2	O5T316_HUMAN	O5t316 homo sapien	243	97.5	5.9	297	2	Q7PS65_ANOGA	Q7prs65 anopheles g
171	103	6.2	232	2	O5BDD1_EMENI	O5bdd1 aspergillus	244	97.5	5.9	298	2	Q9Z0P0_EAT	Q9z0p0 rattus norv
172	102.5	6.2	182	2	Q8I0D8_DROME	Q8i0d8 drosophila	245	97.5	5.9	318	2	O86RN3_DICDI	O86rn3 dictyosteli
173	102.5	6.2	183	2	Q9VT37_DROME	Q9vt37 drosophila	246	97.5	5.9	385	2	Q9NHU9_DROMI	Q9nhu9 drosophila
174	102.5	6.2	497	2	Q8QVC4_9REOV	Q8qvc4 eyach virus	247	97.5	5.9	836	2	O55DF3_DICDI	O55df3 dictyosteli
175	102.5	6.2	553	2	Q8F932_LEPIN	Q8f932 leptospira	248	97.5	5.9	909	1	LDLR1_XENLA	Q99087 xenopus lae
176	102.5	6.2	557	2	Q72V13_LEPIC	Q72v13 leptospira	249	97	5.9	294	2	Q54FY4_DICDI	Q54fy4 dictyosteli
177	102.5	6.2	590	2	Q5BG25_EMENI	Q5bg25 aspergillus	250	97	5.9	316	2	Q9U9J0_TOXCA	Q9u9j0 toxocara ca

251	97	5.9	404	2	Q702Y6_HHV1	Q702Y6 human herpe	324	94.5	5.7	383	2	Q702Y4_HHV1	Q702Y4 human herpe
252	97	5.9	604	2	Q6E9K8_LISMO	Q6E9K8 listeria mo	325	94.5	5.7	395	2	Q70220_HHV1	Q70220 human herpe
253	97	5.9	604	2	Q6E9X2_LISMO	Q6E9X2 listeria mo	326	94.5	5.7	405	2	Q41NQ5_GIBZE	Q41NQ5 gibberella
254	97	5.9	604	2	Q6EA16_LISMO	Q6EA16 listeria mo	327	94.5	5.7	494	2	Q4WG24_ASFPU	Q4WG24 aspergillus
255	97	5.9	648	2	Q4QG32_LEIMA	Q4QG32 leishmania	328	94.5	5.7	510	2	Q5YFP0_5VIRU	Q5YFP0 singapore g
256	97	5.9	1159	2	Q5GG09_DICDI	Q5GG09 dictyosteli	329	94.5	5.7	519	2	Q7YTR7_CABEL	Q7YTR7 caenorhabdi
257	97	5.9	1604	2	Q4SNK3_TETNG	Q4SNK3 tetraodon n	330	94.5	5.7	539	2	Q54GL8_DICDI	Q54GL8 dictyosteli
258	96.5	5.8	268	2	Q5ATR9_EMENI	Q5ATR9 aspergillus	331	94.5	5.7	698	2	Q61SH2_CABBR	Q61SH2 caenorhabdi
259	96.5	5.8	276	2	Q54NG3_DICDI	Q54NG3 dictyosteli	332	94.5	5.7	814	2	Q5AG78_CANAL	Q5AG78 candida alb
260	96.5	5.8	385	2	Q9N666_DROMI	Q9N666 drosophila	333	94.5	5.7	1007	2	Q55CR8_DICDI	Q55CR8 dictyosteli
261	96.5	5.8	385	2	Q9NHU6_DROMI	Q9NHU6 drosophila	334	94.5	5.7	1007	2	Q5POB5_AZOSE	Q5POB5 azarcus sp
262	96.5	5.8	397	2	Q702Y5_HHV1	Q702Y5 human herpe	335	94.5	5.7	1066	2	Q76NW3_DICDI	Q76NW3 dictyosteli
263	96.5	5.8	407	2	Q564S9_CABEL	Q564S9 caenorhabdi	336	94.5	5.7	1079	2	Q9N4S7_CABEL	Q9N4S7 caenorhabdi
264	96.5	5.8	465	1	YHU6_YEAST	Y38845 saccharomyc	337	94.5	5.7	1390	2	Q17602_CABEL	Q17602 dictyosteli
265	96.5	5.8	604	2	Q8GNS1_LISMO	Q8GNS1 listeria mo	338	94.5	5.7	1622	2	Q54G21_DICDI	Q54G21 dictyosteli
266	96.5	5.8	731	1	NOG2_CRYGA	Q6T918 cryptococcu	339	94.5	5.7	1942	2	Q8G1Z7_LACDL	Q8G1Z7 lactobacill
267	96.5	5.8	961	2	Q5ATY9_EMENI	Q5ATY9 aspergillus	340	94.5	5.7	3370	2	Q811N9_PLAP7	Q811N9 plasmodium
268	96.5	5.8	961	2	Q92223_EMENI	Q92223 emericella	341	94	5.7	239	2	Q55C69_DICDI	Q55C69 dictyosteli
269	96.5	5.8	1031	2	Q925N8_MOUSE	Q925N8 mus musculu	342	94	5.7	639	2	Q8GNR8_LISMO	Q8GNR8 listeria mo
270	96.5	5.8	1031	2	Q9D071_MOUSE	Q9D071 m mus muscu	343	94	5.7	639	2	Q6E8W8_LISMO	Q6E8W8 listeria mo
271	96.5	5.8	1065	2	Q50ZP1_ENTHI	Q50ZP1 entamoeba h	344	94	5.7	639	2	Q6E922_LISMO	Q6E922 listeria mo
272	96.5	5.8	1403	1	LARP_DROME	Q9VAU5 drosophila	345	94	5.7	639	2	Q6E9G6_LISMO	Q6E9G6 listeria mo
273	96	5.8	173	2	Q4KXZ2_CEREL	Q4KXZ2 cervus elap	346	94	5.7	639	2	Q6EA26_LISMO	Q6EA26 listeria mo
274	96	5.8	232	2	Q4V322_DROME	Q4V322 drosophila	347	94	5.7	639	2	Q6EAF0_LISMO	Q6EAF0 listeria mo
275	96	5.8	236	2	Q4V400_DROME	Q4V400 drosophila	348	94	5.7	639	2	Q6EAF0_LISMO	Q6EAF0 listeria mo
276	96	5.8	429	2	Q76430_CABEL	Q76430 caenorhabdi	349	94	5.7	769	2	Q00816_TOXGO	Q00816 toxoplasma
277	96	5.8	449	2	Q71UN8_CABEL	Q71UN8 caenorhabdi	350	94	5.7	989	2	Q83U76_CHLTR	Q83U76 chlamydia c
278	96	5.8	481	2	Q9XUP4_CABEL	Q9XUP4 caenorhabdi	351	94	5.7	989	2	Q84FUG_CHLTR	Q84FUG chlamydia c
279	96	5.8	549	2	Q54WC8_DICDI	Q54WC8 dictyosteli	352	94	5.7	1067	2	Q5BGE6_EMENI	Q5BGE6 aspergillus
280	96	5.8	553	2	Q95X13_CABEL	Q95X13 caenorhabdi	353	94	5.7	1241	1	PER_DROPS	P12348 drosophila
281	96	5.8	556	2	Q6DEK7_BRARE	Q6DEK7 brachydanio	354	94	5.7	1241	1	Q75JCO_DICDI	Q75JCO dictyosteli
282	96	5.8	604	2	Q6E9R2_LISMO	Q6E9R2 listeria mo	355	93.5	5.6	278	2	Q4WIP3_ASFPU	Q4WIP3 aspergillus
283	96	5.8	604	2	Q6E9R8_LISMO	Q6E9R8 listeria mo	356	93.5	5.6	296	2	Q6P9X9_RAT	Q6P9X9 ratius norv
284	96	5.8	604	2	Q6E9A7_LISMO	Q6E9A7 listeria mo	357	93.5	5.6	383	2	Q702W5_HHV1	Q702W5 human herpe
285	96	5.8	604	2	Q724K9_LISNF	Q724K9 listeria mo	358	93.5	5.6	385	2	Q9NHU8_DROMI	Q9NHU8 drosophila
286	96	5.8	625	2	Q58SF3_DROSI	Q58SF3 drosophila	359	93.5	5.6	498	2	Q6FWR9_CANGA	Q6FWR9 candida gla
287	96	5.8	625	2	Q58SH8_DROSI	Q58SH8 drosophila	360	93.5	5.6	607	2	Q8GNS0_LISMO	Q8GNS0 listeria mo
288	96	5.8	625	2	Q5ELN3_DROSI	Q5ELN3 drosophila	361	93.5	5.6	613	2	Q51TE4_MAGGR	Q51TE4 magnaporthe
289	96	5.8	625	2	Q6V6E1_DROSI	Q6V6E1 drosophila	362	93.5	5.6	626	2	Q9NDD1_LEITR	Q9NDD1 leishmania
290	96	5.8	732	2	Q54FU3_DICDI	Q54FU3 dictyosteli	363	93.5	5.6	802	2	Q60LR3_CABBR	Q60LR3 caenorhabdi
291	96	5.8	804	2	Q54126_DICDI	Q54126 dictyosteli	364	93.5	5.6	980	2	Q54T19_DICDI	Q54T19 dictyosteli
292	96	5.8	1038	2	Q4T3K8_TETNG	Q4T3K8 tetraodon n	365	93.5	5.6	1033	2	Q4HYG6_GIBZE	Q4HYG6 gibberella
293	96	5.8	1088	1	NCA11_XENLA	P16170 xenopus lae	366	93.5	5.6	1595	2	Q5SBM3_LACSC	Q5SBM3 lactobacill
294	96	5.8	1155	2	Q4JA20_SULAC	Q4JA20 sulfolobus	367	93	5.6	261	2	Q70CC2_EINTE	Q70CC2 emieria ten
295	96	5.8	1569	2	Q4DM4_DICDI	Q4DM4 dictyosteli	368	93	5.6	311	2	Q4E019_CABEL	Q4E019 caenorhabdi
296	95.5	5.8	266	2	Q4HZD3_GIBZE	Q4HZD3 gibberella	369	93	5.6	385	2	Q8T817_DROPS	Q8T817 drosophila
297	95.5	5.8	376	1	MID2_YEAST	P36027 saccharomyc	370	93	5.6	385	2	Q8T819_DROPS	Q8T819 drosophila
298	95.5	5.8	385	2	Q9NHU5_DROMI	Q9NHU5 drosophila	371	93	5.6	405	2	Q5EFZ7_CHICK	Q5EFZ7 gallus gall
299	95.5	5.8	385	2	Q9NHU7_DROMI	Q9NHU7 drosophila	372	93	5.6	448	2	Q56H22_BRARE	Q56H22 brachydanio
300	95.5	5.8	469	2	Q54P62_DICDI	Q54P62 dictyosteli	373	93	5.6	572	2	Q58SM0_DROME	Q58SM0 drosophila
301	95.5	5.8	589	2	Q5S879_9MONO	Q5S879 avian pneum	374	93	5.6	572	2	Q58SM7_DROME	Q58SM7 drosophila
302	95.5	5.8	996	2	Q5BF33_EMENI	Q5BF33 aspergillus	375	93	5.6	576	2	Q61MD1_CABBR	Q61MD1 caenorhabdi
303	95.5	5.8	1259	2	Q869X4_DICDI	Q869X4 dictyosteli	376	93	5.6	608	2	Q50MX9_ENTHI	Q50MX9 entamoeba h
304	95.5	5.8	5374	2	Q99ND0_MOUSE	Q99ND0 mus musculu	377	93	5.6	629	2	Q24017_DROME	Q24017 drosophila
305	95	5.7	273	2	Q61002_MOUSE	Q61002 mus musculu	378	93	5.6	629	2	Q5ELT0_DROME	Q5ELT0 drosophila
306	95	5.7	281	2	Q4KSI9_9ADEN	Q4KSI9 human adeno	379	93	5.6	629	2	Q5ELT4_DROME	Q5ELT4 drosophila
307	95	5.7	281	2	Q702W9_HHV1	Q702W9 human herpe	380	93	5.6	629	2	Q5ELV0_DROME	Q5ELV0 drosophila
308	95	5.7	424	2	Q9FCW0_ARATH	Q9FCW0 arabidopsis	381	93	5.6	639	2	Q8GNR5_LISMO	Q8GNR5 listeria mo
309	95	5.7	538	2	Q69379_LISMO	Q69379 listeria mo	382	93	5.6	639	2	Q8GNR6_LISMO	Q8GNR6 listeria mo
310	95	5.7	601	2	Q5ZKX1_CHICK	Q5ZKX1 gallus gall	383	93	5.6	639	2	Q6E8X4_LISMO	Q6E8X4 listeria mo
311	95	5.7	604	2	Q9RQ13_LISMO	Q9RQ13 listeria mo	384	93	5.6	758	2	Q54UR7_DICDI	Q54UR7 dictyosteli
312	95	5.7	604	2	Q6EAD8_LISMO	Q6EAD8 listeria mo	385	93	5.6	791	2	Q51UQ4_MAGGR	Q51UQ4 magnaporthe
313	95	5.7	639	2	Q8GNR2_LISMO	Q8GNR2 listeria mo	386	93	5.6	916	2	Q7VZ10_MONBE	Q7VZ10 monosiga br
314	95	5.7	639	2	Q6E904_LISMO	Q6E904 listeria mo	387	93	5.6	928	2	Q4SL40_TETNG	Q4SL40 tetraodon n
315	95	5.7	639	2	Q6E982_LISMO	Q6E982 listeria mo	388	93	5.6	930	2	Q9YBL5_ASRPE	Q9YBL5 aeropyrum p
316	95	5.7	639	2	Q6E9Q6_LISMO	Q6E9Q6 listeria mo	389	93	5.6	1034	2	Q613E9_CABBR	Q613E9 caenorhabdi
317	95	5.7	753	2	Q6PPF4_BRARE	Q6PPF4 brachydanio	390	93	5.6	1285	2	Q4RXD7_TETNG	Q4RXD7 tetraodon n
318	95	5.7	1203	2	Q6C028_YARLI	Q6C028 yarrowia li	391	93	5.6	1292	2	Q4RHM3_TETNG	Q4RHM3 tetraodon n
319	95	5.7	1578	2	Q55C84_DICDI	Q55C84 dictyosteli	392	93	5.6	1349	2	Q8WQ04_HUMAN	Q8WQ04 homo sapien
320	95	5.7	1748	2	Q54FL9_DICDI	Q54FL9 dictyosteli	393	93	5.6	1413	2	Q54F12_DICDI	Q54F12 dictyosteli
321	94.5	5.7	345	2	Q691Y8_ANOSA	Q691Y8 anolis sagr	394	92.5	5.6	215	2	Q614I3_CABBR	Q614I3 caenorhabdi
322	94.5	5.7	359	2	TIMDI_HUMAN	Q964d42 homo sapien	395	92.5	5.6	247	2	Q8MKY7_DROME	Q8MKY7 drosophila
323	94.5	5.7	383	2	Q702X5_HHV1	Q702X5 human herpe	396	92.5	5.6	296	2	Q923D3_MOUSE	Q923D3 mus musculu

397	92.5	5.6	299	2	Q4HYT1_GIBZE	Q4hyt1 gibberella	470	91.5	5.5	639	2	Q6E8V0_LISMO	Q6e8v0 listeria mo
398	92.5	5.6	300	1	JAM1_MOUSE	Q8f792 mus musculus	471	91.5	5.5	639	2	Q6E9I4_LISMO	Q6e9i4 listeria mo
399	92.5	5.6	385	2	Q9NHV2_DROMI	Q9nhv2 drosophila	472	91.5	5.5	639	2	Q6E9X8_LISMO	Q6e9x8 listeria mo
400	92.5	5.6	400	1	HPLN4_MOUSE	Q80wm4 mus musculus	473	91.5	5.5	639	2	Q6EA56_LISMO	Q6ea56 listeria mo
401	92.5	5.6	446	2	Q6EMV3_OCEIH	Q6emv3 oceanobacil	474	91.5	5.5	639	2	Q6EAA4_LISMO	Q6eaa4 listeria mo
402	92.5	5.6	448	2	Q61C01_CAEBR	Q61c01 caenorhabdi	475	91.5	5.5	639	2	Q8GNS2_LISMO	Q8gns2 listeria mo
403	92.5	5.6	453	2	Q5KCR5_CRYNE	Q5kcr5 cryptococcu	476	91.5	5.5	639	2	Q6E8T8_LISMO	Q6e8t8 listeria mo
404	92.5	5.6	466	2	Q5SI17_CRYNE	Q5si17 cryptococcu	477	91.5	5.5	651	2	Q6E8T8_LISMO	Q6e8t8 listeria mo
405	92.5	5.6	466	2	Q5KCR4_CRYNE	Q5kcr4 cryptococcu	478	91.5	5.5	681	1	Q61Y25_CAEBR	Q61y25 caenorhabdi
406	92.5	5.6	487	2	Q54G14_DICDI	Q54g14 dictyosteli	479	91.5	5.5	681	1	Q71VM1_9MONO	Q71vm1 lake victor
407	92.5	5.6	487	2	Q4UHA9_THEAN	Q4uha9 theilleria a	480	91.5	5.5	860	2	Q7RZN3_NEUCR	Q7rzn3 neurospora
408	92.5	5.6	569	2	Q5KGV9_LISMO	Q5kgv9 listeria mo	481	91.5	5.5	1138	2	Q4UNB8_RICFE	Q4unb8 rickettsia
409	92.5	5.6	604	2	Q6EAA4_LISMO	Q6eaa4 listeria mo	482	91.5	5.5	1148	2	Q6CBJ2_YARLI	Q6cbj2 yarrowia li
410	92.5	5.6	623	2	Q57602_ICTPU	Q57602 icतालurus p	483	91.5	5.5	1167	2	Q7RWQ7_NEUCR	Q7rwq7 neurospora
411	92.5	5.6	629	2	Q4QG70_LEIMA	Q4qg70 leishmania	484	91.5	5.5	1481	2	Q4PI52_USTMA	Q4pi52 ustilago ma
412	92.5	5.6	638	2	Q55FT4_DICDI	Q55ft4 dictyosteli	485	91.5	5.5	1783	2	Q51UR4_MAGGR	Q51ur4 magnaporthe
413	92.5	5.6	704	2	Q73H41_WOLPM	Q73h41 wolbachia p	486	91	5.5	174	2	Q7YTP1_CAEBL	Q7ytp1 caenorhabdi
414	92.5	5.6	784	2	Q7S3V6_NEUCR	Q7s3v6 neurospora	487	91	5.5	198	2	Q7X3M4_LISMO	Q7x3m4 listeria mo
415	92.5	5.6	812	2	Q55D98_DICDI	Q55d98 dictyosteli	488	91	5.5	213	2	Q5T317_HUMAN	Q5t317 homo sapien
416	92.5	5.6	927	2	Q2I811_CAEBL	Q2i811 caenorhabdi	489	91	5.5	246	2	Q9UAV4_CAEBL	Q9uav4 caenorhabdi
417	92.5	5.6	1491	2	Q4QDK4_LEIMA	Q4qdk4 leishmania	490	91	5.5	346	2	Q52J88_9SAUR	Q52j88 heteronotia
418	92.5	5.6	1636	1	BUD3_YEAST	P25558 saccharomyc	491	91	5.5	346	2	Q52J76_9SAUR	Q52j76 heteronotia
419	92.5	5.6	2048	2	Q55GCI_DICDI	Q55gci dictyosteli	492	91	5.5	450	2	Q8CV85_OCEIH	Q8cv85 oceanobacil
420	92.5	5.6	2138	2	Q759S3_ASHGO	Q759s3 ashbya goss	493	91	5.5	488	2	Q09586_CAEBL	Q09586 caenorhabdi
421	92	5.6	347	2	Q85YW5_DROME	Q85yw5 drosophila	494	91	5.5	591	2	Q4WHJ8_ASPTU	Q4whj8 aspergillus
422	92	5.6	429	2	P79046_9ASCO	P79046 humicola gr	495	91	5.5	596	2	Q6PIT0_XENTR	Q6pit0 xenopus tro
423	92	5.6	500	2	Q864U4_BOVIN	Q864u4 bos taurus	496	91	5.5	600	2	Q4VBEO_XENTR	Q4vbeo xenopus tro
424	92	5.6	504	2	Q54F08_DICDI	Q54fd8 dictyosteli	497	91	5.5	620	2	Q4SVR3_ENCCU	Q4svr3 encephalito
425	92	5.6	567	2	Q4P6Q2_USTMA	Q4p6q2 ustilago ma	498	91	5.5	629	2	Q5ELR5_DROME	Q5elr5 drosophila
426	92	5.6	574	2	Q58SM3_DROME	Q58sm3 drosophila	499	91	5.5	629	2	Q5ELR7_DROME	Q5elr7 drosophila
427	92	5.6	586	2	Q5B1Y4_EMENI	Q5b1y4 aspergillus	500	91	5.5	629	2	Q5ELS3_DROME	Q5els3 drosophila
428	92	5.6	604	2	Q3JNA2_LISMO	Q3jna2 listeria mo	501	91	5.5	639	2	Q6E964_LISMO	Q6e964 listeria mo
429	92	5.6	629	2	Q5ELR9_DROME	Q5elr9 drosophila	502	91	5.5	639	2	Q6EAI0_LISMO	Q6eai0 listeria mo
430	92	5.6	629	2	Q5ELS5_DROME	Q5els5 drosophila	503	91	5.5	644	2	Q54D31_DICDI	Q54d31 dictyosteli
431	92	5.6	629	2	Q5ELU4_DROME	Q5elu4 drosophila	504	91	5.5	693	2	Q7PYV7_ANOGA	Q7pyv7 anopheles g
432	92	5.6	639	2	Q6EA92_LISMO	Q6ea92 listeria mo	505	91	5.5	701	2	Q8ZMG4_PYRAE	Q8zmg4 pyrobaculum
433	92	5.6	644	2	Q6CF33_YARLI	Q6cf33 yarrowia li	506	91	5.5	730	2	Q86A28_DICDI	Q86a28 dictyosteli
434	92	5.6	659	2	Q95X82_CAEBL	Q95x82 caenorhabdi	507	91	5.5	876	2	Q619L5_CAEBR	Q619l5 caenorhabdi
435	92	5.6	668	2	Q4QCH4_LEIMA	Q4qch4 leishmania	508	91	5.5	1246	2	Q51FG7_ENTHI	Q51fg7 entamoeba h
436	92	5.6	741	2	Q6CH88_YARLI	Q6ch88 yarrowia li	509	91	5.5	1398	2	Q869T5_DICDI	Q869t5 dictyosteli
437	92	5.6	828	2	Q5B819_EMENI	Q5b819 aspergillus	510	91	5.5	1842	2	Q4N830_THEPA	Q4n830 theileria p
438	92	5.6	846	2	O01699_CAEBL	O01699 caenorhabdi	511	91	5.5	2162	2	Q09515_CAEBL	Q09515 caenorhabdi
439	92	5.6	907	2	Q6CT08_KJULA	Q6ctd8 kiuyveromyc	512	91	5.5	2176	2	Q54VP0_DICDI	Q54vp0 dictyosteli
440	92	5.6	966	1	SSN6_YEAST	P14922 saccharomyc	513	91	5.5	4262	2	Q685J2_HUMAN	Q685j2 homo sapien
441	92	5.6	1170	2	Q54PK2_DICDI	Q54pk2 dictyosteli	514	91	5.5	4493	2	Q685J3_HUMAN	Q685j3 homo sapien
442	92	5.6	1269	2	Q54CA1_DICDI	Q54cal dictyosteli	515	90.5	5.5	306	2	Q54UW3_DICDI	Q54uw3 plasmodium
443	92	5.6	1343	2	Q54XT5_DICDI	Q54xt5 dictyosteli	516	90.5	5.5	336	2	Q4Z0P5_PLABE	Q4z0p5 plasmodium
444	92	5.6	1505	2	Q54VU4_DICDI	Q54vu4 dictyosteli	517	90.5	5.5	360	2	Q4WG94_ASPTU	Q4wg94 aspergillus
445	92	5.6	1720	2	Q81486_PLAF7	Q81486 plasmodium	518	90.5	5.5	385	2	Q9NHV0_DROMI	Q9nhv0 drosophila
446	92	5.6	2829	1	APC_XENLA	P70039 xenopus lae	519	90.5	5.5	385	2	Q9NHV3_DROMI	Q9nhv3 drosophila
447	91.5	5.5	161	2	Q6CP23_KJULA	Q6cp23 kiuyveromyc	520	90.5	5.5	406	2	Q528W4_MAGGR	Q528w4 magnaporthe
448	91.5	5.5	198	2	Q7WRT1_LISMO	Q7wrt1 listeria mo	521	90.5	5.5	408	2	Q6UDF5_9HERP	Q6udf5 psittacid h
449	91.5	5.5	198	2	Q7X384_LISMO	Q7x384 listeria mo	522	90.5	5.5	461	2	Q6C2X8_YARLI	Q6c2x8 yarrowia li
450	91.5	5.5	300	2	Q8VC39_MOUSE	Q8vc39 mus musculu	523	90.5	5.5	496	2	Q55D06_DICDI	Q55d06 dictyosteli
451	91.5	5.5	305	2	Q8R183_MOUSE	Q8r183 mus musculu	524	90.5	5.5	575	1	CH61_CUCMA	Q05045 cucurbita m
452	91.5	5.5	338	2	Q6EAA4_LISMO	Q6eaa4 listeria mo	525	90.5	5.5	595	2	Q5ANA0_CANAL	Q5ana0 candida alb
453	91.5	5.5	383	2	Q51693_HHV1	Q51693 human herpe	526	90.5	5.5	659	2	Q59R26_CANAL	Q59r26 candida alb
454	91.5	5.5	383	2	Q702X8_HHV1	Q702x8 human herpe	527	90.5	5.5	662	1	MUC1_XENLA	Q50549 xenopus lae
455	91.5	5.5	385	2	Q9NHV1_DROMI	Q9nhv1 drosophila	528	90.5	5.5	678	2	Q54U48_DICDI	Q54u48 dictyosteli
456	91.5	5.5	411	1	LAMP2_RAT	P17046 rattus norv	529	90.5	5.5	690	2	Q66S18_9UROC	Q66s18 oikopleura
457	91.5	5.5	411	2	Q6P6W1_RAT	Q6p6w1 rattus norv	530	90.5	5.5	862	2	Q615W4_CAEBR	Q615w4 caenorhabdi
458	91.5	5.5	497	2	Q8QVC5_9REOV	Q8qvc5 eyach virus	531	90.5	5.5	952	2	Q9U3P1_CAEBL	Q9u3p1 caenorhabdi
459	91.5	5.5	538	2	Q76H84_STRMU	Q76h84 streptococc	532	90.5	5.5	972	2	Q60Q42_CAEBR	Q60q42 caenorhabdi
460	91.5	5.5	573	2	Q69380_LISMO	Q69380 listeria mo	533	90.5	5.5	1084	2	Q55A66_DICDI	Q55a66 dictyosteli
461	91.5	5.5	579	2	Q5CYK7_CRYPV	Q5cyk7 cryptospori	534	90.5	5.5	1084	2	Q86LA6_DICDI	Q86la6 dictyosteli
462	91.5	5.5	588	2	Q5ANG0_CANAL	Q5ang0 candida alb	535	90.5	5.5	1126	2	Q5CIS2_CRYHO	Q5cis2 cryptospori
463	91.5	5.5	604	2	Q8GNR3_LISMO	Q8gnr3 listeria mo	536	90.5	5.5	1175	2	Q9VRL7_DROME	Q9vrl7 drosophila
464	91.5	5.5	604	2	Q8E8U4_LISMO	Q8e8u4 listeria mo	537	90.5	5.5	1400	2	Q5FBC4_DICDI	Q5fbc4 dictyosteli
465	91.5	5.5	627	2	Q7RW72_NEUCR	Q7rw72 neurospora	538	90.5	5.5	1711	1	NUT214_DROME	Q9wix4 drosophila
466	91.5	5.5	633	2	Q9JMV6_LISMO	Q9jmv6 listeria mo	539	90.5	5.5	1976	2	Q9V9I8_DROME	Q9v9i8 neurospora
467	91.5	5.5	633	2	Q4TVQ6_LISMO	Q4tvq6 listeria mo	540	90.5	5.5	2300	2	Q7SFP6_NEUCR	Q7sfp6 neurospora
468	91.5	5.5	639	1	ACTA_LISMO	P33379 listeria mo	541	90	5.4	294	2	Q4V3X0_DROME	Q4v3x0 drosophila
469	91.5	5.5	639	2	Q8GNR9_LISMO	Q8gnr9 listeria mo	542	90	5.4	388	1	VE2_HPVT27	P36789 human papil

543	90	5.4	474	2	Q417B2_GIBZE	Q417b2 gibberella	616	89	5.4	516	2	Q5CM29_CRYHO	Q5cm29 cryptospori
544	90	5.4	488	2	Q4V3Z8_DROME	Q4v3z8 drosophila	617	89	5.4	589	2	Q4N7T4_THRPA	Q4n7t4 theleria p
545	90	5.4	508	2	Q54BP8_DICDI	Q54bp8 dictyostelli	618	89	5.4	603	2	Q6CE49_YARLI	Q6ce49 yarrowia li
546	90	5.4	511	2	Q5A7R7_CANAL	Q5a7r7 candida alb	619	89	5.4	666	2	Q7QXK0_GIALA	Q7qxk0 giardia lam
547	90	5.4	540	2	Q7SF17_NEUCR	Q7sf17 neurospora	620	89	5.4	714	2	Q9NGW9_DICDI	Q9ngw9 dictyostelli
548	90	5.4	560	2	Q54LP6_DICDI	Q54lp6 dictyostelli	621	89	5.4	770	2	Q5SG55_DICDI	Q5sg55 dictyostelli
549	90	5.4	572	2	Q58SM4_DROME	Q58sm4 drosophila	622	89	5.4	833	2	Q8IRC1_DROME	Q8irc1 drosophila
550	90	5.4	572	2	Q58SM6_DROME	Q58sm6 drosophila	623	89	5.4	851	2	Q9VZ10_DROME	Q9vz10 drosophila
551	90	5.4	598	2	Q5ELV8_DROS1	Q5elv8 drosophila	624	89	5.4	860	2	Q5WNQ1_CAEBR	Q5wnq1 caenorhabdi
552	90	5.4	604	2	Q6E900_LISMO	Q6e900 listeria mo	625	89	5.4	880	2	Q54UK3_DICDI	Q54uk3 dictyostelli
553	90	5.4	612	2	Q7QJB6_ANOGA	Q7qjb6 anopheles g	626	89	5.4	887	2	Q9I7T2_DROME	Q9i7t2 drosophila
554	90	5.4	616	2	Q4WC60_ASPPU	Q4wc60 aspergillus	627	89	5.4	898	2	Q8IRC0_DROSIPH	Q8irc0 drosophila
555	90	5.4	626	2	Q8IQV5_DROME	Q8iqv5 drosophila	628	89	5.4	917	2	Q4X105_ASPPU	Q4x105 aspergillus
556	90	5.4	629	2	Q9V3H7_DROME	Q9v3h7 drosophila	629	89	5.4	951	2	Q9FVK8_ORYSA	Q9fvk8 oryza sativ
557	90	5.4	629	2	Q9V3H7_DROME	Q9v3h7 drosophila	630	89	5.4	958	2	Q4WTT4_ASPPU	Q4wtt4 aspergillus
558	90	5.4	630	2	Q5ELS1_DROME	Q5els1 drosophila	631	89	5.4	983	2	Q8IRB9_DROME	Q8irb9 drosophila
559	90	5.4	639	2	Q6E8S6_LISMO	Q6e8s6 listeria mo	632	89	5.4	1081	2	Q59EAL_HUMAN	Q59eal homo sapien
560	90	5.4	740	2	Q54HB4_DICDI	Q54hb4 dictyostelli	633	89	5.4	1116	2	Q5AJH8_CANAL	Q5ajh8 candida alb
561	90	5.4	812	2	Q61KE5_CAEBR	Q61ke5 caenorhabdi	634	89	5.4	1473	2	Q54TV0_DICDI	Q54tv0 dictyostelli
562	90	5.4	823	2	Q54Y28_DICDI	Q54y28 dictyostelli	635	89	5.4	1483	2	Q7KWU3_DICDI	Q7kwu3 dictyostelli
563	90	5.4	877	2	Q9H3O6_HUMAN	Q9h3o6 homo sapien	636	89	5.4	1493	2	Q559I7_DICDI	Q559i7 dictyostelli
564	90	5.4	878	2	Q9H3O7_HUMAN	Q9h3o7 homo sapien	637	89	5.4	1521	2	Q7Q1W8_ANOGA	Q7q1w8 anopheles g
565	90	5.4	948	2	Q86AV9_DICDI	Q86av9 d phosphati	638	89	5.4	1708	2	Q7XWZ9_ORYSA	Q7xwz9 oryza sativ
566	90	5.4	954	2	Q61OZ8_CAEBR	Q61oz8 caenorhabdi	639	89	5.4	2273	2	Q63HU2_BURPS	Q63hu2 burkholderi
567	90	5.4	957	2	Q14651_HUMAN	Q14651 homo sapien	640	89	5.4	6994	2	Q17343_CAEBL	Q17343 caenorhabdi
568	90	5.4	965	2	Q22286_CAEBL	Q22286 caenorhabdi	641	89	5.4	6994	2	Q17490_CAEBL	Q17490 caenorhabdi
569	90	5.4	1086	2	Q54X99_DICDI	Q54x99 dictyostelli	642	88.5	5.3	193	2	Q23366_ARATH	Q23366 arabidopsis
570	90	5.4	1170	2	Q4IC26_GIBZE	Q4ic26 gibberella	643	88.5	5.3	264	2	Q80XS5_MOUSE	Q80xs5 mus musculus
571	90	5.4	1217	2	Q4UKX9_HUMAN	Q4ukx9 homo sapien	644	88.5	5.3	321	2	Q25939_PLAPA	Q25939 plasmodium
572	90	5.4	1293	1	Q4Q6D9_LEIMA	Q4q6d9 leishmania	645	88.5	5.3	359	2	Q55JF9_CRYNE	Q55jef9 cryptococcu
573	90	5.4	1367	1	MUC1_YEAST	P08640 saccharomyc	646	88.5	5.3	389	2	Q611Z9_CAEBR	Q611z9 caenorhabdi
574	90	5.4	1367	2	Q6LCS8_SACDI	Q6lcs8 saccharomyc	647	88.5	5.3	448	2	Q6AQD8_DESPS	Q6aqd8 desulfotale
575	90	5.4	1593	2	Q8XK82_DROME	Q8xk82 drosophila	648	88.5	5.3	481	2	Q9VWK3_DROME	Q9vwk3 drosophila
576	90	5.4	2282	2	Q9NK56_DROME	Q9nk56 drosophila	649	88.5	5.3	494	2	Q618M1_CAEBR	Q618m1 caenorhabdi
577	90	5.4	2871	2	Q8IM87_DROME	Q8im87 drosophila	650	88.5	5.3	518	2	Q8NJS3_CANAL	Q8nj93 candida alb
578	90	5.4	2874	2	Q9V483_DROME	Q9v483 drosophila	651	88.5	5.3	569	2	Q7IXI0_LISMO	Q7ixi0 listeria mo
579	89.5	5.4	195	2	Q9QX82_RAT	Q9qx82 rattus norv	652	88.5	5.3	582	2	Q8IR74_DROME	Q8ir74 drosophila
580	89.5	5.4	276	2	Q52B16_MAGGR	Q52b16 magnaporthe	653	88.5	5.3	596	1	UBOL4_MOUSE	Q99nb8 mus musculus
581	89.5	5.4	305	2	Q8VBW0_MOUSE	Q8vbw0 mus musculus	654	88.5	5.3	598	2	Q9JMY5_LISMO	Q9jmy5 listeria mo
582	89.5	5.4	319	1	CJ078_MOUSE	Q8bp27 mus musculus	655	88.5	5.3	615	2	Q9MGE8_PHAVU	Q9mge8 phaseolus v
583	89.5	5.4	326	2	Q7SCN5_NEUCR	Q7scn5 neurospora	656	88.5	5.3	622	2	Q58SF6_DROS1	Q58sf6 drosophila
584	89.5	5.4	359	2	Q5KCB0_CRYNE	Q5kcb0 cryptococcu	657	88.5	5.3	653	2	Q8IJX0_PLAF7	Q8ijx0 plasmodium
585	89.5	5.4	440	2	Q9P566_NEUCR	Q9p566 neurospora	658	88.5	5.3	699	2	Q6CSM7_KLULA	Q6csm7 kluyveromyc
586	89.5	5.4	443	2	Q6P111_BRARE	Q6p111 brachydanio	659	88.5	5.3	721	2	Q97UG7_SULSO	Q97ug7 sulfolobus
587	89.5	5.4	455	2	Q7VNN0_HAEDU	Q7vnn0 haemophilus	660	88.5	5.3	722	2	Q59644_SULSO	Q59644 sulfolobus
588	89.5	5.4	456	2	Q25242_LUCCU	Q25242 lucilia cup	661	88.5	5.3	722	2	Q6FTP4_CANGA	Q6ftp4 candida gla
589	89.5	5.4	471	2	Q9VMG7_DROME	Q9vmg7 drosophila	662	88.5	5.3	752	2	Q52CRI_MAGGR	Q52cri magnaporthe
590	89.5	5.4	480	2	Q25241_LUCCU	Q25241 lucilia cup	663	88.5	5.3	764	2	Q4WYI0_ASPPU	Q4wyi0 aspergillus
591	89.5	5.4	492	2	Q6CGC6_YARLI	Q6cgc6 yarrowia li	664	88.5	5.3	901	2	Q9H195_HUMAN	Q9h195 homo sapien
592	89.5	5.4	510	2	Q6SGJ8_ASPPU	Q6scj8 aspergillus	665	88.5	5.3	980	2	Q84FU6_CHLTR	Q84fu6 chlamydia t
593	89.5	5.4	548	2	Q61CS6_CAEBR	Q61cs6 caenorhabdi	666	88.5	5.3	980	2	Q84FU8_CHLTR	Q84fu8 chlamydia t
594	89.5	5.4	558	2	Q4JK70_DERPT	Q4jk70 dermatophag	667	88.5	5.3	981	2	Q84FU7_CHLTR	Q84fu7 chlamydia t
595	89.5	5.4	604	2	Q6B9W0_LISMO	Q6b9w0 listeria mo	668	88.5	5.3	1042	2	Q59XZ1_CANAL	Q59xz1 candida alb
596	89.5	5.4	606	2	Q5ZLR8_CHICK	Q5zlr8 gallus gall	669	88.5	5.3	1101	1	GUNC_CELFI	P14090 cellulomona
597	89.5	5.4	634	2	Q7IT11_MOMCH	Q7it11 momordica c	670	88.5	5.3	1106	2	Q4IAX5_GIBZE	Q4iax5 gibberella
598	89.5	5.4	659	2	Q556V6_DICDI	Q556v6 dictyostelli	671	88.5	5.3	1224	2	Q54PM6_DICDI	Q54pm6 dictyostelli
599	89.5	5.4	659	2	Q86A18_DICDI	Q86a18 dictyostelli	672	88.5	5.3	1230	2	Q54JY4_DICDI	Q54jy4 dictyostelli
600	89.5	5.4	917	2	Q7QJ16_ANOGA	Q7qj16 anopheles g	673	88.5	5.3	1346	2	Q54SH1_DICDI	Q54sh1 dictyostelli
601	89.5	5.4	1145	2	Q8JK10_VIRUO	Q8jk10 heliothis z	674	88.5	5.3	2122	2	Q54R92_DICDI	Q54r92 dictyostelli
602	89.5	5.4	1368	2	Q23821_CAEVU	Q23821 caenorhabdi	675	88	5.3	103	2	Q9CTB3_PIG	Q9ctv7 sus scrofa
603	89.5	5.4	1773	2	Q4N437_THEPA	Q4n437 theileria p	676	88	5.3	161	2	Q9CVT7_MOUSE	Q9cvt7 caenorhabdi
604	89.5	5.4	1816	2	Q4NGE9_THEPA	Q4nge9 theileria p	677	88	5.3	259	2	Q9N3B9_CAEBL	Q9n3b9 caenorhabdi
605	89	5.4	307	1	SGS3_DROME	P02840 drosophila	678	88	5.3	302	2	Q5XKX5_CRYNE	Q5xkx5 cryptococcu
606	89	5.4	369	2	Q91E39_9ALPH	Q91e39 phocid herp	679	88	5.3	345	2	Q5KWC3_CRYNE	Q5kwc3 cryptococcu
607	89	5.4	392	2	Q59FZ0_HUMAN	Q59fz0 homo sapien	680	88	5.3	347	2	Q690W2_ANOSA	Q690w2 anolis sagr
608	89	5.4	416	1	LAMP1_HUMAN	P11279 homo sapien	681	88	5.3	362	2	Q9TZV4_PLAPA	Q9tzv4 plasmodium
609	89	5.4	417	2	Q8WU33_HUMAN	Q8wu33 homo sapien	682	88	5.3	382	2	Q9TZV3_PLAPA	Q9tzv3 plasmodium
610	89	5.4	421	2	Q6KCA6_CANDU	Q6kca6 candida dub	683	88	5.3	385	2	Q6C971_YARLI	Q6c971 yarrowia li
611	89	5.4	422	2	Q5CNT4_CRYHO	Q5cnt4 cryptospori	684	88	5.3	385	2	Q8T8I2_DROPB	Q8t8i2 drosophila
612	89	5.4	477	2	Q14887_HUMAN	Q14887 homo sapien	685	88	5.3	385	2	Q8T8I1_DROPB	Q8t8i1 drosophila
613	89	5.4	482	2	Q6BSZ9_DEBHA	Q6bsz9 debaryomyce	686	88	5.3	385	2	Q8T8I6_DROPB	Q8t8i6 drosophila
614	89	5.4	487	2	Q4U479_ANOGA	Q4u479 anopheles g	687	88	5.3	385	2	Q8T8J0_DROPB	Q8t8j0 drosophila
615	89	5.4	503	1	NAS14_CAEBL	Q19269 caenorhabdi	688	88	5.3	385	2	Q8T8J1_DROPB	Q8t8j1 drosophila

689 88 5.3 385 2 Q8T8K3 DROPE  
 690 88 5.3 447 2 Q6CCRI\_YARLI  
 691 88 5.3 449 2 Q6CW26\_KLUULA  
 692 88 5.3 456 2 Q9U2W2\_CAEEL  
 693 88 5.3 463 2 Q7QK86\_ANOHA  
 694 88 5.3 564 2 Q01627\_CAEEL  
 695 88 5.3 577 2 Q6FSJ1\_CANGA  
 696 88 5.3 587 2 Q5IR09\_MAGGR  
 697 88 5.3 587 2 Q4QGJ9\_LEIMA  
 698 88 5.3 588 2 Q13F9\_BACCR  
 699 88 5.3 601 2 Q6V6S2\_DROME  
 700 88 5.3 602 2 Q8YV91\_ANASP  
 701 88 5.3 604 2 Q8E916\_LISMO  
 702 88 5.3 616 2 Q8R0X0\_MOUSE  
 703 88 5.3 656 2 Q8BU97\_MOUSE  
 704 88 5.3 716 2 Q9NYE4\_HUMAN  
 705 88 5.3 761 2 Q22271\_ARATH  
 706 88 5.3 931 2 Q51LJ1\_MAGGR  
 707 88 5.3 995 2 Q91638\_XENLA  
 708 88 5.3 1051 2 Q6C1J9\_YARLI  
 709 88 5.3 1409 2 Q5ALT5\_CANAL  
 710 88 5.3 1630 1 MSP1\_PLAFK  
 711 88 5.3 1790 2 Q81816\_APLCA  
 712 88 5.3 2195 2 Q4SA07\_TETNG  
 713 88 5.3 5703 1 MUC5B\_HUMAN  
 714 87.5 5.3 147 2 Q61043\_TRYCR  
 715 87.5 5.3 244 2 Q54R04\_DICDI  
 716 87.5 5.3 283 2 Q5XUY9\_ARATH  
 717 87.5 5.3 283 2 Q9FKU2\_ARATH  
 718 87.5 5.3 289 2 Q41J90\_GIBZE  
 719 87.5 5.3 299 2 Q8H2T1\_XANOR  
 720 87.5 5.3 338 2 Q6C150\_KLUULA  
 721 87.5 5.3 345 2 Q56W8\_ARATH  
 722 87.5 5.3 357 2 Q4N8P6\_THEPA  
 723 87.5 5.3 366 2 Q6FS18\_CANGA  
 724 87.5 5.3 383 2 Q702Y9\_HV1  
 725 87.5 5.3 442 2 Q7S223\_NEUCR  
 726 87.5 5.3 462 2 Q8TU00\_METAC  
 727 87.5 5.3 463 2 Q5A3K1\_CANAL  
 728 87.5 5.3 498 2 Q6FV08\_CANGA  
 729 87.5 5.3 542 2 Q4V4X7\_DROME  
 730 87.5 5.3 555 2 Q9U6R7\_DERPA  
 731 87.5 5.3 563 2 Q5LK63\_SILPO  
 732 87.5 5.3 571 2 Q4YHW1\_PLABE  
 733 87.5 5.3 622 2 Q58SG2\_DROSI  
 734 87.5 5.3 622 2 Q58SH9\_DROSI  
 735 87.5 5.3 622 2 Q5EL05\_DROSI  
 736 87.5 5.3 622 2 Q5EL09\_DROSI  
 737 87.5 5.3 623 2 Q6T547\_LISMO  
 738 87.5 5.3 625 2 Q5ELP7\_DROSI  
 739 87.5 5.3 634 2 Q7RW80\_NEUCR  
 740 87.5 5.3 639 2 Q6T548\_LISMO  
 741 87.5 5.3 648 2 Q44189\_CAEEL  
 742 87.5 5.3 653 2 Q59YC5\_CANAL  
 743 87.5 5.3 653 2 Q8NK55\_CANAL  
 744 87.5 5.3 665 2 Q41IW3\_GIBZE  
 745 87.5 5.3 682 2 Q60P22\_CAEER  
 746 87.5 5.3 717 2 Q8NAJ6\_HUMAN  
 747 87.5 5.3 752 2 Q8MN82\_DICDI  
 748 87.5 5.3 785 2 Q7QQ15\_GIALA  
 749 87.5 5.3 825 2 Q9LZAG\_ARATH  
 750 87.5 5.3 867 2 Q90X49\_BRARE  
 751 87.5 5.3 906 2 Q8UVU1\_XENLA  
 752 87.5 5.3 908 2 Q59PF9\_CANAL  
 753 87.5 5.3 968 2 Q4SSC4\_TETNG  
 754 87.5 5.3 971 2 Q6W3C4\_CAEEL  
 755 87.5 5.3 989 2 Q19930\_CAEEL  
 756 87.5 5.3 997 1 VGNM\_APMV  
 757 87.5 5.3 1085 1 CASR\_BOVIN  
 758 87.5 5.3 1091 1 NCAMI\_CHICK  
 759 87.5 5.3 1118 2 Q550H5\_DICDI  
 760 87.5 5.3 1129 2 Q6CB75\_YARLI  
 761 87.5 5.3 1313 2 Q55WZ1\_CRYNE

762 87.5 5.3 1370 2 Q6C3B8\_YARLI  
 763 87.5 5.3 1799 2 Q7KUI0\_DROME  
 764 87.5 5.3 1802 1 HKR1\_YEAST  
 765 87.5 5.3 2314 2 Q55F23\_DICDI  
 766 87.5 5.3 2817 2 Q97K42\_CLOAB  
 767 87 5.3 167 2 Q65742\_CICAR  
 768 87 5.3 235 2 Q63349\_RAT  
 769 87 5.3 259 2 Q70CD5\_EIMPE  
 770 87 5.3 362 2 Q6CGU2\_YARLI  
 771 87 5.3 363 2 Q91YK8\_MOUSE  
 772 87 5.3 379 2 Q823B1\_CHLCV  
 773 87 5.3 385 2 Q8T8J9\_DROPS  
 774 87 5.3 406 2 Q413G6\_GIBZE  
 775 87 5.3 442 2 Q758Q5\_ASHGE  
 776 87 5.3 453 2 Q9U301\_CAEEL  
 777 87 5.3 456 2 Q5B7G2\_EMENI  
 778 87 5.3 478 2 Q55RT1\_CRYNE  
 779 87 5.3 484 2 Q4FK07\_9TRYP  
 780 87 5.3 532 2 Q4JK69\_DERPT  
 781 87 5.3 567 2 Q60X66\_CAEER  
 782 87 5.3 585 2 Q58SH0\_DROSI  
 783 87 5.3 639 2 Q6E8S0\_LISMO  
 784 87 5.3 661 2 Q13444\_CLAFU  
 785 87 5.3 686 2 Q61XJ6\_CAEER  
 786 87 5.3 689 2 Q724Q0\_LISNF  
 787 87 5.3 752 2 Q9YC61\_AERPE  
 788 87 5.3 812 2 Q54G74\_DICDI  
 789 87 5.3 841 2 Q6AX88\_XENLA  
 790 87 5.3 881 2 Q8IMS9\_DROME  
 791 87 5.3 919 2 Q51BH5\_ENTHI  
 792 87 5.3 931 2 Q83UW2\_CHLTR  
 793 87 5.3 991 2 Q84FV0\_CHLTR  
 794 87 5.3 991 2 Q84FV1\_CHLTR  
 795 87 5.3 1016 1 PMPH\_CHLTR  
 796 87 5.3 1048 2 Q9LAU3\_LEGPN  
 797 87 5.3 1055 2 Q55G65\_DICDI  
 798 87 5.3 1082 1 YK02\_SCHPO  
 799 87 5.3 1173 2 Q61A60\_CAEER  
 800 87 5.3 1447 2 Q5B4Q8\_EMENI  
 801 87 5.3 1506 2 P79927\_XENLA  
 802 87 5.3 1537 1 FLO1\_YEAST  
 803 87 5.3 1537 2 Q58HH7\_YEAST  
 804 87 5.3 6586 2 Q52F11\_MAGGR  
 805 86.5 5.2 197 2 Q92317\_MOUSE  
 806 86.5 5.2 197 2 Q9R0L9\_MOUSE  
 807 86.5 5.2 245 2 Q61MB0\_CAEER  
 808 86.5 5.2 249 2 Q6BVK5\_DEBHA  
 809 86.5 5.2 277 2 Q4KMD4\_BRARE  
 810 86.5 5.2 390 2 Q73JV8\_TREDE  
 811 86.5 5.2 400 1 MUAI\_XENLA  
 812 86.5 5.2 401 2 Q6BV71\_DEBHA  
 813 86.5 5.2 442 2 Q7MB23\_WOLSU  
 814 86.5 5.2 451 2 Q6DF68\_XENTR  
 815 86.5 5.2 461 2 Q21004\_CAEEL  
 816 86.5 5.2 483 2 Q5AT96\_EMENI  
 817 86.5 5.2 484 1 PAPO2\_XENLA  
 818 86.5 5.2 493 2 Q23330\_CAEEL  
 819 86.5 5.2 503 1 WSC2\_YEAST  
 820 86.5 5.2 582 2 Q58SG7\_DROSI  
 821 86.5 5.2 582 2 Q58SG8\_DROSI  
 822 86.5 5.2 582 2 Q58SG9\_DROSI  
 823 86.5 5.2 582 2 Q58SH3\_DROSI  
 824 86.5 5.2 598 2 Q5ELV4\_DROSI  
 825 86.5 5.2 598 2 Q5ELV5\_DROSI  
 826 86.5 5.2 598 2 Q5ELW0\_DROSI  
 827 86.5 5.2 601 2 Q6V6S4\_DROME  
 828 86.5 5.2 604 2 Q6E8Z8\_LISMO  
 829 86.5 5.2 604 2 Q6E3Z8\_LISMO  
 830 86.5 5.2 624 2 Q58SF9\_DROSI  
 831 86.5 5.2 639 2 Q8GNR0\_LISMO  
 832 86.5 5.2 639 2 Q6E952\_LISMO  
 833 86.5 5.2 639 2 Q6E976\_LISMO  
 834 86.5 5.2 687 2 Q6NHU1\_CORDI

Q6C3B8 yarrowia li  
 Q7kui0 drosophila  
 P41809 saccharomyc  
 Q55F23 dictyosteli  
 Q97k42 clostridium  
 Q65742 cicer ariet  
 Q63349 rattus norv  
 Q70cd5 eimeria ten  
 Q6cgu2 yarrowia li  
 Q91yk8 mus musculu  
 Q823b1 chlamydophi  
 Q8t8j9 drosophila  
 Q413g6 gibberella  
 Q758q5 ashbya goss  
 Q9u301 caenorhabdi  
 Q5b7g2 aspergillus  
 Q55rt1 cryptococcu  
 Q4fk07 trypanosoma  
 Q4jk69 dermatophag  
 Q60x66 caenorhabdi  
 Q58sh0 drosophila  
 Q6e8s0 listeria mo  
 Q61xj6 caenorhabdi  
 Q724q0 listeria mo  
 Q9yc61 aeropyrum p  
 Q54g74 dictyosteli  
 Q6ax88 xenopus lae  
 Q8ims9 drosophila  
 Q51bh5 entamoeba h  
 Q83uw2 chlamydia t  
 Q84fv1 chlamydia t  
 Q84fv1 chlamydia t  
 Q84880 chlamydia t  
 Q9lau3 legionella  
 Q55g65 dictyosteli  
 Q9hd9 schizosacch  
 Q61a60 caenorhabdi  
 Q5b4q8 aspergillus  
 P79927 xenopus lae  
 P32768 saccharomyc  
 Q58hh7 saccharomyc  
 Q52f11 magnaporth  
 Q92317 mus musculu  
 Q9r0l9 mus musculu  
 Q61mb0 caenorhabdi  
 Q6bvk5 debaryomyce  
 Q4kmd4 brachydanio  
 Q73jv8 treponema d  
 P10657 xenopus lae  
 Q6bv71 debaryomyce  
 Q7mb23 wolinnella s  
 Q6df68 xenopus tro  
 Q21004 caenorhabdi  
 Q5at96 aspergillus  
 P51005 xenopus lae  
 Q23330 caenorhabdi  
 P53832 saccharomyc  
 Q58sg7 drosophila  
 Q58sg8 drosophila  
 Q58sg9 drosophila  
 Q58sh3 drosophila  
 Q5elv4 drosophila  
 Q5elv5 drosophila  
 Q5elw0 drosophila  
 Q6v6s4 drosophila  
 Q6e8z8 listeria mo  
 Q6e3z8 listeria mo  
 Q58sf9 drosophila  
 Q8gnr0 listeria mo  
 Q6e952 listeria mo  
 Q6e976 listeria mo  
 Q6nhu1 corynebacte



835	86.5	5.2	733	2	Q5E25	dictyosteli	Q5e25	dictyosteli	908	85.5	5.2	269	2	Q9U9J2_TOXCA	Q9u9j2	toxocara ca
836	86.5	5.2	739	1	GAG_SMRVH	P21411	squierei mo	P21411	909	85.5	5.2	271	2	Q6DGI9_BRARE	Q6dgi9	brachydanio
837	86.5	5.2	779	2	QSTRJ3_ANOGA	Qstrj3	anopheles g	Qstrj3	910	85.5	5.2	345	2	Q691X0_ANOSA	Q691x0	anolis sagr
838	86.5	5.2	780	2	Q18510_TRINI	Q18510	trichoplusi	Q18510	911	85.5	5.2	346	2	Q5R230_9ZIGO	Q5r230	phycomyces
839	86.5	5.2	790	2	Q8TB27_HUMAN	Q8tb27	homo sapien	Q8tb27	912	85.5	5.2	370	2	Q7KRX4_DROME	Q7krx4	drosohphila
840	86.5	5.2	807	2	Q18511_TRINI	Q18511	trichoplusi	Q18511	913	85.5	5.2	378	1	FBSH_MOUSE	Q8r089	mus musculus
841	86.5	5.2	838	2	Q7UNF4_RHOBA	Q7unp4	rhodopirell	Q7unp4	914	85.5	5.2	379	2	Q81050_DROME	Q81050	drosohphila
842	86.5	5.2	843	2	Q4RQMO_TETNG	Q4rqmo	tetraodon n	Q4rqmo	915	85.5	5.2	390	2	Q81QO0_DROME	Q81qo0	drosohphila
843	86.5	5.2	853	2	Q54S28_DICDI	Q54s28	dictyosteli	Q54s28	916	85.5	5.2	405	2	Q51P11_MAGGR	Q51p11	magnaporthe
844	86.5	5.2	941	2	Q9LTH0_ARATH	Q9lth0	arabidopsis	Q9lth0	917	85.5	5.2	419	2	Q5T227_BRARE	Q5t227	brachydanio
845	86.5	5.2	970	2	Q4W973_ASPFU	Q4w973	aspergillus	Q4w973	918	85.5	5.2	427	2	Q4STA8_TETNG	Q4sta8	tetraodon n
846	86.5	5.2	1300	2	Q6BZP6_YARLI	Q6bzp6	yarrowia li	Q6bzp6	919	85.5	5.2	453	2	Q41GE4_GIBZE	Q41ge4	gibberella
847	86.5	5.2	1546	2	Q80S34_MOUSE	Q80s34	mus musculus	Q80s34	920	85.5	5.2	459	2	Q5WG39_BACSK	Q5wg39	bacillus cl
848	86.5	5.2	1579	2	Q99MP1_MOUSE	Q99mp1	mus musculus	Q99mp1	921	85.5	5.2	575	1	CH62_CUCMA	Q50546	cucurbita m
849	86.5	5.2	1683	2	Q810D4_MOUSE	Q810d4	mus musculus	Q810d4	922	85.5	5.2	595	2	Q58S64_DROSI	Q58s64	drosohphila
850	86.5	5.2	1684	2	Q9WT05_MOUSE	Q9wt05	mus musculus	Q9wt05	923	85.5	5.2	622	2	Q7R2J1_GIALA	Q7r2j1	giardia lam
851	86.5	5.2	1822	2	Q7R0W4_GIALA	Q7r0w4	giardia lam	Q7r0w4	924	85.5	5.2	622	2	Q6V6B4_DROSI	Q6v6b4	drosohphila
852	86.5	5.2	1844	2	Q22579_CAEEL	Q22579	caenorhabdi	Q22579	925	85.5	5.2	622	2	Q6V6B4_DROSI	Q6v6b4	drosohphila
853	86.5	5.2	1851	2	Q9ESP3_RAT	Q9esp3	rattus norv	Q9esp3	926	85.5	5.2	623	2	Q89QR8_BRAJA	Q89qr8	bradyrhizob
854	86.5	5.2	2546	2	Q54ERS_DICDI	Q54ers	dictyosteli	Q54ers	927	85.5	5.2	624	2	Q58SF2_DROSI	Q58sf2	drosohphila
855	86.5	5.2	2781	2	Q9UIG2_HUMAN	Q9uig2	homo sapien	Q9uig2	928	85.5	5.2	624	2	Q58SG1_DROSI	Q58sg1	drosohphila
856	86.5	5.2	4509	2	Q54T85_DICDI	Q54t85	dictyosteli	Q54t85	929	85.5	5.2	624	2	Q5ELN1_DROSI	Q5eln1	drosohphila
857	86	5.2	337	2	Q5AF14_CANAL	Q5af14	candida alb	Q5af14	930	85.5	5.2	624	2	Q5ELN5_DROSI	Q5eln5	drosohphila
858	86	5.2	345	2	Q6UUM5_SAUR	Q6ujm5	diploactyl	Q6ujm5	931	85.5	5.2	624	2	Q5ELN5_DROSI	Q5eln5	drosohphila
859	86	5.2	346	2	Q52J82_SAUR	Q52j82	heteronotia	Q52j82	932	85.5	5.2	625	2	Q9LCJ8_STAAU	Q9lcj8	staphylococ
860	86	5.2	347	2	Q9TZV6_PLAFA	Q9tzv6	plasmodium	Q9tzv6	933	85.5	5.2	643	2	Q5JH19_PYKRO	Q5jh19	pyrococcus
861	86	5.2	347	2	Q9TZV6_PLAFA	Q9tzv6	plasmodium	Q9tzv6	934	85.5	5.2	649	2	Q49445_ARATH	Q49445	arabidopsis
862	86	5.2	385	2	Q8TRK4_DROPE	Q8trk4	drosohphila	Q8trk4	935	85.5	5.2	693	2	Q54LR1_DICDI	Q54lr1	dictyosteli
863	86	5.2	390	2	Q70LN3_PHLRA	Q70ln3	phlebia rad	Q70ln3	936	85.5	5.2	716	2	Q54BAL_DICDI	Q54bal	dictyosteli
864	86	5.2	390	2	Q96T55_PHLRA	Q96t55	phlebia rad	Q96t55	937	85.5	5.2	734	2	Q7S939_NEUCR	Q7s939	neurospora
865	86	5.2	431	2	Q51MX9_MAGGR	Q51wx9	magnaporthe	Q51wx9	938	85.5	5.2	746	2	Q54N84_DICDI	Q54n84	dictyosteli
866	86	5.2	434	2	Q872V2_NEUCR	Q872v2	neurospora	Q872v2	939	85.5	5.2	780	1	LMBL3_HUMAN	Q961m7	homo sapien
867	86	5.2	460	2	Q18984_CERAE	Q18984	ceratopithe	Q18984	940	85.5	5.2	780	2	Q4VXE1_HUMAN	Q4vxe1	homo sapien
868	86	5.2	476	2	Q03996_PLACH	Q03996	plasmodium	Q03996	941	85.5	5.2	786	2	Q21027_CAEEL	Q21027	caenorhabdi
869	86	5.2	477	2	Q86VC5_HUMAN	Q86vc5	homo sapien	Q86vc5	942	85.5	5.2	841	2	Q6R8J4_BRARE	Q6r8j4	brachydanio
870	86	5.2	495	2	Q6AK33_DESPS	Q6ak33	desulfotale	Q6ak33	943	85.5	5.2	843	2	Q851G7_DROME	Q851g7	oryza sativ
871	86	5.2	537	2	Q5AH05_CANAL	Q5ah05	candida alb	Q5ah05	944	85.5	5.2	863	2	Q851G7_DROME	Q851g7	oryza sativ
872	86	5.2	537	2	Q5AH05_CANAL	Q5ah05	candida alb	Q5ah05	945	85.5	5.2	866	2	Q4PDE9_USTMA	Q4pde9	ustilago ma
873	86	5.2	551	1	PODXL_RABIT	Q28h65	cryptotlagus	Q28h65	946	85.5	5.2	878	2	Q55GH4_DICDI	Q55gh4	dictyosteli
874	86	5.2	572	2	Q58SM1_DROME	Q58sm1	drosohphila	Q58sm1	947	85.5	5.2	895	2	Q80973_ARATH	Q80973	arabidopsis
875	86	5.2	598	2	Q4TVQ7_LISMO	Q4tvq7	listeria mo	Q4tvq7	948	85.5	5.2	935	2	Q6R8J3_BRARE	Q6r8j3	brachydanio
876	86	5.2	604	2	Q8GNQ9_LISMO	Q8gnq9	listeria mo	Q8gnq9	949	85.5	5.2	954	2	Q55FS4_DICDI	Q55fs4	dictyosteli
877	86	5.2	604	2	Q6E9N2_LISMO	Q6e9n2	listeria mo	Q6e9n2	950	85.5	5.2	977	2	Q6R8J2_BRARE	Q6r8j2	brachydanio
878	86	5.2	625	2	Q58SG0_DROSI	Q58sg0	drosohphila	Q58sg0	951	85.5	5.2	981	2	Q6GQ19_XENLA	Q6gq19	xenopus lae
879	86	5.2	629	2	Q5EL58_DROME	Q5el58	drosohphila	Q5el58	952	85.5	5.2	1052	2	Q91G49_IRV6	Q91g49	chilo iride
880	86	5.2	639	2	Q6EBR4_LISMO	Q6ebr4	listeria mo	Q6ebr4	953	85.5	5.2	1209	2	Q4SFS8_TETNG	Q4sfs8	cacao swoll
881	86	5.2	697	2	Q7S009_NEUCR	Q7s009	neurospora	Q7s009	954	85.5	5.2	1668	2	Q5TJ69_VTRU	Q5tj69	tetraodon n
882	86	5.2	709	2	Q4PYT7_USTMA	Q4pyt7	ustilago ma	Q4pyt7	955	85.5	5.2	2448	2	Q8WWQ5_HUMAN	Q8wwq5	homo sapien
883	86	5.2	714	2	Q59TK9_CANAL	Q59tk9	candida alb	Q59tk9	956	85.5	5.2	2482	2	Q61GF0_CAEER	Q61gf0	caenorhabdi
884	86	5.2	714	2	Q59TP1_CANAL	Q59tp1	candida alb	Q59tp1	957	85.5	5.2	3346	2	Q822X0_CHICV	Q822x0	chlamydomo
885	86	5.2	734	2	Q869R9_DICDI	Q869r9	dictyosteli	Q869r9	958	85.5	5.2	4862	2	Q5R127_BRARE	Q5r127	brachydanio
886	86	5.2	750	2	Q9HFZ4_CANAL	Q9hfz4	candida alb	Q9hfz4	959	85.5	5.2	6995	2	Q96RK2_HUMAN	Q96rk2	homo sapien
887	86	5.2	780	2	Q9LK78_ARATH	Q9lk78	arabidopsis	Q9lk78	960	85	5.1	172	2	Q8VC95_MOUSE	Q8vc95	mus musculus
888	86	5.2	799	2	Q8EXF5_LEPIN	Q8exf5	leptospira	Q8exf5	961	85	5.1	255	2	Q86HS8_DICDI	Q86hs8	dictyosteli
889	86	5.2	799	2	Q75F17_LEPIC	Q75f17	leptospira	Q75f17	962	85	5.1	265	2	Q9GZE5_CAEEL	Q9gze5	caenorhabdi
890	86	5.2	843	2	Q7XJ06_ORYSA	Q7xj06	oryza sativ	Q7xj06	963	85	5.1	300	2	Q95XH5_CAEEL	Q95xh5	caenorhabdi
891	86	5.2	855	2	Q55C58_DICDI	Q55c58	dictyosteli	Q55c58	964	85	5.1	317	2	Q8BEK4_COMPX	Q8bek4	cowpox viru
892	86	5.2	866	2	Q80XL8_MOUSE	Q80xl8	mus musculus	Q80xl8	965	85	5.1	320	2	Q4SCG1_TETNG	Q4scg1	tetraodon n
893	86	5.2	955	2	Q55MM6_CRYNE	Q55mm6	cryptococcu	Q55mm6	966	85	5.1	326	2	Q9VW89_DROME	Q9vw89	drosohphila
894	86	5.2	955	2	Q5KBO1_CRYNE	Q5kbo1	cryptococcu	Q5kbo1	967	85	5.1	343	1	HXDAA_BRARE	Q90469	brachydanio
895	86	5.2	1080	1	UBPB_MOUSE	Q80u87	mus musculus	Q80u87	968	85	5.1	346	2	Q52JEO_9SAUR	Q52je0	heteronotia
896	86	5.2	1266	2	Q6CAR3_YARLI	Q6car3	yarrowia li	Q6car3	969	85	5.1	346	2	Q52JD9_9SAUR	Q52jd9	heteronotia
897	86	5.2	1266	2	Q626F7_CAEER	Q626f7	caenorhabdi	Q626f7	970	85	5.1	346	2	Q52JB6_9SAUR	Q52jb6	heteronotia
898	86	5.2	1324	2	Q8MMQ2_DICDI	Q8mmq2	dictyosteli	Q8mmq2	971	85	5.1	346	2	Q52J84_9SAUR	Q52j84	heteronotia
899	86	5.2	1609	2	Q51DL9_ENTHI	Q51dl9	entamoeba h	Q51dl9	972	85	5.1	346	2	Q52J86_9SAUR	Q52j86	heteronotia
900	86	5.2	1674	2	Q80Z18_MOUSE	Q80z18	mus musculus	Q80z18	973	85	5.1	410	2	Q4R5B5_MACFA	Q4r5b5	macaca fasc
901	86	5.2	1716	2	Q61ZV2_CAEER	Q61zv2	caenorhabdi	Q61zv2	974	85	5.1	456	2	Q5R8Q6_PONPY	Q5r8q6	pongo pygma
902	86	5.2	1785	2	Q25685_PLACH	Q25685	plasmodium	Q25685	975	85	5.1	472	2	Q5B2T1_EMENI	Q5b2t1	aspergillus
903	86	5.2	2044	2	Q4HZP9_GIBZE	Q4hzp9	gibberella	Q4hzp9	976	85	5.1	478	2	Q5XG84_CRYNE	Q5xg84	cryptococcu
904	86	5.2	2247	2	Q55FT4_DICDI	Q55ft4	dictyosteli	Q55ft4	977	85	5.1	503	2	Q8VCF0_MOUSE	Q8vcf0	mus musculus
905	85.5	5.2	193	2	Q8LB00_ARATH	Q8lb00	arabidopsis	Q8lb00	978	85	5.1	510	2	Q8NJT3_KJULA	Q8njt3	kluveromyc
906	85.5	5.2	206	2	Q6TVK4_POXV	Q6tvk4	orf virus.	Q6tvk4	979	85	5.1	526	2	Q51YT8_MAGGR	Q51yt8	magnaporthe
907	85.5	5.2	224	2	Q8KKT9_RHIET	Q8kkt9	rhizobium e	Q8kkt9	980	85	5.1					



981	85	5.1	531	2	Q5TXG4_ANOGA	Q5txg4 anopheles g	1054	84.5	5.1	657	2	Q86ID0_DICDI	Q86id0 dictyosteli
982	85	5.1	573	2	Q8H7K9_ORISA	Q8h7k9 oryza sativ	1055	84.5	5.1	658	1	SHKJ_SCHPO	P50527 schizosacch
983	85	5.1	576	2	Q06604_YEAST	Q06604 saccharomyc	1056	84.5	5.1	709	2	Q5CVY0_CRYPV	Q5cvy0 cryptocpori
984	85	5.1	597	2	Q5AA66_CANAL	Q5aa66 candida alb	1057	84.5	5.1	706	2	O16783_CAEBL	O16783 caenorhabdi
985	85	5.1	599	2	Q6C2K2_YARLI	Q6c2k2 yarrowia li	1058	84.5	5.1	729	2	O51WE3_MAGGR	O51we3 magnaporth
986	85	5.1	601	2	Q6V6S1_DROME	Q6v6s1 drosophila	1059	84.5	5.1	773	2	Q8TGH3_9BASI	Q8tgh3 malassezia
987	85	5.1	612	2	Q82289_CAEBR	Q82289 caenorhabdi	1060	84.5	5.1	803	1	IF2_COXBU	Q83b51 coxiella bu
988	85	5.1	625	2	Q58SF8_DROSI	Q58sf8 drosophila	1061	84.5	5.1	806	2	Q9VCQ7_DROME	Q9vcq7 drosophila
989	85	5.1	627	1	FXNB_LACIA	Q9cef5 lactococcus	1062	84.5	5.1	814	2	Q6C247_YARLI	Q6c247 yarrowia li
990	85	5.1	629	2	Q7ZTW7_BRARE	Q7ztw7 brachydanio	1063	84.5	5.1	834	2	O5LHK9_BACFN	Q877b7 aspergillus
991	85	5.1	639	2	Q6E9T0_LISMO	Q6e9t0 listeria mo	1064	84.5	5.1	931	2	Q5LHK9_BACFN	Q5lkh9 bacteroides
992	85	5.1	655	2	Q4SOL5_TETNG	Q4sol5 tetrasodon n	1065	84.5	5.1	931	2	Q64Y17_BACFR	Q64y17 bacteroides
993	85	5.1	657	2	Q54E45_DICDI	Q54e45 dictyosteli	1066	84.5	5.1	956	2	Q4POT6_USTWA	Q4p0t6 ustilago ma
994	85	5.1	782	2	Q8GX37_ARATH	Q8gx37 arabidopsis	1067	84.5	5.1	956	2	Q4SFS4_TETNG	Q4sf04 tetrasodon n
995	85	5.1	852	2	Q6CIA5_YARLI	Q6cias5 yarrowia li	1068	84.5	5.1	1047	2	Q874L3_CANAL	Q874l3 candida alb
996	85	5.1	860	1	VG12_BP803	Q37893 bacterioph	1069	84.5	5.1	1057	2	Q5KEB3_CRYNE	Q5keb3 cryptococcu
997	85	5.1	879	2	Q4IC17_GIBZE	Q4ic17 gibberella	1070	84.5	5.1	1102	2	Q08964_YEAST	Q08964 saccharomyc
998	85	5.1	911	2	Q7KML1_DICDI	Q7kml1 dictyosteli	1071	84.5	5.1	1103	2	Q6CA70_YARLI	Q6ca70 yarrowia li
999	85	5.1	927	2	Q52F88_MAGGR	Q52f88 magnaporth	1072	84.5	5.1	1161	1	DAN4_YEAST	P47179 saccharomyc
1000	85	5.1	989	2	Q9M184_ARATH	Q9m1e4 arabidopsis	1073	84.5	5.1	1186	2	Q54194_DICDI	Q54194 dictyosteli
1001	85	5.1	990	2	Q91803_XENLA	Q91803 xenopus lae	1074	84.5	5.1	1189	2	Q54CM2_DICDI	Q54cm2 dictyosteli
1002	85	5.1	993	2	Q83TJ6_CHLTR	Q83tj6 chlamydia t	1075	84.5	5.1	1218	2	Q54YZ6_DICDI	Q54yz6 dictyosteli
1003	85	5.1	1002	2	Q6OYJ3_CAEBR	Q6oyj3 caenorhabdi	1076	84.5	5.1	1355	2	Q86AM1_DICDI	Q86am1 dictyosteli
1004	85	5.1	1004	2	Q4RX1_TETNG	Q4rx1 tetrasodon n	1077	84.5	5.1	1380	2	Q55617_DICDI	Q55617 dictyosteli
1005	85	5.1	1013	2	Q6CKG8_KLULA	Q6ckg8 kluyveromyc	1078	84.5	5.1	1420	2	Q4FWR7_LEIMA	Q4fwr7 leishmania
1006	85	5.1	1025	2	Q626Q9_CAEBR	Q626q9 caenorhabdi	1079	84.5	5.1	1629	2	Q4IB96_GIBZE	Q4ib96 gibberella
1007	85	5.1	1049	2	Q960B6_DROME	Q960e6 drosophila	1080	84.5	5.1	1743	2	Q811L9_PLAVI	Q811l9 plasmodium
1008	85	5.1	1049	2	Q3V6L1_DROME	Q3v6l1 drosophila	1081	84.5	5.1	1827	2	Q4Y6M8_PLACH	Q4y6m8 plasmodium
1009	85	5.1	1061	2	Q5RA99_PONPY	Q5ra99 pongo pygma	1082	84.5	5.1	1878	2	Q6CPZ4_KLULA	Q6cpz4 kluyveromyc
1010	85	5.1	1139	2	Q54Z39_DICDI	Q54z39 dictyosteli	1083	84.5	5.1	1984	1	SCN9A_RAT	Q08562 rattus norv
1011	85	5.1	1170	2	Q95011_CAEBL	Q95011 caenorhabdi	1084	84.5	5.1	2163	2	Q61TS1_CAEBR	Q61ts1 caenorhabdi
1012	85	5.1	1216	2	Q54LU4_DICDI	Q54lu4 dictyosteli	1085	84.5	5.1	2180	2	Q9VAS8_DROME	Q9vas8 drosophila
1013	85	5.1	1286	2	Q3VR49_DROME	Q3vr49 drosophila	1086	84.5	5.1	2205	2	Q54C75_DICDI	Q54c75 dictyosteli
1014	85	5.1	1324	2	Q9VKA7_DROME	Q9vka7 drosophila	1087	84.5	5.1	2206	2	Q4REQ4_TETNG	Q4req4 tetrasodon n
1015	85	5.1	1429	2	Q61Y04_CAEBR	Q61y04 caenorhabdi	1088	84.5	5.1	2378	2	Q7N7Y6_PHOLL	Q7n7y6 photorhabdu
1016	85	5.1	1693	2	Q51ZG9_MAGGR	Q51zg9 magnaporth	1089	84.5	5.1	2481	2	Q7A4B1_STAAN	Q7a4b1 staphylococ
1017	85	5.1	1779	2	Q52374_9FIRM	Q52374 caldicellul	1090	84.5	5.1	2481	2	Q99Q66_STAAM	Q99qr6 staphylococ
1018	85	5.1	17352	2	Q95YM2_PROCL	Q95ym2 procambarus	1091	84.5	5.1	2761	2	Q19522_CAEBL	Q19522 caenorhabdi
1019	84.5	5.1	187	2	Q5CYR7_CRYPV	Q5cyr7 cryptocpori	1092	84.5	5.1	3443	2	Q8JXZ8_MOUSE	Q8jxm8 mus musculu
1020	84.5	5.1	220	2	Q9EQG0_MOUSE	Q9eqg0 mus musculu	1093	84.5	5.1	22152	2	Q8WXI7_HUMAN	Q8wx17 homo sapien
1021	84.5	5.1	245	2	Q56423_CAEBL	Q56423 caenorhabdi	1094	84	5.1	197	2	Q54GR3_DICDI	Q54gr3 dictyosteli
1022	84.5	5.1	250	2	Q5AP52_CANAL	Q5ap52 candida alb	1095	84	5.1	262	2	P74577_SYND3	P74577 synechocyst
1023	84.5	5.1	274	2	Q54W22_DICDI	Q54w22 dictyosteli	1096	84	5.1	305	2	Q4WUZ7_ASPFU	Q4wuz7 aspergillus
1024	84.5	5.1	278	2	Q51QC1_MAGGR	Q51qc1 magnaporth	1097	84	5.1	309	2	Q63549_RAT	Q63549 rattus norv
1025	84.5	5.1	313	2	Q8BEJ1_9POXV	Q8bej1 skunkpox vi	1098	84	5.1	335	2	Q9C7W2_ARATH	Q9c7w2 arabidopsis
1026	84.5	5.1	333	2	Q60JT6_CAEBR	Q60jt6 caenorhabdi	1099	84	5.1	346	2	Q52J83_9SAUR	Q52j83 heteronotia
1027	84.5	5.1	345	2	Q691T8_ANOSA	Q691t8 anolis sagr	1100	84	5.1	346	2	Q52J75_9SAUR	Q52j75 heteronotia
1028	84.5	5.1	378	2	Q6FNP6_CANGA	Q6fnp6 candida gla	1101	84	5.1	346	2	Q52J73_9SAUR	Q52j73 heteronotia
1029	84.5	5.1	396	2	Q51T12_MAGGR	Q51t12 magnaporth	1102	84	5.1	359	1	MTDH_MEDSA	Q82515 medicago sa
1030	84.5	5.1	423	2	Q6CTJ9_KLULA	Q6ctj9 kluyveromyc	1103	84	5.1	359	2	Q53X16_MEDSA	Q53x16 medicago sa
1031	84.5	5.1	456	2	Q8R5M8_MOUSE	Q8r5m8 mus musculu	1104	84	5.1	376	2	Q54N82_DICDI	Q54n82 dictyosteli
1032	84.5	5.1	463	2	Q9JX25_NFIMA	Q9jx25 neisseria m	1105	84	5.1	385	2	Q8T8I3_DROPB	Q8t8i3 drosophila
1033	84.5	5.1	493	1	TNR8_RAT	P97525 rattus norv	1106	84	5.1	385	2	Q8T8I5_DROPE	Q8t8i5 drosophila
1034	84.5	5.1	506	2	Q53Q78_HUMAN	Q53q78 homo sapien	1107	84	5.1	385	2	Q8T8K2_DROPE	Q8t8k2 drosophila
1035	84.5	5.1	522	2	Q4VAS1_HUMAN	Q4vas1 homo sapien	1108	84	5.1	385	2	Q8T8L0_DROPE	Q8t8l0 drosophila
1036	84.5	5.1	524	2	Q54B97_DICDI	Q54b97 dictyosteli	1109	84	5.1	399	2	Q5MJ02_TETPY	Q5mj02 tetrahymena
1037	84.5	5.1	532	2	Q6P7V2_MOUSE	Q6p7v2 mus musculu	1110	84	5.1	420	2	Q8N7W9_HUMAN	Q8n7w9 homo sapien
1038	84.5	5.1	540	1	CH60_STRAP	Q8kj20 streptococc	1111	84	5.1	420	2	Q8YMH1_ANASP	Q8ymh1 anabaena sp
1039	84.5	5.1	542	2	Q54PF2_DICDI	Q54pf2 dictyosteli	1112	84	5.1	456	1	NRX3B_BOVIN	Q28143 bos taurus
1040	84.5	5.1	547	2	Q4R5X1_MACFA	Q4r5x1 macaca fasc	1113	84	5.1	464	2	Q9VX42_DROME	Q9vx42 corynebacte
1041	84.5	5.1	560	2	Q4VAS3_HUMAN	Q4vas3 homo sapien	1114	84	5.1	475	2	Q8FQJ1_COREF	Q8fqj1 streptococc
1042	84.5	5.1	562	1	NUPL_HUMAN	P52594 homo sapien	1115	84	5.1	487	2	Q8EIP9_STRAS	Q8eip9 streptococc
1043	84.5	5.1	562	2	Q4VASO_HUMAN	Q4vas0 homo sapien	1116	84	5.1	487	2	Q8E764_STRAS	Q8e764 streptococc
1044	84.5	5.1	566	2	Q4UKT5_RICFE	Q4ukt5 rickettsia	1117	84	5.1	543	2	Q14879_HUMAN	Q14879 homo sapien
1045	84.5	5.1	570	2	Q6GMZ9_XENLA	Q6gmz9 xenopus lae	1118	84	5.1	598	2	Q5ELV9_DROSI	Q5elv9 drosophila
1046	84.5	5.1	582	2	Q58SG6_DROSI	Q58sg6 drosophila	1119	84	5.1	610	2	Q4ILV6_GIBZE	Q4ilv6 gibberella
1047	84.5	5.1	622	2	Q8V6E2_DROSI	Q8v6e2 drosophila	1120	84	5.1	625	2	Q58SH7_DROSI	Q58sh7 drosophila
1048	84.5	5.1	624	2	Q58SF4_DROSI	Q58sf4 drosophila	1121	84	5.1	625	2	Q5ELP1_DROSI	Q5elp1 drosophila
1049	84.5	5.1	624	2	Q675N0_CORSU	Q675n0 cornu suec	1122	84	5.1	636	1	ENV_MCFE	P15073 mink cell f
1050	84.5	5.1	625	2	Q58SF7_DROSI	Q58sf7 drosophila	1123	84	5.1	639	2	Q6EB93_LISMO	Q6eb93 listeria mo
1051	84.5	5.1	632	2	Q5ELU2_DROME	Q5elu2 drosophila	1124	84	5.1	640	2	Q55G71_DICDI	Q55g71 dictyosteli
1052	84.5	5.1	636	2	Q66H25_BRARE	Q66hz5 brachydanio	1125	84	5.1	641	2	Q6AJU8_DESPS	Q6aju8 desulfotale
1053	84.5	5.1	653	2	Q4P819_USTWA	Q4p819 ustilago ma	1126	84	5.1	648	2	Q95QX0_CAEBL	Q95qx0 caenorhabdi

1127	84	5.1	668	2	Q5B5D4_EMENI	Q5B5d4 aspergillus	1200	83.5	5.0	812	2	Q86AW3_DICDI	Q86aw3 dictyosteli
1128	84	5.1	677	2	Q5B9K5_EMENI	Q5B9k5 aspergillus	1201	83.5	5.0	822	2	Q54Z52_DICDI	Q54z52 dictyosteli
1129	84	5.1	713	2	Q55RT5_CRYNE	Q55rt5 cryptococcus	1202	83.5	5.0	838	2	Q90YM1_BRARE	Q90ym1 brachydanio
1130	84	5.1	730	2	Q6CPU9_KLULA	Q6cpu9 kluyveromyc	1203	83.5	5.0	899	2	Q58CJ5_DROME	Q58cj5 drosophila
1131	84	5.1	758	2	Q51JF4_WAGGR	Q51jf4 magnaporth	1204	83.5	5.0	915	2	Q54BC9_DICDI	Q54bc9 dictyosteli
1132	84	5.1	793	2	Q8YAG7_LISMO	Q8yag7 listeria mo	1205	83.5	5.0	935	2	Q9VGN4_DROME	Q9vgn4 drosophila
1133	84	5.1	809	2	Q54J73_DICDI	Q54j73 dictyosteli	1206	83.5	5.0	967	2	Q8A294_DROME	Q8a294 saccharomyc
1134	84	5.1	812	2	Q5TT09_ANOGA	Q5tt09 anopheles g	1207	83.5	5.0	976	2	Q9A531_CAUCR	Q9a531 caulobacter
1135	84	5.1	827	2	Q61WN3_USTWA	Q61wn3 ustilago ma	1208	83.5	5.0	984	2	Q4UEB9_THEAN	Q4ueb9 theileria a
1136	84	5.1	827	2	Q4PBV7_USTWA	Q4pbv7 ustilago ma	1209	83.5	5.0	1001	2	Q05164_YEAST	Q05164 saccharomyc
1137	84	5.1	836	2	Q56DP0_PLABE	Q56dp0 plasmodium	1210	83.5	5.0	1043	2	Q97E41_CLOAB	Q97e41 clostridium
1138	84	5.1	854	2	Q5ZKA3_CHICK	Q5zka3 gallus gall	1211	83.5	5.0	1056	2	Q55P74_CRYNE	Q55p74 cryptococcus
1139	84	5.1	855	2	Q4P3C5_USTWA	Q4p3c5 ustilago ma	1212	83.5	5.0	1235	2	Q54HF3_DICDI	Q54hf3 dictyosteli
1140	84	5.1	864	1	AT7L1_HUMAN	Q9ulk2 homo sapien	1213	83.5	5.0	1286	2	Q9TXR6_CABEL	Q9txr6 caenorhabdi
1141	84	5.1	880	2	Q7YU85_DROME	Q7yu85 drosophila	1214	83.5	5.0	1570	2	Q61L27_CABER	Q61l27 caenorhabdi
1142	84	5.1	933	2	Q6ZM25_HUMAN	Q6zm25 h cdna flj1	1215	83.5	5.0	1589	2	Q54134_DICDI	Q54134 dictyosteli
1143	84	5.1	961	1	ENC1_MOUSE	Q55914 mus musculu	1216	83.5	5.0	1607	2	Q6CDM9_YARLI	Q6cdm9 yarrowia li
1144	84	5.1	996	1	LRP8_MOUSE	Q924X6 mus musculu	1217	83.5	5.0	1713	2	Q8TGE1_YEAST	Q8tge1 saccharomyc
1145	84	5.1	1021	2	Q6CXI2_KLULA	Q6cx12 kluyveromyc	1218	83.5	5.0	1765	2	Q54WL2_DICDI	Q54wl2 dictyosteli
1146	84	5.1	1075	1	FLO5_YEAST	P38894 saccharomyc	1219	83.5	5.0	1820	2	Q54P55_DICDI	Q54p55 dictyosteli
1147	84	5.1	1085	2	Q5BLF7_BRARE	Q5blf7 brachydanio	1220	83.5	5.0	1855	2	Q4L3P2_STAHI	Q4l3p2 staphylococ
1148	84	5.1	1153	2	Q6A1Q0_DROME	Q6alc0 drosophila	1221	83.5	5.0	2823	2	Q54SZ1_DICDI	Q54sz1 dictyosteli
1149	84	5.1	1326	2	Q5KJN8_CRYNE	Q5kja8 cryptococcus	1222	83.5	5.0	2856	2	Q4UEK8_THEAN	Q4uek8 theileria a
1150	84	5.1	1331	1	MANB_CALSA	P22533 caldocellum	1223	83.5	5.0	2764	2	Q727D6_HUMAN	Q727d6 homo sapien
1151	84	5.1	1343	2	Q960V6_DROME	Q960v6 drosophila	1224	83.5	5.0	3026	2	Q81LS9_PLAF7	Q81ls9 plasmodium
1152	84	5.1	1343	2	Q9W2G6_DROME	Q9w2g6 drosophila	1225	83.5	5.0	3175	1	RPOA_EAVBU	P19811 e replicase
1153	84	5.1	1362	2	Q9V294_PYRAB	Q9v294 pyrococcus	1226	83.5	5.0	3172	2	Q86A58_FELCA	Q86a58 felis silve
1154	84	5.1	1366	2	Q86AM2_DICDI	Q86am2 dictyosteli	1227	83.5	5.0	5179	1	MUC2_HUMAN	Q02817 homo sapien
1155	84	5.1	1601	2	Q54L90_DICDI	Q54l90 dictyosteli	1228	83	5.0	197	2	Q8JL62_GVCF	Q8jl62 gvcof
1156	84	5.1	1645	2	Q9U263_CABEL	Q9u263 caenorhabdi	1229	83	5.0	198	2	Q7QB72_ANOGA	Q7qb72 anopheles g
1157	84	5.1	1649	2	Q54LW8_DICDI	Q54lw8 dictyosteli	1230	83	5.0	207	2	Q4X015_ASPFU	Q4x015 aspergillus
1158	84	5.1	1832	2	Q96503_CRYPV	Q96503 cryptospori	1231	83	5.0	257	2	Q54HH8_DICDI	Q54hh8 dictyosteli
1159	84	5.1	2044	2	Q55CR5_DICDI	Q55cr5 dictyosteli	1232	83	5.0	262	2	Q7PRG9_ANOGA	Q7prg9 anopheles g
1160	84	5.1	2215	2	Q81I26_PLAF7	Q81i26 plasmodium	1233	83	5.0	277	2	Q5ASU6_CANAL	Q5asu6 candida alb
1161	84	5.1	2233	2	Q7PRT5_ANOGA	Q7prt5 anopheles g	1234	83	5.0	291	2	Q6QPG5_GADEN	Q6qpg5 simian aden
1162	84	5.1	2306	2	Q4WIS2_ASPFU	Q4wis2 aspergillus	1235	83	5.0	309	2	Q61EL3_CRYSA	Q61el3 cryza sativ
1163	84	5.1	2447	2	Q4RTS7_TETFG	Q4rts7 tetraodon n	1236	83	5.0	309	2	Q7XNY3_ORYSA	Q7xny3 cryza sativ
1164	83.5	5.0	198	2	Q4WAE1_ASPFU	Q4wae1 aspergillus	1237	83	5.0	314	2	Q9H8R7_HUMAN	Q9h8r7 homo sapien
1165	83.5	5.0	203	2	Q4VHF5_9MONO	Q4vhf5 bovine resp	1238	83	5.0	316	2	Q87D14_HUMAN	Q87d14 homo sapien
1166	83.5	5.0	216	2	Q28501_MACMU	Q28501 macaca mula	1239	83	5.0	337	2	Q7Z5K8_HUMAN	Q7z5k8 homo sapien
1167	83.5	5.0	274	2	Q9EX24_ETRCO	Q9ex24 streptomyce	1240	83	5.0	342	2	Q54LV1_DICDI	Q54lv1 dictyosteli
1168	83.5	5.0	279	2	Q14888_HUMAN	Q14888 homo sapien	1241	83	5.0	345	2	Q691Y6_ANOSA	Q691y6 anolis sagr
1169	83.5	5.0	292	2	Q68668_BACME	Q68668 bacillus me	1242	83	5.0	378	2	Q8SHB2_RHABR	Q8shb2 rhampholeon
1170	83.5	5.0	306	2	Q88V34_LACPL	Q88v34 lactobacill	1243	83	5.0	368	2	Q8SKS5_DROME	Q8sk5 drosophila
1171	83.5	5.0	306	2	Q9QYL4_MOUSE	Q9qyl4 mus musculu	1244	83	5.0	382	2	Q9XZ28_LITSI	Q9xz28 litomosoide
1172	83.5	5.0	352	1	MYB86_ARATH	Q8lph6 arabidopsis	1245	83	5.0	385	2	Q8T8K5_DROPE	Q8t8k5 drosophila
1173	83.5	5.0	385	2	Q8T8L3_DROMI	Q8t8l3 drosophila	1246	83	5.0	409	1	RD23B_HUMAN	P54727 homo sapien
1174	83.5	5.0	385	2	Q83NC5_TROM8	Q83nc5 tropheryma	1247	83	5.0	409	2	Q53F10_HUMAN	Q53f10 homo sapien
1175	83.5	5.0	405	2	Q95XV0_CAEEL	Q95xv0 caenorhabdi	1248	83	5.0	410	2	Q5AYD3_EMENI	Q5ayd3 aspergillus
1176	83.5	5.0	446	2	Q9Y849_KLULA	Q9y849 kluyveromyc	1249	83	5.0	419	2	Q87D11_HUMAN	Q87d11 homo sapien
1177	83.5	5.0	448	2	Q83FT5_TROWT	Q83ft5 tropheryma	1250	83	5.0	422	2	Q87D13_HUMAN	Q87d13 homo sapien
1178	83.5	5.0	455	2	Q4INK6_GIBZE	Q4ink6 gibberella	1251	83	5.0	463	2	Q42665_SCHPO	Q42665 schizosacch
1179	83.5	5.0	465	2	Q84DR0_LISMO	Q84dr0 listeria mo	1252	83	5.0	485	2	Q9V8B0_DROME	Q9v8b0 drosophila
1180	83.5	5.0	476	2	Q7SEJ2_NEUCR	Q7sej2 neurospora	1253	83	5.0	512	2	Q41756_GIBZE	Q41756 gibberella
1181	83.5	5.0	486	2	Q6APY5_RAT	Q6apy5 rattus norv	1254	83	5.0	547	2	Q54SA9_DICDI	Q54sa9 dictyosteli
1182	83.5	5.0	486	2	Q84DR1_LISMO	Q84dr1 listeria mo	1255	83	5.0	547	2	Q623V9_CABER	Q623v9 caenorhabdi
1183	83.5	5.0	498	1	TNR8_MOUSE	Q60846 mus musculu	1256	83	5.0	552	2	Q4NGB9_THEPA	Q4nqb9 theileria p
1184	83.5	5.0	498	2	Q6C977_YARLI	Q6c977 yarrowia li	1257	83	5.0	559	2	Q9VN36_DROME	Q9vn36 drosophila
1185	83.5	5.0	516	2	Q7YIC5_CRYPV	Q7yic5 cryptospori	1258	83	5.0	564	2	Q5CQC1_CRYPV	Q5ccq1 cryptospori
1186	83.5	5.0	575	2	Q58SM2_DROME	Q58sm2 drosophila	1259	83	5.0	585	2	Q58SG3_DROSI	Q58sg3 drosophila
1187	83.5	5.0	585	2	Q58S80_9MONO	Q58s80 avian pneum	1260	83	5.0	585	2	Q58SG5_DROSI	Q58sg5 drosophila
1188	83.5	5.0	585	2	Q58S81_9MONO	Q58s81 avian pneum	1261	83	5.0	585	2	Q58SH2_DROSI	Q58sh2 drosophila
1189	83.5	5.0	623	2	Q7XND3_ORYSA	Q7xnd3 cryza sativ	1262	83	5.0	599	2	Q5ELV7_DROME	Q5elv7 drosophila
1190	83.5	5.0	624	2	Q58SP5_DROSI	Q58sp5 drosophila	1263	83	5.0	599	2	Q5ELV8_DROME	Q5elv8 drosophila
1191	83.5	5.0	624	2	Q5ELP3_DROSI	Q5elp3 drosophila	1264	83	5.0	600	2	Q59F94_HUMAN	Q59f94 homo sapien
1192	83.5	5.0	624	2	Q5VIF5_9ASTE	Q5vif5 cornus cf.	1265	83	5.0	601	1	UBQL4_HUMAN	Q9nr15 homo sapien
1193	83.5	5.0	632	2	Q5ELT8_DROME	Q5elt8 drosophila	1266	83	5.0	601	2	Q5VYAI_HUMAN	Q5vyai homo sapien
1194	83.5	5.0	641	2	Q86SD2_CIOIN	Q86sd2 ciona intes	1267	83	5.0	605	1	WSC4_YEAST	P38739 saccharomyc
1195	83.5	5.0	669	2	Q7EZY9_ORYSA	Q7ezy9 cryza sativ	1268	83	5.0	632	2	Q5ELU0_DROME	Q5elu0 drosophila
1196	83.5	5.0	674	2	Q6APL0_DESPS	Q6apl0 desulfofocale	1269	83	5.0	632	2	Q5ELU8_DROME	Q5elu8 drosophila
1197	83.5	5.0	789	2	Q57ZE5_9TRYP	Q57ze5 trypanosoma	1270	83	5.0	639	2	Q6E8Z2_LISMO	Q6e8z2 listeria mo
1198	83.5	5.0	791	2	Q66VC3_GALPH	Q66vc3 equid herpe	1271	83	5.0	653	1	NUMB_MOUSE	Q9qrs3 mus musculu
1199	83.5	5.0	800	2	Q8TFG4_SCHPO	Q8tf4 schizosacch	1272	83	5.0	661	2	Q9V8S2_DROME	Q9v8s2 drosophila

1273	83	5.0	679	2	Q59DM1_CAEEL	Q59dm1 caenorhabdi	1346	82.5	5.0	456	1	Y883_HAEIN	P44917 haemophilus
1274	83	5.0	737	1	KNS1_YEAST	P32350 saccharomyc	1347	82.5	5.0	456	2	Q4QM25_HAE18	Q4qm25 haemophilus
1275	83	5.0	738	1	VU47_HHV6Z	P52549 human herpe	1348	82.5	5.0	459	2	Q5S828_CRYNE	Q5s828 cryptococcu
1276	83	5.0	762	2	Q86AG3_DICDI	Q86ag3 dictyosteli	1349	82.5	5.0	464	2	Q9C247_NEUCR	Q9c247 neuospora
1277	83	5.0	769	2	Q17921_CAEEL	Q17921 caenorhabdi	1350	82.5	5.0	508	2	Q6VNX4_DROSA	Q6vnx4 drosophila
1278	83	5.0	771	2	Q4WCD2_ASPFU	Q4wcd2 aspergillus	1351	82.5	5.0	517	2	Q5AF50_CANAL	Q5af50 candida alb
1279	83	5.0	786	2	Q9FDM5_STRAG	Q9fdm5 streptococc	1352	82.5	5.0	540	1	CH60_STRAS	Q8cx22 streptococc
1280	83	5.0	794	2	Q5SCQ4_DICDI	Q5scq4 dictyosteli	1353	82.5	5.0	540	1	CH60_STRAS	Q8cx22 streptococc
1281	83	5.0	797	1	VGLX_EHVLB	Q5SCQ4 dictyosteli	1354	82.5	5.0	540	1	CH60_STRAS	Q8cx22 streptococc
1282	83	5.0	806	2	Q5R6R3_PONPY	P28968 equine herp	1355	82.5	5.0	569	2	Q9SL10_ARATH	Q9sl10 arabidopsais
1283	83	5.0	814	2	Q5SAJ1_DICDI	Q5raj1 dictyosteli	1356	82.5	5.0	582	2	Q54W91_DICDI	Q54w91 dictyosteli
1284	83	5.0	826	2	Q8V0L5_GALPH	Q8v0l5 equid herpe	1357	82.5	5.0	598	2	Q5ELW5_DROSI	Q5elw5 drosophila
1285	83	5.0	832	2	Q6QJ51_CAEER	Q6qj51 caenorhabdi	1358	82.5	5.0	599	2	Q5ELY0_DROME	Q5ely0 drosophila
1286	83	5.0	858	2	Q3H8D9_HUMAN	Q3h8d9 homo sapien	1359	82.5	5.0	602	2	Q4V707_DROME	Q4v707 drosophila
1287	83	5.0	866	1	VGLX_EHVLV	Q666w0 equine herp	1360	82.5	5.0	607	2	Q8GNR4_LISMO	Q8gnr4 listeria mo
1288	83	5.0	866	2	Q39781_GALPH	Q39781 equid herpe	1361	82.5	5.0	623	2	Q5LYX7_STRT1	Q5lyx7 streptococc
1289	83	5.0	867	2	Q39782_GALPH	Q39782 equid herpe	1362	82.5	5.0	623	2	Q5M3J0_STRT2	Q5m3j0 streptococc
1290	83	5.0	904	2	Q5SM65_HUMAN	Q5sm65 homo sapien	1363	82.5	5.0	624	2	Q5VRJ4_CORSU	Q5vrf4 cornus suet
1291	83	5.0	955	2	Q5SQ29_HUMAN	Q5sq29 homo sapien	1364	82.5	5.0	624	2	Q5VRJ6_CORSU	Q5vrf6 cornus suet
1292	83	5.0	963	1	LRP8_HUMAN	Q4114 homo sapien	1365	82.5	5.0	624	2	Q5VFJ7_CORSU	Q5vff7 cornus suet
1293	83	5.0	963	2	Q5SM67_HUMAN	Q5sm67 homo sapien	1366	82.5	5.0	624	2	Q5VFJ9_9ASTE	Q5vff9 cornus unal
1294	83	5.0	985	2	Q5KL22_CRYNE	Q5kl22 cryptococcu	1367	82.5	5.0	624	2	Q5VFK1_9ASTE	Q5vfk1 cornus cf.
1295	83	5.0	985	2	Q5V60_CRYNE	Q5v60 cryptococcu	1368	82.5	5.0	624	2	Q675N1_CORSU	Q675n1 cornus suet
1296	83	5.0	1002	2	Q6CBP5_YARLI	Q6cbd5 yarrowia li	1369	82.5	5.0	635	2	Q66065_FIBSU	Q66065 fibrobacter
1297	83	5.0	1030	2	Q7QV30_GIALA	Q7qv30 giardia lam	1370	82.5	5.0	639	2	Q6E910_LISMO	Q6e910 listeria mo
1298	83	5.0	1069	2	Q519R3_ENTHI	Q519r3 entamoeba h	1371	82.5	5.0	639	2	Q6E940_LISMO	Q6e940 listeria mo
1299	83	5.0	1080	2	Q510Y4_ENTHI	Q510y4 entamoeba h	1372	82.5	5.0	641	2	Q5KHD0_CRYNE	Q5khd0 cryptococcu
1300	83	5.0	1126	2	Q8E6U1_STRA3	Q8e6u1 streptococc	1373	82.5	5.0	646	2	Q4J6E4_SULAC	Q4j6e4 sulfolobus
1301	83	5.0	1183	2	Q8GCD1_CHLAU	Q8gcd1 chloroflexu	1374	82.5	5.0	686	2	Q8NVE4_STAAM	Q8nve4 staphylococ
1302	83	5.0	1184	2	Q4IHX0_GIBZE	Q4ihx0 gibberella	1375	82.5	5.0	698	2	Q74LM8_LACJO	Q74lm8 lactobacill
1303	83	5.0	1215	1	G2158_HUMAN	Q5t848 homo sapien	1376	82.5	5.0	706	2	Q5CL90_CRYHO	Q5cl90 cryptospori
1304	83	5.0	1221	2	Q8X1D8_ASPFU	Q8xid8 aspergillus	1377	82.5	5.0	711	2	Q7YYX9_CRYPV	Q7yyx9 cryptospori
1305	83	5.0	1265	2	Q9P2G7_HUMAN	Q9p2g7 homo sapien	1378	82.5	5.0	726	1	NF11_YEAST	Q12216 saccharomyc
1306	83	5.0	1266	2	Q4X245_ASPFU	Q4x245 aspergillus	1379	82.5	5.0	728	2	Q7NB51_MYCULA	Q7nb51 mycoplasma
1307	83	5.0	1377	2	Q54ND2_DICDI	Q54nd2 dictyosteli	1380	82.5	5.0	782	2	Q6CNV3_KLUGA	Q6cnv3 kluyveromyc
1308	83	5.0	1458	2	Q54P34_DICDI	Q54pj4 dictyosteli	1381	82.5	5.0	790	1	ADA30_HUMAN	Q5ukf2 homo sapien
1309	83	5.0	1646	2	Q5CF26_CRYHO	Q5cf26 cryptospori	1382	82.5	5.0	790	2	Q5T3X6_HUMAN	Q5t3x6 homo sapien
1310	83	5.0	1686	2	Q7RZ86_NEUCR	Q7rzc6 neuospora	1383	82.5	5.0	808	2	Q81123_CAEEL	Q81123 caenorhabdi
1311	83	5.0	2081	2	Q5SQ28_HUMAN	Q5sq28 homo sapien	1384	82.5	5.0	825	2	Q30088_SACCHAROMYC	Q30088 saccharomyc
1312	83	5.0	2162	2	Q8N3U0_HUMAN	Q8n3u0 homo sapien	1385	82.5	5.0	833	2	Q602T7_METCA	Q602t7 methylococc
1313	83	5.0	2210	2	Q7Z3E7_HUMAN	Q7z3e7 homo sapien	1386	82.5	5.0	848	2	Q6GP20_XENLA	Q6gp20 xenopus lae
1314	83	5.0	2478	2	Q9LCH2_STAAM	Q9lch2 staphylococ	1387	82.5	5.0	871	1	POB1_SCHPO	Q64653 schizosacch
1315	83	5.0	2478	2	Q9RL69_STAAM	Q9rl69 staphylococ	1388	82.5	5.0	876	2	Q6XLT5_BRARE	Q6xlt5 brachydanio
1316	83	5.0	2478	2	Q9HE44_STAAC	Q9he44 staphylococ	1389	82.5	5.0	886	2	Q52B52_MAGGR	Q52b52 magnaportha
1317	83	5.0	3300	2	Q4N127_THEPA	Q4n127 theileria p	1390	82.5	5.0	988	2	Q8UVU2_XENLA	Q8uvu2 xenopus lae
1318	83	5.0	6011	2	Q4U447_POLCB	Q4u447 polyangium	1391	82.5	5.0	993	2	Q92JUC5_RICKETTSIA	Q92juc5 rickettsia
1319	82.5	5.0	184	2	Q7PRM2_ANOGA	Q7prm2 anopheles g	1392	82.5	5.0	1042	2	Q54IH7_DICDI	Q54ih7 dictyosteli
1320	82.5	5.0	197	2	Q26878_TRYCR	Q26878 trypanosoma	1393	82.5	5.0	1091	2	Q7SDT8_NEUCR	Q7sd88 neuospora
1321	82.5	5.0	231	2	Q86LC2_9CNID	Q86lc2 zoanthus sp	1394	82.5	5.0	1124	2	Q50XX8_ENTHI	Q50xx8 entamoeba h
1322	82.5	5.0	252	2	Q6GZ06_9MONO	Q6gz06 avian pneum	1395	82.5	5.0	1163	2	Q7PY32_ANOGA	Q7py32 anopheles g
1323	82.5	5.0	258	2	Q7SGP8_NEUCR	Q7sgp8 neuospora	1396	82.5	5.0	1167	2	Q54CK8_DICDI	Q54ck8 dictyosteli
1324	82.5	5.0	286	2	Q7SNA27_NEUCR	Q7saz7 neuospora	1397	82.5	5.0	1181	2	Q52A92_MAGGR	Q52a92 magnaportha
1325	82.5	5.0	290	1	LECR_CLALU	Q7xa59 lilium long	1398	82.5	5.0	1206	1	FMN1B_MOUSE	Q05859 mus musculu
1326	82.5	5.0	308	2	Q7XA59_LILLO	Q7xa59 ceratitidis c	1399	82.5	5.0	1258	2	Q4HVR5_GIBZE	Q4hvr5 gibberella
1327	82.5	5.0	326	2	Q9NFX5_CERCA	Q9nfx5 anolis sagr	1400	82.5	5.0	1258	2	Q86IA2_DICDI	Q86ia2 dictyosteli
1328	82.5	5.0	345	2	Q690V6_ANOSA	Q690v6 anolis sagr	1401	82.5	5.0	1259	2	Q614L3_CAEER	Q614l3 caenorhabdi
1329	82.5	5.0	345	2	Q690V7_ANOSA	Q690v7 anolis sagr	1402	82.5	5.0	1260	2	Q5G5G1_DICDI	Q5g5g1 dictyosteli
1330	82.5	5.0	345	2	Q690X3_ANOSA	Q690x3 anolis sagr	1403	82.5	5.0	1261	2	Q7R2F4_GIALA	Q7r2f4 giardia lam
1331	82.5	5.0	345	2	Q691U6_ANOSA	Q691u6 anolis sagr	1404	82.5	5.0	1267	2	Q54VU8_DICDI	Q54v8 dictyosteli
1332	82.5	5.0	345	2	Q691L2_ANOSA	Q691l2 anolis sagr	1405	82.5	5.0	1343	2	Q61MH3_CAEER	Q61mh3 caenorhabdi
1333	82.5	5.0	345	2	Q692A4_ANOSA	Q692a4 anolis sagr	1406	82.5	5.0	1371	2	Q9VU22_DROME	Q9vu22 drosophila
1334	82.5	5.0	345	2	Q692C2_9SAUR	Q692c2 anolis quad	1407	82.5	5.0	1383	2	Q5BLU5_EMENI	Q5blu5 apergillus
1335	82.5	5.0	346	2	Q5CE07_CRYHO	Q5ce07 cryptospori	1408	82.5	5.0	1468	1	FMPC_CHLMU	Q05860 mus musculu
1336	82.5	5.0	383	1	V82_HPV57	P22155 human papil	1409	82.5	5.0	1468	1	FMN1A_MOUSE	Q05860 mus musculu
1337	82.5	5.0	389	2	Q64BB8_9ARCH	Q64bb8 uncultured	1410	82.5	5.0	1472	2	Q6V9R4_STRPU	Q6v9r4 strongyloce
1338	82.5	5.0	389	2	Q6GX00_9VIRU	Q6gx00 swine hepat	1411	82.5	5.0	1478	1	LPHN2_BOVIN	Q97817 bos taurus
1339	82.5	5.0	389	2	Q6GX32_9VIRU	Q6gx32 swine hepat	1412	82.5	5.0	1809	2	Q4Q8Z5_LEIMA	Q4q8z9 leishmania
1340	82.5	5.0	389	2	Q6GX33_9VIRU	Q6gx33 swine hepat	1413	82.5	5.0	1969	2	Q7SEZ5_NEUCR	Q7se25 neuospora
1341	82.5	5.0	391	2	Q54XR0_DICDI	Q54xf0 dictyosteli	1414	82.5	5.0	2311	1	ROS_CHICK	P08941 gallus gall
1342	82.5	5.0	400	2	Q9SQ87_BRAJU	Q9sqf7 brassica ju	1415	82.5	5.0	2381	2	Q54QC0_DICDI	Q54qc0 dictyosteli
1343	82.5	5.0	416	2	Q9K8G4_BACHU	Q9k8g4 bacillus ba	1416	82.5	5.0	4483	2	Q51QB7_MAGGR	Q51qb7 magnaportha
1344	82.5	5.0	425	2	Q54VC3_DICDI	Q54vc3 dictyosteli	1417	82.5	4.9	166	2	Q5IE00_PINTA	Q5ie00 pinus taeda
1345	82.5	5.0	452	2	Q6CE56_YARLI	Q6ce56 yarrowia li	1418	82.5	4.9	166	2	Q5IE20_PINTA	Q5ie20 pinus taeda





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Matches 319; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARCFSLVLLTSTWTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTAEKA 60
DB 1 MARCFSLVLLTSTWTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTAEKA 60
QY 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
DB 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
QY 121 SRQFAAYCYNSSDTWNTNSCIPEIITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIPA 180
DB 121 SRQFGAYCYNSSDTWNTNSRIPEIITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIPA 180
QY 181 PTTTPPAPASTSIPRRKKLCVTEVFMETSTMTSTETEPFVENKAAPKNEAAGFGVPTAL 240
DB 181 PTTTPPAPASTSIPRRKKLCVTEVFMETSTMTSTETEPFVENKAAPKNEAAGFGVPTAL 240
QY 241 LVALLPFGAAAGLFCYVKRYKAFPTTNKQKEMIEYKVKKEKANDSNFNEESKKT 300
DB 241 LVALLPFGAAAGLFCYVKRYKAFPTTNKQKEMIEYKVKKEKANDSNFNEESKKT 300
QY 301 DKNPEESKSPSKTTVRCLAEV 322
DB 301 DKNPEESKSPSKTTVRCLAEV 322

RESULT 4
Q8UC88_BOVIN
ID Q8UC88_BOVIN PRELIMINARY; PRT; 322 AA.
AC Q8UC88;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cell surface retention sequence binding protein-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
RA Huang J.S.;
RT Cloning, expression, characterization and role in autocrine cell
RT growth of cell surface retention sequence binding protein-1.;
RL J. Biol. Chem. 278:43855-43869(2003).
DR EMBL; AY372937; AAQ85130.1; -; mRNA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PSS0963; LINK_2; 1.
SQ SEQUENCE 322 AA; 35561 MW; 4901DA1BF92648AE CRC64;

Query Match 70.9%; Score 1174; DB 2; Length 322;
Best Local Similarity 71.1%; Pred. No. 1.6e-86;
Matches 229; Conservative 34; Mismatches 59; Indels 0; Gaps 0;
QY 1 MARCFSLVLLTSTWTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTAEKA 60
DB 1 MARCFSLVLLTSTWTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTAEKA 60
QY 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
DB 61 CRLVGLTASQDQVEARKEFGFTCSYGVGVKQFVVIPRIISNPKCGKNGVVIWRSSL 120
QY 121 SRQFAAYCYNSSDTWNTNSCIPEIITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIPA 180
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DB 121 SSRHRSYCHNSDIWNSCLPEIITTDPLPTEATATYTKLWVSDSTHSELSTDGPDYV 180
QY 181 PTTTPPAPASTSIPRRKKLCVTEVFMETSTMTSTETEPFVENKAAPKNEAAGFGVPTAL 240
DB 181 TTTVAPPLASTTPRRKKLCITTEAFMDTSAVATERESDIQNPAPKNEAVGFGVPTAL 240
QY 241 LVALLPFGAAAGLFCYVKRYKAFPTTNKQKEMIEYKVKKEKANDSNFNEESKKT 300
DB 241 LVALLPFGAAAGLFCYVKRYKAFPTTNKQKEMIEYKVKKEKANDSNFNEESKKT 300
QY 301 DKNPEESKSPSKTTVRCLAEV 322
DB 301 NKTPEEPKSPKTTVRCLAEV 322

RESULT 5
Q8BHC0_MOUSE
ID Q8BHC0_MOUSE PRELIMINARY; PRT; 318 AA.
AC Q8BHC0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Extra cellular link domain-containing 1 [Mus musculus adult male lung
DE cDNA, RIKEN full-length enriched library, clone:1200012G08
DE product:extra cellular link domain-containing 1, full insert
DE sequence].
GN Name=Xlkdi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RA Strausberg R.J.
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Iwawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2003).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1101/1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Oeato N., Saito R., Suzuki H., Yamanaoka I., Quackenbush J.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Schoenbach C., Gojobori T.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis B.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Nagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Vetrardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes";  
RL Genome Res. 10:1617-1630(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC038653; AH38653.1; -; mRNA.  
DR EMBL; BC038892; AH38892.1; -; mRNA.  
DR EMBL; AK004726; BAC25094.1; -; mRNA.  
DR HSP; P98066; 107B.  
DR Ensembl; ENSMUSG0000030787; Mus musculus.  
DR MGI; MGI:2136348; Xlkd1.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005886; C:plasma membrane; IDA.  
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.  
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.  
DR InterPro; IPR000538; Link.  
DR Pfam; PF00193; Xlink; 1.  
DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
DR PROSITE; PS01241; LINK 1; UNKNOWN 1.  
DR PROSITE; PS0963; LINK 2; 1.  
SQ SEQUENCE 318 AA; 34573 MW; 34AA31AEF5430B08 CRC64;

Query Match 66.6%; Score 1103; DB 2; Length 318;  
Best Local Similarity 69.7%; Pred. No. 8.9e-81;  
Matches 221; Conservative 30; Mismatches 62; Indels 4; Gaps 3;

QY 6 SLVLLTTSITWTRLLVQGSRLAEELSLQVSCRTMGITLTKSKANQQLNFTKEACRLLG 65  
Db 6 SLVLLLASITWTRHPVQGDVLQDLSLSTCRIMGVALVGRNKNPNQNFTEAEACKMLG 64  
QY 66 LSLAGKQDVETALKASFETCSYGVWGDGFVVISRI SPNPKCGKNGVGLVVKVPVSRQFA 125  
Db 65 LTLASRDQVESAKSGFETCSYGVWGEQFSVIFRIPSNPCGKNGKGVLIWNPSSQKFK 124  
QY 126 AYCNSSDTWNSCIPEITTKDPIFNQTQTATOTTEFFIVSDTSYVASPYSTIPAPTTTP 185  
Db 125 AYCNSSDTWNSCIPEIVTTFYPVLDTQ--TPATEFVSSSAYLASSPDSPTTVPVSATT- 181  
QY 186 PAPASIPRKKLICTVEVFMETSMSTETEPVENKAFKNEAGFGVPTALLVLAL 245  
Db 182 RAPPLTSMARKTKKICITEVYTFPTETAFVASFAGFAAFKNEAGFGVPTALLVLAL 241  
QY 246 LFFGAAGLGFYKVRVKAFFPTNKQOKEMETKVKKEKANDSNPNESKKTDKNPE 305  
Db 242 LFFGAARAVLCVVKRYKAFPTTNKQOKEMETKVKKEKADNVNANESKKTIKNPE 301  
QY 306 ESKSPSKTIVRCLEAEV 322  
Db 302 EAKSPKPTIVRCLEAEV 318

RESULT 6  
Q99NE4\_MOUSE  
ID Q99NE4\_MOUSE PRELIMINARY; PRT; 318 AA.  
AC Q99NE4;  
DT 01-JUN-2001 (T-EMBLrel. 17, Created)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)









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DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; F:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS50963; LINK_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 437 AA; 49108 MW; 7088441D0E138C10 CRC64;

Query Match 13.9%; Score 229.5; DB 2; Length 437;
Best Local Similarity 26.3%; Pred. No. 5.6e-10;
Matches 82; Conservative 34; Mismatches 111; Indels 85; Gaps 10;

QY 34 VSCRIMGTLVSKKANQOLNTEAKEACRLGLSLAGKQVETALKASFETCSYGVWDG 93
DB 24 ISCRFKGVFHFVEKYDRYALNRNDAIKLCHELTNTIANITLMEIAQDIGFETCRYGWIEDR 83

QY 94 FVWTSRISPNPKCGNGVGLWIKVPVSRQFAAYCYNSSDTWTNSCIP-----E 142
DB 84 -VVIPRIKPNICAAHYTGIFLGNNDLSRYDAICYNASETEDKSCEPVLLNEDTDLSHK 142

QY 143 IITTKDPIFNQTQTATQTTEFIVSDYSTVSASPYSTIPAP-----TTTTPPA-PASTS 192
DB 143 TIDSVDPTLQNPRTQNSDKSGTVDPGFAMITPDGQDWDIDIGTTPDHGDPFSTK 202

QY 193 IPRKKLICVTEFVNETSTMSTE--TEPPVENKAAPKFAAGVGPVPTALLVALLPFGA 250
DB 203 -----GDGSDSTEQTNEFGDIDH-----SGYQEVPG----- 227

QY 251 AAGLGFYVYKRYKAPPTNNQOKMETETKVVKEEKANDSNPEESKK----- 299
DB 228 -----HVFPGTDHEVNE-PDTEHTTENSDDSGHYEHPRHHDQDNTGRD 273

QY 300 -TDKNPESKSP 310
DB 274 YTRPDDESSKEP 285

RESULT 12
O70509 RAT PRELIMINARY; PRT; 364 AA.
AC O70509;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Glycoprotein CD44s (Cd44 protein).
GN Name=CD44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=lumbar spine;
RA Stevens J.W.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RP [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney, and Pituitary gland;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.W., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG NIH MGC Project;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065147; AAC17117.1; -; mRNA.
DR EMBL; BC061531; AAHG1531.1; -; mRNA.
DR EMBL; BC085703; AAH85703.1; -; mRNA.
DR HSSP; P98066; 107B.
DR SMR; O70509; 24-172.
DR Ensembl; ENSRNOC0000006094; Rattus norvegicus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR PROSITE; PS01241; LINK_1; 1.
DR PROSITE; PS50963; LINK_2; 1.
SQ SEQUENCE 364 AA; 39725 MW; BA249776C419AA7 CRC64;

Query Match 13.7%; Score 227; DB 2; Length 364;
Best Local Similarity 24.3%; Pred. No. 7.2e-10;
Matches 86; Conservative 55; Mismatches 153; Indels 60; Gaps 13;

QY 15 WTRFLIVQGSIRAEELSIQVSCRIMGITLVSKKANQOLNTEAKEACRLGLSLAGKDOV 74
DB 10 WGLLCLQLSLAQOQIDNLITCRYAGVFHFVEKNGRYSISRTEAADLCEAFNTTLTPTWAQM 69

QY 75 ETALKASFETCSYGVWDGFWIWSRISPNPKCGNGVGLWIKVPVSRQFAAYCYNSSDT 134
DB 70 ELALSKGFETCRYGFI-EGHVIPRIHPNAICANNTGVVILLASNTSHDYTYCFNASAP 128

QY 135 WTNSCIPEIITTKDPIFNQTQTATQTTEFIVSDST-YSVASPYST-----IPAPT----- 182
DB 129 LEEDC-----TSVTDLPNSPDGPTTITVNRDGRTRYSKGGEYRTHQEDIDASNIIDEDVS 183

QY 183 -----TTPPA-PASTSIPRKKLICVTEFVNETSTMST-ETEPFVENKAAPK-----N 228
DB 184 SGSTIEKSTPEGYILHTDLTPTSQPTGDRDDAFFTGTSATSDGSSMDPRGGFTVTTHGS 243

QY 229 EAAGFGG-----VPTALLVALLPFGAAAGLFCVVKRYKAFPTN 270
DB 244 ELAGHSSGNQDSGVTTTSGPARRPOIPEWILLASL-LALAILAVC-----IAVNSRR 297

QY 271 KNOQKEMIEYK---VVKEEKANDSNPEESKKTKDNPEESKSPKTTVRCLEAE 321
DB 298 CGQKKKLIVNSGNGTVEDRKPSELN-GEASKSQEMVHLVNKEPTETPDQPMFAD 350
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RESULT 13  
CD44\_PAPHA STANDARD; PRT; 362 AA.  
AC P14745;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)  
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte  
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).  
GN Name=CD44;  
OS Papio hamadryas (Hamadryas baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Papio.  
OX NCBI\_TaxID=9557;  
RN [1]  
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 66-74.  
RX MEDLINE=89282830; PubMed=2471974;  
RA Idzerda R.L.; Carter W.G.; Nottenburg C.; Wayner E.A.; Gallatin W.M.;  
RA St John T.;  
RT "Isolation and DNA sequence of a cDNA clone encoding a lymphocyte  
RT adhesion receptor for high endothelium."  
RL Proc. Natl. Acad. Sci. U.S.A. 86:4659-4663(1989).  
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to  
CC mucosal high endothelial venule and to types I and VI collagen.  
CC Probably involved in matrix adhesion, lymphocyte activation and  
CC lymph node homing.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- PM: Extensively modified including N- and O-linked glycosylation,  
CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,  
CC of phosphate to cytoplasmic domain serine residues.  
CC -!- SIMILARITY: Contains 1 Link domain.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; M22452; AAA35385.1; -; mRNA.  
CC HSP; P98066; ITSG.  
DR HSR; P14745; 20-168.  
DR InterPro; IPR001231; CD44 antigen.  
DR InterPro; IPR000538; Link.  
DR Pfam; PF00193; Xlink; 1.  
DR PRINTS; PR00658; CD44.  
DR PRINTS; PR01265; LINKMODULE.  
DR PRODOM; PD000918; Link; 1.  
DR PROSITE; PS01241; LINK\_1; 1.  
DR PROSITE; PS00963; LINK\_2; 1.  
KW Alternative splicing; Cell adhesion; Direct protein sequencing;  
KW Glycoprotein; Phosphorylation; Proteoglycan;  
KW Pyrrolidone carboxylic acid; Receptor; Signal; Transmembrane.  
FT SIGNAL 1 20  
FT CHAIN 21 362  
FT CD44 antigen.  
FT TOPO\_DOM 21 269  
FT TRANSHEM 270 290  
FT TOPO\_DOM 291 362  
FT DOMAIN 32 120  
FT REGION 225 269  
FT COMPBIAS 150 158  
FT MOD\_RES 21 21  
FT MOD\_RES 292 292  
FT MOD\_RES 326 326  
FT CARBOHYD 25 25  
FT CARBOHYD 57 57  
FT CARBOHYD 100 100  
FT CARBOHYD 110 110  
FT CARBOHYD 120 120  
FT CARBOHYD 256 256  
FT DISULFID 53 118

FT DISULFID 77 97 By similarity.  
FT CONFLICT 67 E -> V (in Ref. 1; AA sequence).  
SQ SEQUENCE 362 AA; 39379 MW; 578BFE7C3D52FF CRC64;  
  
Query Match 13.4%; Score 222.5; DB 1; Length 362;  
Best Local Similarity 25.5%; Pred. No. 1.7e-09;  
Matches 92; Conservative 43; Mismatches 127; Indels 99; Gaps 16;  
  
QY 20 LVQSLRAEELSTQVSCRMGITLVSKKANQQNLNFTKEAKCELLGLSLAGKDOVETALK 79  
DB 14 LVQLSL--AQIDLNITCRFEGYHVEKNGRYSISRTEAADLCKAFNSTLTPTMAQMEKALS 71  
QY 80 ASFETCYGKVGDFVVISRIISPNKCGKNGVGLIWKVPVSQFAAYCVNSSDTWTNSC 139  
DB 72 IGPETCRYGFI-EGHVIVPRIHPNSICANNVTGVYLTNTS-QYDTYCFNASAPPGEDC 129  
QY 140 IPEIITTKDPIFNQTQTATQTFIVSDST-YSVASYSYTIPT-----APT----- 182  
DB 130 -----TSVTDLPNADFPTITITVNRDGTTRYVKKGERTNPEDINPSPTDDDDVSGSSS 184  
QY 183 -----TTPAPASTSIPRRKKLICVTEVFMETSTMTSTETEPFVENKAAP 226  
DB 185 ERSSTLGGYIFYNHFTSPPIPEDG-----PWITDTRTPATRDQGA 229  
QY 227 K-----NEAGF-----GG-----VPTALLVLALLFFGAAGLGFY 258  
DB 230 DPGSGSHTHGSESAGSHSGREGGANTTSGPLRTPOIPEWLIILASL-LALALILAVC- 287  
QY 259 VKRYKVAFFPTNNQOKEMIETK---VVIKEKANDSNPNEESKKTDK----NPESKSPS 311  
DB 288 ----IAVNSRRRCQKKLVINNGAVEDRKSSGLN-GEASKSQBMVHLVNKSESTPD 342  
QY 312 K 312  
DB 343 Q 343  
  
RESULT 14  
CD44\_RAT STANDARD; PRT; 503 AA.  
ID AC P26051; Q99021;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)  
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte  
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-  
DE 24).  
GN Name=Cd44;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).  
RC STRAIN=BDIX; TISSUE=Pancreas;  
RX MEDLINE=91191552; PubMed=1707342; DOI=10.1016/0092-8674(91)90403-L;  
RA Guenther U., Hofmann M., Rudy W., Reber S., Zoeller M., Haussmann I.,  
RA Matzku S., Wenzel A., Ponta H., Herrlich P.;  
RT "A new variant of glycoprotein CD44 confers metastatic potential to  
RT rat carcinoma cells".  
RL Cell 65:13-24 (1991).  
RN [2]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RA Stevens J.W., Midura R.J.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SULFATION OF TYR-288.  
RX PubMed=9692903;  
RA Slegman J.P., Rahmsdorf U., Steffen A., Ponta H., Herrlich P.;  
RT "CD44 variant exon v5 encodes a tyrosine that is sulphated".  
RL Eur. J. Biochem. 255:74-80(1998).



Query Match		13.2%;	Score 219.5;	DB 2;	Length 780;
Best Local Similarity		24.9%;	Pred. No. 7.3e-09;		
Matches	86;	Conservative	45;	Mismatches	144;
				Indels	71;
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Qy	15	WTTRELLVQGSURABELSIQVSCRMGITLVSKKANQOLNFTAKEACRLGLSLAGKDQV	74		
Db	10	WGLLCLLQLSLAQOOIDLNITCRYAGVHVVEKNGRYSISRTEADLCFAFNLTLPMAQM	69		
Qy	75	ETALKASFETCSYGMVGDFWISRIISPNCCKGNGVGLIWKVPVSRQFAAYCYNSSDT	134		
Db	70	ELARKGFETCRYGFI-EGHVVIPRIHPNAICANNTGVYILLASNTSHYDTYCFNASAP	128		
Qy	135	WTNSCIPEIITTKDPIENTQTATOTTEFIVSDST-YSVASPYST---IPAPT-----	182		
Db	129	LEEDC-----TSVTDLNSFDGPVTITIVNRDGTIRSKGGEYRTHQEDIDASNIIDEDVS	183		
Qy	183	-----TTPPA-PASTSIPIRRKKLICVTEVFMETSTMSTETETPFVENKAAFKNEAAG--	232		
Db	184	SGSTIEKSTPEGYILHTDLPTSOPTGDRDDAFFIGSTLAT-----IASTVYSKSHATAOK	238		
Qy	233	-----FCG-----VPTALLVLALFPGAA-----AGLGFYVYKRYKAPFFT	269		
Db	239	QNNWISWFGNSOSTTQTQDSPTTATTALMTTPTPPKQEAQNWFSW-----PF	289		
Qy	270	NKNQCKEMIEKVVKEEKANDSN-----PNEESK-KTDKNPEESKS	309		
Db	290	QPSESKSHLHTTKMPCGTESNTNPTGWKPNENEDETDKYPNFGS	335		

Search completed: March 20, 2006, 14:12:56  
Job time : 127.488 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:07:29 ; Search time 14.4292 Seconds

(without alignments)

2147.153 Million cell updates/sec

Title: US-10-063-510-6

Perfect score: 1657

Sequence: 1 MARCFSLVLLLTSLITRLL.....NPBESKSPSKTIVRCLEAEV 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	229.5	13.9	363	2 A37009	CD44 homolog membr
2	222.5	13.4	362	2 A30901	lymphocyte adhesio
3	222.5	13.4	365	2 A34424	CD44 membrane glyco
4	222	13.4	503	2 B38745	cell adhesion mole
5	217.5	13.1	362	2 A35616	T-cell surface glyco
6	208.5	12.6	366	2 A53286	cell-surface glyco
7	205	12.4	361	2 JH0417	cell adhesion mole
8	202.5	12.2	351	2 S45305	CD44 antigen precu
9	202	12.2	742	2 A47195	lymphocyte homing
10	199.5	12.0	426	2 JH0518	lymphocyte homing
11	199.5	12.0	493	2 S13530	CD44E protein, epi
12	198	11.9	395	2 I77371	CD44R5 - human
13	196.5	11.9	699	2 I37369	epican - human
14	185	11.2	359	2 S24240	lymphocyte surface
15	148.5	9.0	2109	1 I50421	aggreccan precursor
16	145.5	8.8	3562	2 A47171	chondroitin sulfat
17	145	8.8	277	2 A41735	hyaluronate-bindin
18	145	8.8	1069	2 T42681	hypothetical prote
19	144	8.7	275	2 JC6506	tumor necrosis fac
20	143	8.6	2327	2 T42630	aggreccan - bovine
21	137	8.3	276	2 A47290	TSG-6 homolog PS4
22	131.5	7.9	2124	2 A28452	proteoglycan core
23	131	7.9	2132	1 A55182	aggreccan precursor
24	130.5	7.9	883	2 S57653	brevican precursor
25	130.5	7.9	883	2 S49126	brevican precursor
26	130.5	7.9	2415	1 A39086	aggreccan precursor
27	128.5	7.8	912	2 A54423	brevican precursor
28	121	7.3	1340	2 A39808	proteoglycan core
29	117	7.1	340	2 JC7505	brain link protein

versican precursor  
aggreccan - pig (fr  
versican precursor  
versican precursor  
neutocan precursor  
glycoprotein 1 pre  
dihydroliopamide a  
LDL receptor 2 pre  
versican precursor  
proteoglycan link  
hypothetical prote  
hypothetical prote  
proteoglycan link  
brevican precursor  
proteoglycan link  
neutocan - mouse  
chondroitin sulfat  
versican - pig-tai  
proteoglycan link  
proteoglycan link  
hypothetical prote  
hypothetical prote  
hypothetical prote  
brevican precursor  
hypothetical prote  
neural cell adhesi  
hypothetical prote  
zonadhesin - mouse  
hypothetical prote  
hypothetical prote  
LDL receptor 1 pre  
LDL receptor 1 pre  
hypothetical prote  
chitinase (EC 3.2.  
hypothetical prote  
neural cell adhesi  
MID2 protein - yea  
neurexin III-alpha  
neurofascin - chic  
hypothetical prote  
period clock prote  
hypothetical prote  
mucin 5AC (clone J  
hypothetical prote  
hypothetical prote  
hypothetical prote  
BUD3 protein - yea  
endo-1,4-beta-xyla  
hypothetical prote  
CvC8 protein - yea  
96K lysosomal memb  
actA protein precu  
actin-assembly ind  
hypothetical prote  
structural protein  
hypothetical prote  
hypothetical prote  
hypothetical prote  
chaperonin 60 - cu  
E2 protein - human  
mucin FIM-C.1 - Af  
glucan 1,4-alpha-g  
hypothetical prote  
protein-tyrosine k  
salivary glue prot  
lysosome-associate  
probable zinc meta  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
endoglucanase C (E



103	88	5.3	456	2	T31483	hypoethetical prote	176	83	5.0	738	2	T44194	hypoethetical prote
104	88	5.3	564	2	T25945	hypoethetical prote	177	83	5.0	797	1	TGBEX1	glycoprotein X pre
105	88	5.3	602	2	AD2067	hypoethetical prote	178	83	5.0	866	2	T45462	membrane glycoprot
106	88	5.3	761	2	T00940	hypoethetical prote	179	83	5.0	867	2	T45463	membrane glycoprot
107	88	5.3	1631	1	SAZQK1	major merozoite su	180	83	5.0	977	2	T16232	hypoethetical prote
108	88	5.3	3507	2	T34513	hypoethetical prote	181	82.5	5.0	290	2	S66355	lectin-related stro
109	88	5.3	3570	2	T45025	mucin MUC5B, trach	182	82.5	5.0	383	1	S15624	E2 protein - human
110	87.5	5.3	825	2	T48431	hypoethetical prote	183	82.5	5.0	416	2	B84030	stage VI sporulati
111	87.5	5.3	1085	2	SA0476	Ca(2+)-sensing rec	184	82.5	5.0	456	1	H64099	probable amino aci
112	87.5	5.3	1091	1	IJCHNL	neural cell adhesi	185	82.5	5.0	569	2	B84470	Mutator-like trans
113	87.5	5.3	1802	2	S69703	HKR1 protein precu	186	82.5	5.0	726	2	S67044	NF11 protein - yea
114	87.5	5.3	2817	2	B97033	uncharacterized pr	187	82.5	5.0	825	2	S62042	probable membrane
115	87	5.3	2335	2	PC2022	mucin like protein	188	82.5	5.0	871	2	T43427	pob1 protein - fis
116	87	5.3	752	2	H72616	hypoethetical prote	189	82.5	5.0	993	2	S97717	hypoethetical prote
117	87	5.3	1016	2	H71460	probable outer mem	190	82.5	5.0	1206	2	S24407	formin isoform IV
118	87	5.3	1506	2	T30886	integumentary muc	191	82.5	5.0	1407	2	T18381	latrophilin-2 (spl
119	87	5.3	1537	2	S53465	flocculation prote	192	82.5	5.0	1407	2	T18385	latrophilin-2 (spl
120	86.5	5.2	400	1	A28172	spasmolysin precu	193	82.5	5.0	1422	2	T18383	latrophilin-2, spl
121	86.5	5.2	461	2	T22946	hypoethetical prote	194	82.5	5.0	1435	2	T18387	latrophilin-2 (spl
122	86.5	5.2	503	2	S63257	probable membrane	195	82.5	5.0	1450	2	T18382	latrophilin-2 (spl
123	86.5	5.2	550	2	T29919	hypoethetical prote	196	82.5	5.0	1460	2	D81675	polymorphic membra
124	86.5	5.2	740	1	FOIJD	gag polyprotein -	197	82.5	5.0	1463	2	T18386	latrophilin-2 (spl
125	86.5	5.2	1777	2	T34369	hypoethetical prote	198	82.5	5.0	1465	2	T18384	latrophilin-2 (spl
126	86.5	5.2	2616	2	A57096	nudel protein prec	199	82.5	5.0	1468	2	S11515	latrophilin-2 (spl
127	86	5.2	333	2	T27883	hypoethetical prote	200	82.5	5.0	1478	2	T18388	latrophilin-2 (spl
128	86	5.2	1785	2	A45546	major merozoite su	201	82.5	5.0	2311	1	TVCHSR	formin - mouse
129	85.5	5.2	575	2	S29316	chaperonin 60 - cu	202	82	4.9	260	1	G69223	kinase-related pro
130	85.5	5.2	649	2	T04606	protein kinase hom	203	82	4.9	389	2	T33340	hypoethetical prote
131	85.5	5.2	786	2	T16509	hypoethetical prote	204	82	4.9	410	1	B31959	lysosome-associate
132	85.5	5.2	895	2	T02597	Mutator-like trans	205	82	4.9	410	1	JC4317	lysosome-associate
133	85	5.1	265	2	T33695	hypoethetical prote	206	82	4.9	476	2	A46118	myosin-binding pro
134	85	5.1	576	2	S59829	hypoethetical prote	207	82	4.9	544	2	T15175	hypoethetical prote
135	85	5.1	627	2	G86860	serine/threonine p	208	82	4.9	577	2	G89430	protein K02E2.3 li
136	85	5.1	989	2	T47503	hypoethetical prote	209	82	4.9	584	2	T19061	hypoethetical prote
137	85	5.1	990	2	T51618	nucleolar phosphop	210	82	4.9	693	2	T19551	mucin-like protein
138	85	5.1	1162	2	T21557	hypoethetical prote	211	82	4.9	720	2	S51340	nucleoporin NUP2-1
139	85	5.1	1779	2	T31085	xylanase - Caldice	212	82	4.9	761	2	A96810	probable Mutator-1
140	84.5	5.1	463	2	B82001	probable amino-aci	213	82	4.9	894	2	B96557	probable receptor
141	84.5	5.1	493	2	JC5486	membrane glycoprot	214	82	4.9	911	2	B86438	hypoethetical prote
142	84.5	5.1	562	2	A57088	nucleoporin-like p	215	82	4.9	926	2	T38198	COPII coated vesic
143	84.5	5.1	658	2	T39500	serine/threonine-s	216	82	4.9	973	2	A97522	ribonuclease E, RN
144	84.5	5.1	658	2	S60170	protein kinase Pak	217	82	4.9	977	2	AC2741	ribonuclease E, RN
145	84.5	5.1	709	2	T28712	hypoethetical prote	218	82	4.9	1021	2	S64506	protein kinase BUB
146	84.5	5.1	1102	2	S65235	probable membrane	219	82	4.9	1023	2	JC4013	major acidic nucle
147	84.5	5.1	1161	2	S57180	probable membrane	220	82	4.9	1083	2	S59780	hypoethetical prote
148	84.5	5.1	2181	2	D90011	FnkB protein limpo	221	82	4.9	1127	2	T25804	hypoethetical prote
149	84.5	5.1	2761	2	T21064	hypoethetical prote	222	82	4.9	1672	2	C81675	polymorphic membra
150	84	5.1	262	2	T67772	hypoethetical prote	223	82	4.9	2738	2	B88320	protein F07A11.6 l
151	84	5.1	335	2	H96667	AP2-containing DNA	224	82	4.9	26926	1	T38344	titin, cardiac mus
152	84	5.1	420	2	AB2426	hypoethetical prote	225	81.5	4.9	235	2	T47379	hypoethetical prote
153	84	5.1	426	2	B53580	neurexin III beta	226	81.5	4.9	369	2	T01196	transcription fact
154	84	5.1	543	2	S35047	mucin JUL7 - human	227	81.5	4.9	386	2	B97212	protein containing
155	84	5.1	636	1	VCWVFS	env polyprotein -	228	81.5	4.9	463	2	B81228	sodium/alanine sym
156	84	5.1	793	2	AH1094	probable peptidogl	229	81.5	4.9	636	2	S63131	probable membrane
157	84	5.1	996	2	JE0237	apolipoprotein E r	230	81.5	4.9	687	2	A40711	RNA polymerase II
158	84	5.1	1075	2	S48992	flocculation prote	231	81.5	4.9	860	2	AG1612	DNA mismatch repai
159	84	5.1	1331	2	A48954	mannan endo-1,4-be	232	81.5	4.9	869	2	T22422	hypothetical prote
160	84	5.1	1362	2	A75207	amylopolyluanase p	233	81.5	4.9	1151	2	T18297	zinc-finger protei
161	84	5.1	1832	2	T31113	mucin-like glycopre	234	81.5	4.9	1212	2	T13804	sns protein - frui
162	84	5.1	3020	2	A43932	mucin 2 precursor,	235	81.5	4.9	1216	2	F88473	protein F40H6.5 li
163	83.5	5.0	216	2	I51920	mucin - rheus mac	236	81.5	4.9	1419	2	T30531	agglutinin-like ad
164	83.5	5.0	279	2	S53363	mucin 5AC (clone J	237	81.5	4.9	1445	1	A48148	protein-tyrosine-p
165	83.5	5.0	446	2	T45525	WSC4 homolog limpo	238	81.5	4.9	1513	2	T23681	hypothetical prote
166	83.5	5.0	967	2	S66852	hypoethetical prote	239	81.5	4.9	2282	2	T42717	DNA-binding protei
167	83.5	5.0	976	2	A87576	peptidase, M16 fam	240	81	4.9	339	2	T25562	hypothetical prote
168	83.5	5.0	1043	2	F97302	hypoethetical prote	241	81	4.9	413	2	S55890	plasma protein rec
169	83.5	5.0	1286	2	A88396	protein M01E10.2 l	242	81	4.9	422	1	BMRT2Y	synaptotagmin II -
170	83.5	5.0	3175	1	RRWVSV	genome polyprotein	243	81	4.9	651	2	C56653	membrane glycoprot
171	83	5.0	221	2	S53649	ribosomal protein	244	81	4.9	683	2	T10720	NADPH-ferrihemopro
172	83	5.0	409	2	S43446	RAD23 protein homo	245	81	4.9	683	2	T86358	membrane glycoprot
173	83	5.0	463	2	T38444	hypoethetical prote	246	81	4.9	911	2	S46497	aspartate kinase (
174	83	5.0	605	2	S48940	hypoethetical prote	247	81	4.9	1047	2	A55617	maquarade precurs
175	83	5.0	737	1	S64767	probable serine/th	248	81	4.9	1128	2	A49960	bud emergence prec

249	81	4.9	1169	2	S38181	flocculation prote	322	78.5	4.7	423	2	S69583	hypothetical prote
250	81	4.9	1367	2	S51959	hypothetical prote	323	78.5	4.7	542	2	S64030	probable membrane
251	81	4.9	1609	2	S25345	probable membrane	324	78.5	4.7	591	1	WMBPQ2	gene P2 protein -
252	81	4.9	1726	2	R39401	merozoite surface	325	78.5	4.7	599	2	S46630	hypothetical prote
253	81	4.9	6642	2	T29757	protein UNC-89 - C	326	78.5	4.7	688	2	B42161	myosin-light-chain
254	80.5	4.9	148	1	T07723	immediate-early se	327	78.5	4.7	815	2	JG0197	cGMP-gated cation
255	80.5	4.9	391	1	S15617	E2 protein - human	328	78.5	4.7	825	2	T29634	hypothetical prote
256	80.5	4.9	441	2	T31482	hypothetical prote	329	78.5	4.7	919	1	FX2P1P	H+-exporting ATPas
257	80.5	4.9	543	2	T22585	hypothetical prote	330	78.5	4.7	1011	1	JH0581	NAD ADP-ribosyltra
258	80.5	4.9	592	2	T34446	hypothetical prote	331	78.5	4.7	1356	2	T16754	hypothetical prote
259	80.5	4.9	595	2	A42086	CD30 antigen precu	332	78.5	4.7	1420	2	T17158	CL2AB protein - ra
260	80.5	4.9	742	2	T33514	hypothetical prote	333	78.5	4.7	1435	2	T46611	CL2BB protein - ra
261	80.5	4.9	798	2	T34248	hypothetical prote	334	78.5	4.7	1452	2	T17157	CL2AA protein - ra
262	80.5	4.9	918	2	I58178	glutamate receptor	335	78.5	4.7	1463	2	T17159	CL2AC protein - ra
263	80.5	4.9	1124	2	F71719	hypothetical prote	336	78.5	4.7	1467	2	T17160	CL2BA protein - ra
264	80.5	4.9	1159	1	A44280	inner layer protei	337	78.5	4.7	1478	2	T17185	CL2BC protein - ra
265	80.5	4.9	2225	2	T26083	hypothetical prote	338	78.5	4.7	1487	2	T14324	alpha-latrotoxin r
266	80	4.8	153	2	S67294	hypothetical prote	339	78.5	4.7	1876	2	E97944	zinc metalloprotei
267	80	4.8	177	1	RGBYGI	regulatory protein	340	78.5	4.7	3224	1	S58884	Ran-binding protei
268	80	4.8	345	2	T21776	hypothetical prote	341	78	4.7	253	2	S76719	hypothetical prote
269	80	4.8	359	2	T13478	hypothetical prote	342	78	4.7	260	2	AG2238	hypothetical prote
270	80	4.8	415	2	AE2237	hypothetical prote	343	78	4.7	266	2	T30919	hypothetical prote
271	80	4.8	451	2	S71754	cellular hepatitis	344	78	4.7	287	2	T12471	hypothetical prote
272	80	4.8	468	2	A55116	vacuolar ATPase (E	345	78	4.7	293	2	G87018	probable membrane
273	80	4.8	521	2	S69559	hypothetical prote	346	78	4.7	321	2	T26152	hypothetical prote
274	80	4.8	650	2	T41681	probable serine/th	347	78	4.7	340	2	AH0940	probable ABC trans
275	80	4.8	667	2	A40713	cyclicin I - bovine	348	78	4.7	372	2	T48660	heat shock protein
276	80	4.8	688	2	T18263	S-layer protein -	349	78	4.7	373	2	F81333	chaperone DnaJ Cj1
277	80	4.8	702	2	T34313	hypothetical prote	350	78	4.7	384	2	T21929	hypothetical prote
278	80	4.8	725	2	A41258	a-agglutinin core	351	78	4.7	425	2	T48724	hypothetical prote
279	80	4.8	881	2	S56032	probable membrane	352	78	4.7	434	2	B84684	hypothetical prote
280	80	4.8	1013	1	S04200	NAD ADP-ribosyltra	353	78	4.7	530	2	A45690	transactivator EBN
281	80	4.8	1348	2	S27812	probable epidermal	354	78	4.7	627	1	VCVM2	env polyprotein -
282	79.5	4.8	152	2	T15170	hypothetical prote	355	78	4.7	655	2	T30044	hypothetical prote
283	79.5	4.8	165	2	A27195	histone H1 - Tetra	356	78	4.7	786	1	A47547	serine proteinase
284	79.5	4.8	194	2	T75255	hypothetical prote	357	78	4.7	1050	2	T31853	hypothetical prote
285	79.5	4.8	354	2	T46740	microfilarial shea	358	78	4.7	1337	2	T30291	dextranase - Strep
286	79.5	4.8	461	1	A35356	tumor necrosis fac	359	78	4.7	1360	2	T33922	hypothetical prote
287	79.5	4.8	510	2	R72007	conserved hypothet	360	78	4.7	1442	1	B48148	protein-tyrosine-p
288	79.5	4.8	510	2	A86618	Cr861 hypothetical	361	78	4.7	1634	2	T26517	hypothetical prote
289	79.5	4.8	534	2	G84713	hypothetical prote	362	78	4.7	1723	2	H85657	polymorphic membra
290	79.5	4.8	554	2	JW0094	neurofilament prot	363	78	4.7	1723	2	E72067	polymorphic membra
291	79.5	4.8	580	2	T20716	hypothetical prote	364	78	4.7	1732	2	C81601	polymorphic membra
292	79.5	4.8	693	2	T25878	hypothetical prote	365	78	4.7	1955	1	AGCH	agrin precursor -
293	79.5	4.8	827	2	T04789	hypothetical prote	366	78	4.7	1995	2	T08166	probable membrane
294	79.5	4.8	860	2	AC1250	hypothetical prote	367	78	4.7	5327	2	T13564	microtubule-associ
295	79.5	4.8	998	2	S31735	DNA mismatch repai	368	77.5	4.7	275	2	T21933	hypothetical prote
296	79.5	4.8	1011	2	T20785	NAD ADP-ribosyltra	369	77.5	4.7	396	2	F83130	probable MFS trans
297	79.5	4.8	1280	2	E95031	hypothetical prote	370	77.5	4.7	401	2	AG3552	branched-chain ami
298	79.5	4.8	1365	2	S14871	alkaline amylopull	371	77.5	4.7	474	1	BMPFSY	synaptotagmin - fr
299	79	4.8	215	2	S26363	suppressor two of	372	77.5	4.7	476	2	T32032	hypothetical prote
300	79	4.8	249	2	G84781	histone H1.1 - hum	373	77.5	4.7	496	2	B41322	N-acetyluramoyl-L
301	79	4.8	352	2	T51659	hypothetical prote	374	77.5	4.7	514	2	JQ1317	activin receptor p
302	79	4.8	534	2	T39903	myb-related transc	375	77.5	4.7	519	2	T45764	hypothetical prote
303	79	4.8	575	2	T21775	serine-rich protei	376	77.5	4.7	526	2	A56573	hypothetical prote
304	79	4.8	611	2	AB1497	hypothetical prote	377	77.5	4.7	607	2	S01939	nuclear pore compl
305	79	4.8	710	2	S67098	internalin protein	378	77.5	4.7	623	2	T18892	hypothetical prote
306	79	4.8	738	2	T44007	probable membrane	379	77.5	4.7	816	2	S64439	hypothetical prote
307	79	4.8	739	2	T49456	hypothetical prote	380	77.5	4.7	860	2	JC4566	hypothetical prote
308	79	4.8	822	2	JC4076	dextranase (EC 3.2	381	77.5	4.7	906	2	G90281	conserved hypothet
309	79	4.8	836	2	S49940	cell division cont	382	77.5	4.7	938	2	A56731	chromatin assembly
310	79	4.8	949	2	S19808	glutamate receptor	383	77.5	4.7	975	2	T08606	protein phosphatas
311	79	4.8	1098	2	T08599	probable transcrip	384	77.5	4.7	993	1	PIVXTA	RNA 1 protein - to
312	79	4.8	1849	2	C41859	IgA-specific metal	385	77.5	4.7	1127	2	E86386	probable mutator-1
313	79	4.8	1904	2	T13256	tail-host specific	386	77.5	4.7	1156	2	T23748	hypothetical prote
314	78.5	4.7	152	2	T28759	hypothetical prote	387	77.5	4.7	1312	2	A97879	beta-N-acetylhexos
315	78.5	4.7	164	2	I53661	hypothetical prote	388	77.5	4.7	1475	2	S42718	nuclear pore compl
316	78.5	4.7	232	2	A60095	mucin 5AC - human	389	77.5	4.7	368	2	A44265	trichorax homolog
317	78.5	4.7	294	2	A37232	larval glue protei	390	77	4.6	257	2	G72690	probable spermidin
318	78.5	4.7	314	1	HNQZVW	mucin, tracheal (A	391	77	4.6	350	2	E75341	pepidyl-prolyl ci
319	78.5	4.7	314	1	JQ1793	hemagglutinin prec	392	77	4.6	353	2	S22805	env polyprotein -
320	78.5	4.7	322	2	A53715	apomucin precursor	393	77	4.6	453	2	F75206	maltose-binding pe
321	78.5	4.7	387	2	A53586	albumin-binding pr	394	77	4.6	528	2	S69589	hypothetical prote

395	77	4.6	553	2	T19894	hypothetical prote	468	76	4.6	1014	1	A29725	NAD ADP-ribosyltra
396	77	4.6	598	2	T22610	hypothetical prote	469	76	4.6	1041	2	H71617	SERA antigen/papai
397	77	4.6	623	2	A48123	cell cycle regulat	470	76	4.6	1046	2	T29776	hypothetical prote
398	77	4.6	639	2	T33166	hypothetical prote	471	76	4.6	1216	2	B90580	hypothetical prote
399	77	4.6	669	1	VCVWEK	env polyprotein -	472	76	4.6	1263	2	AH2011	heterocyst glycoli
400	77	4.6	734	2	B42680	nucleolus-cytoplas	473	76	4.6	1338	2	S09982	protein-tyrosine k
401	77	4.6	742	2	T42614	probable envelope	474	76	4.6	1348	2	A43917	probable epidermal
402	77	4.6	771	2	JC7388	M83 protein - huma	475	76	4.6	1388	2	A53317	collagen alpha 1(X
403	77	4.6	861	2	T23810	hypothetical prote	476	76	4.6	1401	2	T17452	werner syndrome pr
404	77	4.6	862	2	B36786	hypothetical prote	477	76	4.6	1422	2	T42636	protein-tyrosine-p
405	77	4.6	892	2	T09193	ataxin 7 - human	478	76	4.6	1438	2	B71610	WD40 WEB-1 homolog
406	77	4.6	897	2	S50550	SIN1-associated pr	479	76	4.6	1489	2	G71406	probable retroviro
407	77	4.6	967	2	G86229	hypothetical prote	480	76	4.6	1513	2	T44045	hypothetical prote
408	77	4.6	977	2	S49004	tyrosine kinase Mp	481	76	4.6	1890	2	T04556	hypothetical prote
409	77	4.6	1016	2	T11720	hypothetical prote	482	76	4.6	2570	2	T17451	fibriae-associate
410	77	4.6	1237	2	T14633	hypothetical prote	483	75.5	4.6	261	2	T30170	hypothetical prote
411	77	4.6	1401	2	T30247	Werner syndrome pr	484	75.5	4.6	273	2	T44657	protein GP80 [impo
412	77	4.6	1513	2	A54895	mucin 2, intestina	485	75.5	4.6	319	1	A35163	carbonate dehydrat
413	77	4.6	2187	2	T30826	nascent polypeptid	486	75.5	4.6	343	2	T40306	hypothetical prote
414	76.5	4.6	284	2	T42357	a-agglutinin core	487	75.5	4.6	348	1	B46216	transcription fact
415	76.5	4.6	349	2	T43457	hypothetical prote	488	75.5	4.6	364	1	OOHUG	opsin, green-sensi
416	76.5	4.6	382	2	S27388	neuropeptide Y rec	489	75.5	4.6	387	2	A86302	hypothetical prote
417	76.5	4.6	391	2	C69673	penicillin-binding	490	75.5	4.6	411	2	T03154	DNA polymerase pro
418	76.5	4.6	421	2	A60058	neural cell adhesi	491	75.5	4.6	412	2	B97279	TPR-repeat-contain
419	76.5	4.6	433	2	H84120	methyl-accepting c	492	75.5	4.6	430	1	A46216	transcription fact
420	76.5	4.6	482	2	AG1147	P60 extracellular	493	75.5	4.6	435	2	S40993	hypothetical prote
421	76.5	4.6	484	2	A41487	protein P60 precur	494	75.5	4.6	443	2	D72383	NADH oxidase - The
422	76.5	4.6	505	2	B46629	mucin 6, gastric (	495	75.5	4.6	445	2	I38521	inwardly rectifyin
423	76.5	4.6	518	2	G8961	protein F59A7.8 [i	496	75.5	4.6	448	2	S17370	DNA-binding protei
424	76.5	4.6	542	2	I39540	chitinase (EC 3.2.	497	75.5	4.6	468	2	S70297	SPS2 protein homol
425	76.5	4.6	549	2	S04845	Ig heavy chain pre	498	75.5	4.6	511	1	VGBBF4	glycoprotein C - h
426	76.5	4.6	640	1	VCVWML	env polyprotein -	499	75.5	4.6	609	2	G87496	peptidase, M23/M37
427	76.5	4.6	679	2	S64258	hypothetical prote	500	75.5	4.6	639	2	T13151	adaptor protein CM
428	76.5	4.6	718	2	T29708	hypothetical prote	501	75.5	4.6	665	2	G97213	probable membrane-
429	76.5	4.6	727	2	A88131	protein F10G7.9 [i	502	75.5	4.6	709	2	T32089	hypothetical prote
430	76.5	4.6	749	2	B86403	probable mutator-1	503	75.5	4.6	778	2	T43223	hypothetical prote
431	76.5	4.6	773	2	T00502	hypothetical prote	504	75.5	4.6	780	2	A48143	HF-1 regulatory el
432	76.5	4.6	806	2	E69424	hypothetical prote	505	75.5	4.6	963	2	T40290	hypothetical prote
433	76.5	4.6	990	2	T16554	hypothetical prote	506	75.5	4.6	1131	2	T41144	hypothetical serin
434	76.5	4.6	1154	1	VGIHIB	E2 glycoprotein pr	507	75.5	4.6	1166	2	S37692	probable tumor sup
435	76.5	4.6	1379	2	T45119	F1M protein [impor	508	75.5	4.6	1235	2	T13710	protein-tyrosine k
436	76.5	4.6	1736	2	F86178	hypothetical prote	509	75.5	4.6	1237	2	E86457	probable RNA helic
437	76.5	4.6	1946	2	JC6032	lactocepin (EC 3.4	510	75.5	4.6	1473	2	T31422	C-terminal domain-
438	76.5	4.6	3869	2	A48205	All-1 protein +GTE	511	75.5	4.6	1655	2	T32633	hypothetical prote
439	76.5	4.6	5037	2	B35041	ryanodine receptor	512	75.5	4.6	1737	2	A59235	unconventional myo
440	76	4.6	167	2	A33532	mucin SMCUC-40 - hu	513	75.5	4.6	1881	2	H95076	zinc metalloprotei
441	76	4.6	172	2	T21753	hypothetical prote	514	75.5	4.6	2526	2	T20531	hypothetical prote
442	76	4.6	243	2	B41710	promastigote surfa	515	75.5	4.6	3176	2	CGHJ3A	collagen alpha 3(V
443	76	4.6	356	2	D38979	hypothetical prote	516	75	4.5	94	2	S53365	mucin 5AC (clone C
444	76	4.6	368	2	S36584	protein F37B4.9 [i	517	75	4.5	128	2	T05035	hypothetical prote
445	76	4.6	378	2	A12180	E2 protein - human	518	75	4.5	205	2	S55670	hypothetical prote
446	76	4.6	382	2	B88561	hypothetical prote	519	75	4.5	248	2	AF1914	carbon dioxide con
447	76	4.6	384	2	A41710	protein F58A4.7b [	520	75	4.5	256	2	T09034	hypothetical prote
448	76	4.6	389	2	E97305	promastigote surfa	521	75	4.5	295	2	T28078	hypothetical prote
449	76	4.6	389	2	A47013	NADH-dependent but	522	75	4.5	310	1	H71054	hypothetical prote
450	76	4.6	499	2	T47722	butanol dehydrogen	523	75	4.5	313	2	AH0734	hypothetical prote
451	76	4.6	515	2	AD1162	probable protein k	524	75	4.5	353	2	S33322	Probable bacteriop
452	76	4.6	532	2	T28784	flagellar motor sw	525	75	4.5	388	2	T16861	(S)-2-hydroxy-acid
453	76	4.6	536	2	T37544	hypothetical prote	526	75	4.5	390	2	A72108	hypothetical prote
454	76	4.6	539	2	T02512	hypothetical serin	527	75	4.5	390	2	B86514	hypothetical prote
455	76	4.6	549	2	T49298	hypothetical prote	528	75	4.5	418	2	T16713	hypothetical prote
456	76	4.6	592	2	T16725	hypothetical prote	529	75	4.5	425	1	A26431	nerve growth facto
457	76	4.6	615	2	T47395	hypothetical prote	530	75	4.5	435	2	C40511	hypothetical prote
458	76	4.6	687	2	A49636	soluble vascular e	531	75	4.5	475	2	B84745	probable splicing
459	76	4.6	699	2	I38073	nucleolar phosphop	532	75	4.5	477	2	T32938	hypothetical prote
460	76	4.6	700	2	A54641	interspersed repea	533	75	4.5	481	2	T38149	pre-mrna splicing
461	76	4.6	763	2	T08929	hypothetical prote	534	75	4.5	554	2	A56596	chitinase (EC 3.2.
462	76	4.6	766	2	B85440	receptor kinase-li	535	75	4.5	604	2	T37984	probable splicing
463	76	4.6	824	2	T23923	hypothetical prote	536	75	4.5	607	2	S63395	probable membrane
464	76	4.6	929	2	G72677	hypothetical prote	537	75	4.5	651	2	T16450	hypothetical prote
465	76	4.6	940	2	AD1374	internalin protein	538	75	4.5	679	2	T19703	hypothetical prote
466	76	4.6	960	1	JN0677	protein-tyrosine k	539	75	4.5	739	2	I56187	transcription fact
467	76	4.6	994	1	MNVVM	nonstructural prot	540	75	4.5	775	1	WMBE19	ribonucleoside-dip

541	75	4.5	778	2	T45221	DNA damage checkpo	614	74	4.5	621	2	T20307	hypothetical prote
542	75	4.5	796	2	E96654	hypothetical prote	615	74	4.5	622	2	AC1236	acyltransferase (c
543	75	4.5	858	1	IJRTNC	neural cell adhesi	616	74	4.5	665	1	VCWVKA	env polyprotein pr
544	75	4.5	904	2	T03806	hypothetical prote	617	74	4.5	672	2	T20310	hypothetical prote
545	75	4.5	916	2	T20909	hypothetical prote	618	74	4.5	681	2	A45705	type I transmembr
546	75	4.5	940	2	D89723	protein F39D8.1b [	619	74	4.5	689	2	B43491	env polyprotein -
547	75	4.5	945	2	T21998	hypothetical prote	620	74	4.5	731	1	T04455	hypothetical prote
548	75	4.5	1048	1	S61388	dotA protein - Leg	621	74	4.5	739	1	A34873	transcription fact
549	75	4.5	1118	2	A48292	mucin, tracheobron	622	74	4.5	775	2	A32494	transposable eleme
550	75	4.5	1253	2	T18528	probable pyruvate	623	74	4.5	823	2	G90848	probable exonuclea
551	75	4.5	1741	2	T13610	parallel sister ch	624	74	4.5	823	2	E85706	probable exonuclea
552	75	4.5	1768	2	T13349	parallel sister ch	625	74	4.5	852	2	T06310	hypothetical prote
553	75	4.5	1838	1	CGHUIV	collagen alpha 1(V	626	74	4.5	862	2	S51493	major nitrogen reg
554	75	4.5	1979	2	T16222	hypothetical prote	627	74	4.5	903	2	T00705	N-chimerin homolog
555	75	4.5	3122	2	T17202	DNA-directed DNA p	628	74	4.5	1016	2	T19006	ankyrin related pr
556	75	4.5	3375	2	T19821	hypothetical prote	629	74	4.5	1018	2	T40253	hypothetical prote
557	74.5	4.5	148	2	S50553	hypothetical prote	630	74	4.5	1099	2	G90546	conserved hypotet
558	74.5	4.5	211	2	S28046	hypothetical prote	631	74	4.5	1104	2	S59310	probable membrane
559	74.5	4.5	254	2	D88560	protein F59A4.1 [i	632	74	4.5	1110	2	I51116	NF-180 - sea lamp
560	74.5	4.5	262	2	T33597	hypothetical prote	633	74	4.5	1115	1	IJMSNL	neural cell adhesi
561	74.5	4.5	276	-2	T51685	myb-related transc	634	74	4.5	1159	2	S62562	probable nuclear p
562	74.5	4.5	281	2	T49337	hypothetical prote	635	74	4.5	1164	2	B71429	phytochrome D - Ar
563	74.5	4.5	294	2	AI2016	hypothetical prote	636	74	4.5	1390	2	T14004	IgA protein - sli
564	74.5	4.5	310	1	YAZ031	300K antigen Ag231	637	74	4.5	1694	2	H64106	microtubule-associ
565	74.5	4.5	321	2	T50966	hypothetical prote	638	74	4.5	1828	2	A40115	myosin heavy chain
566	74.5	4.5	382	2	T25280	hypothetical prote	639	74	4.5	1938	1	MMKW1	transcription adap
567	74.5	4.5	396	2	T50229	probable transmemb	640	74	4.5	2114	2	A54277	prespore-specific
568	74.5	4.5	407	2	T26938	hypothetical prote	641	73.5	4.4	168	2	A31196	hypothetical prote
569	74.5	4.5	416	2	T20448	hypothetical prote	642	73.5	4.4	182	2	T30078	type III secretion
570	74.5	4.5	429	2	S29044	endoglucanase A pr	643	73.5	4.4	253	2	T32879	escu [imported] -
571	74.5	4.5	432	2	T08771	hypothetical prote	644	73.5	4.4	263	2	T38003	hypothetical prote
572	74.5	4.5	478	2	A32555	major merozoite su	645	73.5	4.4	292	2	S24169	hypothetical aet-t
573	74.5	4.5	482	2	T22754	hypothetical prote	646	73.5	4.4	305	2	S44661	mucin - rat
574	74.5	4.5	520	2	S14598	E2 glycoprotein -	647	73.5	4.4	335	2	AE3000	ZK353.4 protein -
575	74.5	4.5	531	2	S09859	hypothetical prote	648	73.5	4.4	345	2	D98283	cell division prot
576	74.5	4.5	551	2	S52287	urbain - silkworm	649	73.5	4.4	345	2	D91201	hypothetical prote
577	74.5	4.5	636	2	T32332	hypothetical prote	650	73.5	4.4	345	2	H86047	type III secretion
578	74.5	4.5	713	2	JE0230	NADPH-cytochrome p	651	73.5	4.4	358	2	AD2378	hypothetical prote
579	74.5	4.5	802	2	T21315	hypothetical prote	652	73.5	4.4	371	2	S20075	promastigote surfa
580	74.5	4.5	808	2	T23129	hypothetical prote	653	73.5	4.4	376	2	T48245	hypothetical prote
581	74.5	4.5	884	2	AE3166	ARP-dependent DNA	654	73.5	4.4	381	2	E69862	hypothetical prote
582	74.5	4.5	998	2	S37627	protein-tyrosine k	655	73.5	4.4	397	2	G69287	hypothetical prote
583	74.5	4.5	1042	2	T48801	endo-1,4-beta-xyla	656	73.5	4.4	405	2	A60534	P2B/LAMP-1 precurs
584	74.5	4.5	1595	2	T31082	hypothetical prote	657	73.5	4.4	445	2	A54852	potassium rectifie
585	74.5	4.5	1630	2	A53577	ascites siolglyco	658	73.5	4.4	447	2	A39321	mucin - rat (fragm
586	74.5	4.5	1902	2	C97702	cell surface antig	659	73.5	4.4	457	2	T20884	hypothetical prote
587	74.5	4.5	1965	2	T33216	hypothetical prote	660	73.5	4.4	458	2	T31631	hypothetical prote
588	74.5	4.5	2688	2	I49477	alpha-A-crystallin	661	73.5	4.4	459	2	I48854	gene murine tumour
589	74.5	4.5	3828	2	T13857	tri thorax protein	662	73.5	4.4	476	2	B44997	merozoite surface
590	74.5	4.5	3944	2	T19997	hypothetical prote	663	73.5	4.4	484	1	A24994	cellulose 1,4-beta
591	74	4.5	147	2	S09762	hypothetical prote	664	73.5	4.4	511	1	VGBE1K	glycoprotein C - h
592	74	4.5	223	2	T21930	hypothetical prote	665	73.5	4.4	540	2	H98086	chaperonin GroEL [
593	74	4.5	257	1	MGNZBR	major surface glyco	666	73.5	4.4	540	2	G95222	chaperonin, 60 kDa
594	74	4.5	264	2	A49149	mesoderm developme	667	73.5	4.4	542	2	T19952	hypothetical prote
595	74	4.5	286	2	S44835	F54H12.3 protein -	668	73.5	4.4	550	1	VG1HD6	E2 glycoprotein pr
596	74	4.5	305	2	AB2149	hypothetical prote	669	73.5	4.4	555	2	T26413	hypothetical prote
597	74	4.5	317	2	C85432	hypothetical prote	670	73.5	4.4	556	2	C87609	sensor histidine k
598	74	4.5	332	2	T31528	hypothetical prote	671	73.5	4.4	569	2	A46462	r cell activation
599	74	4.5	339	1	JT0756	group-V allergen i	672	73.5	4.4	601	2	H90270	hypothetical prote
600	74	4.5	339	2	A56274	sulfur-regulated 3	673	73.5	4.4	602	2	T39866	hypothetical prote
601	74	4.5	344	2	T13975	NADH2 dehydrogenas	674	73.5	4.4	626	2	AB1328	probable peptidogl
602	74	4.5	346	2	H84512	hypothetical prote	675	73.5	4.4	654	2	T33044	hypothetical prote
603	74	4.5	390	2	C97889	UDPGlucose 6-dehyd	676	73.5	4.4	696	2	G81262	probable integral
604	74	4.5	337	2	E97176	N-terminal domain	677	73.5	4.4	708	2	F87245	penicillin-binding
605	74	4.5	412	1	AJBORS	argininosuccinate	678	73.5	4.4	713	2	T44447	neuregulin-3 (impo
606	74	4.5	413	2	S28066	sexual differentiation	679	73.5	4.4	756	2	JCS586	signaling mediator
607	74	4.5	417	2	T20327	hypothetical prote	680	73.5	4.4	799	2	H71255	probable cell divi
608	74	4.5	435	2	AG1028	prepilin (imported	681	73.5	4.4	819	2	R95136	conserved domain p
609	74	4.5	454	2	T02100	hypothetical prote	682	73.5	4.4	901	2	A44825	phosphoprotein, sy
610	74	4.5	540	1	FOVWHL	gag polyprotein -	683	73.5	4.4	901	2	T02205	Lu-ECAM-1 protein
611	74	4.5	575	2	S39484	DNA-binding protei	684	73.5	4.4	990	2	H88733	protein F32E10.3 [
612	74	4.5	586	2	S66697	probable membrane	685	73.5	4.4	1004	2	T38074	hypothetical prote
613	74	4.5	600	2	T06292	hypothetical prote	686	73.5	4.4	1139	1	E64234	cytadherence-acces

687	73.5	4.4	1291	2	T22382	hypothenical prote	760	72.5	4.4	642	2	T39607	fork head protein
688	73.5	4.4	2232	2	T34434	hypothenical prote	761	72.5	4.4	648	2	PC4395	mucin 3 - human (f
689	73.5	4.4	4385	2	T29043	hypothenical prote	762	72.5	4.4	657	2	A82415	conserved hypothen
690	73	4.4	188	2	C96593	unknown protein, 9	763	72.5	4.4	663	2	T18631	hypothenical prote
691	73	4.4	198	2	E71837	protein-expo mem	764	72.5	4.4	710	2	A99486	ABC transporter, b
692	73	4.4	213	2	S43949	histone H1 - mouse	765	72.5	4.4	728	2	T72693	probable phosphoes
693	73	4.4	260	2	I50109	gastrulation prote	766	72.5	4.4	729	2	G96559	hypothenical prote
694	73	4.4	288	2	J02365	polyprotein - Bean	767	72.5	4.4	743	2	D86888	penicillin-binding
695	73	4.4	315	1	HNZV5V	hemagglutinin prec	768	72.5	4.4	765	1	T44946	transducer protein
696	73	4.4	316	2	G86333	hypothetical prote	769	72.5	4.4	896	2	S36326	clathrin assembly
697	73	4.4	327	2	S20074	promastigote surfa	770	72.5	4.4	907	1	Q08K21	membrane antigen g
698	73	4.4	359	2	S42787	serine/threonine-r	771	72.5	4.4	915	2	S36327	clathrin assembly
699	73	4.4	369	2	E84291	iron (III) ABC tra	772	72.5	4.4	944	2	C70839	probable ampol3 pro
700	73	4.4	422	2	A55417	synaptotagmin II -	773	72.5	4.4	982	2	A53253	microtubule-associ
701	73	4.4	428	1	Q4ECAD	damx protein (arob	774	72.5	4.4	1016	1	S70428	NAD ADP-ribosyltra
702	73	4.4	441	2	A43555	GAP-43-related pro	775	72.5	4.4	1036	2	S73601	protein P200 - Myc
703	73	4.4	448	2	G88639	protein C3H4.2 [i	776	72.5	4.4	1116	2	S77213	DNA-directed DNA p
704	73	4.4	461	2	T51044	related to spore c	777	72.5	4.4	1148	2	T09073	splicing factor Si
705	73	4.4	469	2	E64456	hypothenical prote	778	72.5	4.4	1152	2	A33183	microtubule-associ
706	73	4.4	482	2	A44997	merozoite surface	779	72.5	4.4	1180	2	E86719	hypothenical prote
707	73	4.4	486	2	S66097	cell-cycle protein	780	72.5	4.4	1199	2	A40670	nuclear envelope p
708	73	4.4	486	2	A89927	elastin binding pr	781	72.5	4.4	1219	2	T14578	nucleoporin Nup153
709	73	4.4	492	1	CHBOA3	gamma-aminobutyric	782	72.5	4.4	1222	2	T22490	hypothenical prote
710	73	4.4	496	2	E90181	hypothenical prote	783	72.5	4.4	1309	1	BVBVD9	RAD9 protein - yea
711	73	4.4	509	1	A37259	membrane glycoprot	784	72.5	4.4	1312	2	E95006	beta-N-acetylhexos
712	73	4.4	550	2	C75557	hypothenical prote	785	72.5	4.4	1555	2	T18688	hypothenical prote
713	73	4.4	558	2	A98199	translocated intim	786	72.5	4.4	1635	2	T14075	chitinase (BC 3.2.
714	73	4.4	558	2	E86045	probable transloca	787	72.5	4.4	1847	2	T18308	probable vitellogel
715	73	4.4	600	2	E72027	phosphoenolpyruvat	788	72.5	4.4	1973	2	G89608	protein B0272.5 [i
716	73	4.4	600	2	A86597	phosphoenolpyruvat	789	72.5	4.4	1973	2	T18686	hypothenical prote
717	73	4.4	669	2	A46511	envelope protein -	790	72.5	4.4	2305	2	B89608	protein C23f12.1 [
718	73	4.4	688	2	A43491	env polyprotein -	791	72.5	4.4	2305	2	T15571	hypothenical prote
719	73	4.4	720	2	T51007	hypothenical prote	792	72.5	4.4	2314	1	A46151	protein-tyrosine-p
720	73	4.4	728	2	T20561	hypothenical prote	793	72.5	4.4	2897	2	B48666	cell proliferation
721	73	4.4	781	2	T49472	hormone-sensitive	794	72.5	4.4	3069	2	H70656	fatty-acid synthas
722	73	4.4	814	2	T33140	hypothenical prote	795	72.5	4.4	3256	2	A48666	cell proliferation
723	73	4.4	880	2	S44833	F54H12.5 protein -	796	72.5	4.4	3256	2	G98226	hypothenical prote
724	73	4.4	918	2	A36337	membrane glycoprot	797	72.5	4.3	139	2	A13059	hypothenical prote
725	73	4.4	932	1	VGBEBC	glycoprotein gi pr	798	72.5	4.3	159	2	F72758	hypothenical prote
726	73	4.4	958	2	T10679	hypothenical prote	799	72.5	4.3	197	2	T33525	hypothenical prote
727	73	4.4	1055	2	H90023	hypothenical prote	800	72.5	4.3	199	2	JE0351	OX40 ligand protei
728	73	4.4	1071	2	T22327	hypothenical prote	801	72.5	4.3	216	2	T03041	hypothenical prote
729	73	4.4	1256	1	A43829	muramidase-release	802	72.5	4.3	246	2	PC4397	mucin 3 T10 - huma
730	73	4.4	1320	2	JC5630	TCOF1 protein - mo	803	72.5	4.3	282	2	B37994	bone sialoprotein
731	73	4.4	1345	2	S46817	hypothenical prote	804	72.5	4.3	317	1	GEHUS	phage-related prot
732	73	4.4	1702	2	A41859	IGA-specific metal	805	72.5	4.3	322	2	G69946	integrin-associate
733	73	4.4	1993	2	AF1450	probable peptidogl	806	72.5	4.3	324	2	S36646	hypothenical prote
734	73	4.4	2179	1	GNNYH4	genome polyprotein	807	72.5	4.3	330	2	T49644	hypothenical prote
735	73	4.4	2285	2	T12796	probable transglyc	808	72.5	4.3	334	2	T19637	hypothenical prote
736	73	4.4	2416	2	T13825	adenomatous polypo	809	72.5	4.3	425	1	F0MVG	gag polyprotein -
737	73	4.4	2468	2	A83412	hypothenical prote	810	72.5	4.3	428	2	D86003	hypothenical prote
738	73	4.4	2722	2	T20532	hypothenical prote	811	72.5	4.3	428	2	F91157	probable membrane
739	73	4.4	263	2	I51225	snail protein - z	812	72.5	4.3	460	2	A44154	amino acid transpo
740	72.5	4.4	303	2	S40973	hypothenical prote	813	72.5	4.3	508	2	A33378	fascilin III prec
741	72.5	4.4	314	2	B95034	dihydropterate sy	814	72.5	4.3	509	2	A96563	probable protein k
742	72.5	4.4	321	2	T26153	hypothenical prote	815	72.5	4.3	544	2	S07144	neurofilament trip
743	72.5	4.4	328	2	S35336	transcription fact	816	72.5	4.3	548	1	QFPGL	neurofilament trip
744	72.5	4.4	340	2	C90894	probable LACI-type	817	72.5	4.3	576	2	S38293	hypothenical serin
745	72.5	4.4	340	2	F85793	probable LACI-type	818	72.5	4.3	587	2	S38634	chaperonin, mitoch
746	72.5	4.4	340	2	G54905	sugar-binding prot	819	72.5	4.3	592	2	D70863	hypothenical prote
747	72.5	4.4	382	2	T27058	hypothenical prote	820	72.5	4.3	622	2	A90570	lipoprotein [impor
748	72.5	4.4	391	2	T35470	probable integral	821	72.5	4.3	674	2	S74506	ribonuclease E - S
749	72.5	4.4	406	2	T23294	hypothenical prote	822	72.5	4.3	677	2	T00369	hypothenical prote
750	72.5	4.4	415	2	T32490	hypothenical prote	823	72.5	4.3	736	2	T41259	hypothenical prote
751	72.5	4.4	463	1	A36479	milk fat globule m	824	72.5	4.3	770	1	S30293	transcription fact
752	72.5	4.4	487	2	S40820	probable permease	825	72.5	4.3	817	2	T21336	hypothenical prote
753	72.5	4.4	498	1	VGXPLM	surface glycoprote	826	72.5	4.3	855	2	D98004	histidine Motif-Co
754	72.5	4.4	499	2	A12449	hypothenical prote	827	72.5	4.3	876	2	T49801	hypothenical prote
755	72.5	4.4	507	2	S05542	hypothenical prote	828	72.5	4.3	884	2	T20405	hypothenical prote
756	72.5	4.4	511	2	T35194	transcription init	829	72.5	4.3	958	2	T26258	hypothenical prote
757	72.5	4.4	560	2	T32661	hypothenical prote	830	72.5	4.3	1034	2	S49947	SWT4 protein - yea
758	72.5	4.4	580	2	B38418	jockey protein 1 -	831	72.5	4.3	1038	2	AG2187	hypothenical prote
759	72.5	4.4	610	2	S35049	mucin JER57 - huma	832	72.5	4.3	1146	2	S46837	hypothenical prote

833	72	4.3	1176	2	T49482	hypothetical prote	906	71	4.3	370	2	S49008	fork head protein
834	72	4.3	1196	2	H85061	hypothetical prote	907	71	4.3	378	2	S00842	leukostatin precur
835	72	4.3	1203	2	T17415	mycelial surface a	908	71	4.3	379	1	S71571	alcohol dehydrogen
836	72	4.3	1388	2	A57655	tim (timeless) pro	909	71	4.3	394	2	T21752	hypothetical prote
837	72	4.3	1489	2	T31108	cyst germination s	910	71	4.3	410	1	S68153	cellulase (EC 3.2.
838	72	4.3	1547	2	T28657	blackjack protein,	911	71	4.3	415	2	A35560	lysosomal membrane
839	72	4.3	1570	2	T18272	1-phosphatidylinos	912	71	4.3	433	2	S19996	hypothetical prote
840	72	4.3	1778	2	T50074	probable nucleopor	913	71	4.3	455	2	A87913	protein B0205.10 [
841	72	4.3	1829	2	T24583	hypothetical prote	914	71	4.3	462	2	T32751	hypothetical prote
842	72	4.3	2441	2	S39161	CREB-binding prote	915	71	4.3	474	1	TVR7C4	Ca2+/calmodulin-de
843	72	4.3	2578	2	A56922	transcription fact	916	71	4.3	496	2	T30976	hypothetical prote
844	72	4.3	2971	2	T08026	non-structural hyp	917	71	4.3	500	1	S60929	probable aldehyde
845	71.5	4.3	141	2	A38196	hypothetical prote	918	71	4.3	502	2	I52637	Ca2+/calmodulin-de
846	71.5	4.3	146	2	S52800	hypothetical prote	919	71	4.3	530	2	S62439	hypothetical serin
847	71.5	4.3	162	2	C84948	NADH2 dehydrogenas	920	71	4.3	534	2	G97703	hypothetical prote
848	71.5	4.3	164	2	A26490	histone H1, macron	921	71	4.3	622	2	T15467	hypothetical prote
849	71.5	4.3	178	2	TQ1547	stripe disease-spe	922	71	4.3	626	1	NCHUIA	platelet glycoprot
850	71.5	4.3	231	2	F84311	hypothetical prote	923	71	4.3	665	1	NCMVVR	hypothetical prote
851	71.5	4.3	263	2	S01360	salivary glue prot	924	71	4.3	669	2	T08827	env polyprotein pr
852	71.5	4.3	313	2	TQ1862	31R protein - vari	925	71	4.3	670	2	T13739	hypothetical prote
853	71.5	4.3	313	2	T28598	hypothetical prote	926	71	4.3	711	2	T48335	probable hormone r
854	71.5	4.3	313	2	A34677	secretory pathway	927	71	4.3	719	2	T27977	receptor like prot
855	71.5	4.3	363	2	T25278	hypothetical prote	928	71	4.3	738	2	I40719	lin-15A protein -
856	71.5	4.3	372	2	F43674	US7 protein - huma	929	71	4.3	751	2	T21967	isocitrate dehydro
857	71.5	4.3	373	2	S43455	hypothetical prote	930	71	4.3	751	2	T21967	hypothetical prote
858	71.5	4.3	381	2	S65212	hypothetical prote	931	71	4.3	767	1	JU0474	glucan 1,4-alpha-g
859	71.5	4.3	385	2	T38113	hypothetical serin	932	71	4.3	778	1	ALBYG	glucan 1,4-alpha-g
860	71.5	4.3	392	2	T49471	mucin (muc3) relat	933	71	4.3	784	2	AH2560	hypothetical prote
861	71.5	4.3	393	2	T49578	hypothetical prote	934	71	4.3	785	2	S54016	hypothetical prote
862	71.5	4.3	395	2	I52842	CD43 lp-3 antigen	935	71	4.3	791	2	T39924	SOK2 protein - yea
863	71.5	4.3	395	2	A43545	leukosialin CD43 p	936	71	4.3	814	1	KXBY	hypothetical prote
864	71.5	4.3	408	2	A46712	glycoprotein Iia -	937	71	4.3	880	2	D89756	protein T23E7.2b [
865	71.5	4.3	414	2	B84600	hypothetical prote	938	71	4.3	968	2	T00353	hypothetical prote
866	71.5	4.3	423	2	T22865	hypothetical prote	939	71	4.3	977	2	H84469	hypothetical prote
867	71.5	4.3	442	1	S11712	transcription init	940	71	4.3	982	2	T15171	hypothetical prote
868	71.5	4.3	443	1	D64584	heat shock protein	941	71	4.3	1032	2	T18293	guanylate kinase-1
869	71.5	4.3	466	2	AI0957	chromosomal replic	942	71	4.3	1200	1	SNFSO	ice nucleation pro
870	71.5	4.3	482	2	T48397	S-receptor kinase-	943	71	4.3	1204	2	C75015	probable pyrolysin
871	71.5	4.3	503	2	G75262	hypothetical prote	944	71	4.3	1244	2	T19615	hypothetical prote
872	71.5	4.3	507	2	T50398	hypothetical serin	945	71	4.3	1256	2	G97902	alpha-amylase (EC
873	71.5	4.3	540	1	A55145	thiamine-phosphate	946	71	4.3	1302	2	T23236	hypothetical prote
874	71.5	4.3	584	2	T19565	hypothetical prote	947	71	4.3	1326	2	H89134	protein F25G6.9 [1
875	71.5	4.3	631	2	I52257	episialin - mouse	948	71	4.3	1367	2	T33819	hypothetical prote
876	71.5	4.3	661	1	VCMVCB	env polyprotein -	949	71	4.3	1533	2	T00344	hypothetical prote
877	71.5	4.3	665	2	B81444	probable methyl-ac	950	71	4.3	1583	2	S59644	sister chromatid c
878	71.5	4.3	675	2	T47378	probable transposa	951	71	4.3	1751	2	A45604	major blood-stage
879	71.5	4.3	755	2	T20950	hypothetical prote	952	71	4.3	1819	2	T32008	hypothetical prote
880	71.5	4.3	760	1	S07896	transcription fact	953	71	4.3	1842	2	T34309	probable fatty-aci
881	71.5	4.3	882	2	T01168	hypothetical prote	954	71	4.3	1842	2	T38781	fatty acid synthas
882	71.5	4.3	1043	2	T23875	hypothetical prote	955	71	4.3	2035	2	A40718	host cell factor C
883	71.5	4.3	1121	2	T02764	myosin-I binding p	956	71	4.3	2090	2	S26058	probable transform
884	71.5	4.3	1156	2	T43326	germline RNA helic	957	71	4.3	2848	2	T33550	hypothetical prote
885	71.5	4.3	1172	2	T32759	hypothetical prote	958	71	4.3	2957	2	T33152	hypothetical prote
886	71.5	4.3	1234	2	T31623	hypothetical prote	959	71	4.3	3035	1	I46646	ryanodine receptor
887	71.5	4.3	1260	2	A87046	hypothetical prote	960	70.5	4.3	118	2	S49913	cryptogein - Phyto
888	71.5	4.3	1297	2	T30274	proteoliasin - se	961	70.5	4.3	128	2	A35690	mucin 3 (Clone SIB
889	71.5	4.3	1459	2	T32271	hypothetical prote	962	70.5	4.3	146	1	ERAD32	early E3 16K glyco
890	71.5	4.3	1557	2	D41214	protein-tyrosine-p	963	70.5	4.3	172	2	F49247	merozoite surface
891	71.5	4.3	1566	2	T20058	hypothetical prote	964	70.5	4.3	174	2	E49247	merozoite surface
892	71.5	4.3	1630	2	C41214	protein-tyrosine-p	965	70.5	4.3	193	2	G90125	hypothetical prote
893	71	4.3	98	2	S53367	mucin 5AC (clone M	966	70.5	4.3	204	2	S67295	probable membrane
894	71	4.3	135	2	T49996	AtAGP4 - Arabidops	967	70.5	4.3	209	2	C89850	conserved hypothet
895	71	4.3	168	2	JN0073	glycophorin A - no	968	70.5	4.3	211	2	C71482	probable endonucle
896	71	4.3	177	2	G75285	hypothetical prote	969	70.5	4.3	212	2	F86545	hypothetical prote
897	71	4.3	213	2	A86228	hypothetical prote	970	70.5	4.3	212	2	F72077	hypothetical prote
898	71	4.3	240	2	T33698	hypothetical prote	971	70.5	4.3	235	2	PC4396	mucin 3 T9 - human
899	71	4.3	242	2	T27226	hypothetical prote	972	70.5	4.3	236	2	I46606	MHC SLA-DQ alpha c
900	71	4.3	304	2	T15922	hypothetical prote	973	70.5	4.3	264	2	T09377	hypothetical prote
901	71	4.3	310	2	T20535	hypothetical prote	974	70.5	4.3	284	2	T28018	hypothetical prote
902	71	4.3	329	2	T43012	conserved hypothec	975	70.5	4.3	288	2	T41112	hypothetical prote
903	71	4.3	343	2	S75435	hypothetical prote	976	70.5	4.3	308	2	T29756	hypothetical prote
904	71	4.3	349	2	T05857	hypothetical prote	977	70.5	4.3	312	2	T25994	hypothetical prote
905	71	4.3	360	2	T33835	hypothetical prote	978	70.5	4.3	314	2	B97905	dihydropteroate sy
										316	1	A43661	dihydropteroate sy

979	70.5	4.3	321	2	T19259	hypothetical prote	1052	70	4.2	350	2	S22456	hydroxyproline-ric
980	70.5	4.3	330	2	S28102	rix protein - Scap	1053	70	4.2	350	2	AH3043	dehydrogenase Atu3
981	70.5	4.3	350	2	A10139	urp-hexose-1-phosp	1054	70	4.2	350	2	D98242	lipopolysaccharide
982	70.5	4.3	380	1	D34285	ubiquinol-cytochro	1055	70	4.2	355	2	D26883	neural cell adhesi
983	70.5	4.3	382	2	A28067	lysosomal membrane	1056	70	4.2	357	2	E72245	hydrolase, ama/hip
984	70.5	4.3	385	2	F70591	probable kefB prot	1057	70	4.2	358	2	A80802	protein T05A8.7 [i
985	70.5	4.3	393	2	S62335	Irl-7 protein - fr	1058	70	4.2	360	2	T08673	hypothetical prote
986	70.5	4.3	402	2	E86195	hypothetical prote	1059	70	4.2	409	2	T18726	hypothetical prote
987	70.5	4.3	403	1	S35541	transcription fact	1060	70	4.2	424	2	I51210	synaptotagmin p65
988	70.5	4.3	427	2	C98883	protein Jc8.10 [im	1061	70	4.2	425	2	T18723	hypothetical prote
989	70.5	4.3	431	1	JC2002	transcription fact	1062	70	4.2	426	2	T04985	probable transamin
990	70.5	4.3	431	2	T11911	NADH2 dehydrogenas	1063	70	4.2	445	2	S45713	potassium channel
991	70.5	4.3	433	2	S37790	probable serine/th	1064	70	4.2	446	2	S66268	inward rectifier p
992	70.5	4.3	445	2	T23139	hypothetical prote	1065	70	4.2	455	2	AE0181	hypothetical prote
993	70.5	4.3	462	2	A48933	gamma-aminobutyric	1066	70	4.2	456	2	T38221	hypothetical serin
994	70.5	4.3	465	2	H82345	mannose-1-phosphat	1067	70	4.2	458	2	T26630	hypothetical prote
995	70.5	4.3	491	2	T52398	hypothetical prote	1068	70	4.2	461	2	T38698	noc1 protein - fis
996	70.5	4.3	522	2	S41819	nucleoporin p62 -	1069	70	4.2	462	2	T19830	hypothetical prote
997	70.5	4.3	526	2	A34896	adenylate cyclase-	1070	70	4.2	487	2	AI1505	hypothetical cell
998	70.5	4.3	526	2	C84532	hypothetical prote	1071	70	4.2	497	2	T51195	hypothetical prote
999	70.5	4.3	562	2	A85042	hypothetical prote	1072	70	4.2	529	2	S18453	variant surface gl
1000	70.5	4.3	608	2	A46312	gag polyprotein -	1073	70	4.2	542	2	B47022	chitinase [BC 3.2.
1001	70.5	4.3	616	2	T29234	hypothetical prote	1074	70	4.2	584	2	JC7809	sulfakinin recepto
1002	70.5	4.3	629	2	AB1525	probable peptidogl	1075	70	4.2	589	2	AI0684	hypothetical prote
1003	70.5	4.3	649	2	T24505	hypothetical prote	1076	70	4.2	599	2	G17481	probable phosphoen
1004	70.5	4.3	675	2	D85065	receptor protein k	1077	70	4.2	609	2	S62518	hypothetical prote
1005	70.5	4.3	716	2	T26998	hypothetical prote	1078	70	4.2	611	2	T22456	hypothetical prote
1006	70.5	4.3	809	2	T18970	hypothetical prote	1079	70	4.2	613	2	B90294	hypothetical prote
1007	70.5	4.3	814	2	F59430	GTPase regulator a	1080	70	4.2	617	2	T15408	hypothetical prote
1008	70.5	4.3	839	2	I50590	class I INCENP pro	1081	70	4.2	625	2	S34035	hypothetical prote
1009	70.5	4.3	845	2	T38840	hypothetical trp-a	1082	70	4.2	651	2	S18874	nucleolin - Africa
1010	70.5	4.3	874	2	B86322	FGA1.8 protein -	1083	70	4.2	653	2	E86787	hypothetical prote
1011	70.5	4.3	877	2	I50591	class II INCENP pr	1084	70	4.2	662	2	T50464	glucose-regulated
1012	70.5	4.3	893	2	T18271	hypothetical prote	1085	70	4.2	697	2	E96752	hypothetical prote
1013	70.5	4.3	899	2	C84765	hypothetical prote	1086	70	4.2	706	2	S33761	transferrin precu
1014	70.5	4.3	910	1	S73361	dhaj homolog prote	1087	70	4.2	714	2	T22454	hypothetical prote
1015	70.5	4.3	942	2	S53963	MCS1 protein - yea	1088	70	4.2	753	2	T24869	hypothetical prote
1016	70.5	4.3	979	2	A35913	regulatory factor	1089	70	4.2	768	2	E86417	unknown protein, 5
1017	70.5	4.3	999	1	IUH053	desmoglein 3 precu	1090	70	4.2	770	2	T51024	related to C2H2 zi
1018	70.5	4.3	1015	2	JC6552	DNA topoisomerase	1091	70	4.2	822	2	T51049	related to nucleol
1019	70.5	4.3	1028	2	E85089	probable transposo	1092	70	4.2	833	2	F90914	hypothetical prote
1020	70.5	4.3	1032	2	G89427	protein T08D2.3 [i	1093	70	4.2	835	2	JC6140	cell surface-asso
1021	70.5	4.3	1052	2	C64221	hypothetical 114K	1094	70	4.2	937	2	A56517	nucleoporin Nup98
1022	70.5	4.3	1106	2	T31742	hypothetical prote	1095	70	4.2	971	2	T19431	hypothetical prote
1023	70.5	4.3	1115	2	A47541	protein kinase IRE	1096	70	4.2	971	2	F88448	protein C45G9.10 [
1024	70.5	4.3	1123	2	T18270	hypothetical prote	1097	70	4.2	1004	2	A55142	myosin-light-chain
1025	70.5	4.3	1131	2	T15787	hypothetical prote	1098	70	4.2	1186	2	T19050	hypothetical prote
1026	70.5	4.3	1221	2	A10193	ribonuclease E (EC	1099	70	4.2	1213	2	A41724	limb deformity (ld
1027	70.5	4.3	1520	2	T44231	hypothetical prote	1100	70	4.2	1274	2	JN0015	trp protein - frui
1028	70.5	4.3	1603	2	S17983	gene posterior sex	1101	70	4.2	1275	2	JU0092	trp protein - frui
1029	70.5	4.3	1742	2	T17120	cellulase (BC 3.2.	1102	70	4.2	1415	2	T08945	hypothetical prote
1030	70.5	4.3	1872	2	T00339	hypothetical prote	1103	70	4.2	1420	1	A44361	amiloride-sensitiv
1031	70.5	4.3	2271	2	F90073	hypothetical prote	1104	70	4.2	1589	2	C47666	defective chorion-
1032	70.5	4.3	2717	2	A34203	DNA-binding protei	1105	70	4.2	1784	2	T10532	gag-pol polyprotei
1033	70.5	4.3	3054	1	GNBVEV	genome polyprotein	1106	70	4.2	1868	2	S48938	hypothetical prote
1034	70	4.2	147	2	JC7938	Type II antifreeze	1107	70	4.2	2440	2	S39162	transcription coac
1035	70	4.2	148	2	T32682	hypothetical prote	1108	70	4.2	3163	1	JQ1895	genome polyprotein
1036	70	4.2	150	2	T52587	probable arabinoga	1109	69.5	4.2	120	1	W4WL42	E4 protein - human
1037	70	4.2	150	2	T48611	agp6 protein - Ara	1110	69.5	4.2	124	2	E84613	hypothetical prote
1038	70	4.2	209	2	AB2218	hypothetical prote	1111	69.5	4.2	146	2	S52810	hypothetical prote
1039	70	4.2	210	2	JC7830	cytokine-inducible	1112	69.5	4.2	171	2	H86413	hypothetical prote
1040	70	4.2	214	2	A46629	mucin 6, gastric (	1113	69.5	4.2	202	2	AB2378	hypothetical prote
1041	70	4.2	221	2	T47592	hypothetical prote	1114	69.5	4.2	217	2	S01358	salivary glue prot
1042	70	4.2	234	2	G64858	probable membrane	1115	69.5	4.2	219	2	B72291	hypothetical prote
1043	70	4.2	239	2	B83709	hypothetical prote	1116	69.5	4.2	266	2	H55590	hypothetical prote
1044	70	4.2	256	2	AC2283	hypothetical prote	1117	69.5	4.2	271	2	B96773	hypothetical prote
1045	70	4.2	298	2	C55223	minor tail protein	1118	69.5	4.2	299	2	G70784	probable mmpS3 pro
1046	70	4.2	310	2	T26267	hypothetical prote	1119	69.5	4.2	313	2	H36854	hemagglutinin - va
1047	70	4.2	311	2	H96002	probable sugar kin	1120	69.5	4.2	316	2	S58719	probable membrane
1048	70	4.2	321	2	T42750	hypothetical prote	1121	69.5	4.2	326	2	I48351	fos-related antige
1049	70	4.2	329	2	S38082	pathogenesis-relat	1122	69.5	4.2	338	2	F69437	hypothetical prote
1050	70	4.2	333	2	G98297	ribose ABC transpo	1123	69.5	4.2	338	2	S28004	probable cell surf
1051	70	4.2	333	2	AH2985	ABC transporter, m	1124	69.5	4.2	364	2	T32589	hypothetical prote



1125	69.5	4.2	372	1	QOBB88	glycoprotein I pre	1198	69	4.2	416	2	T34279	hypothetical prote
1126	69.5	4.2	372	2	T06745	hypothetical prote	1199	69	4.2	423	2	T44258	transducer protein
1127	69.5	4.2	400	2	T32705	hypothetical prote	1200	69	4.2	424	1	VGBBE9	glycoprotein gp63
1128	69.5	4.2	417	2	AD0200	isocitrate dehydro	1201	69	4.2	427	2	E83711	hypothetical prote
1129	69.5	4.2	423	2	T24393	hypothetical prote	1202	69	4.2	431	2	G86277	F14117.11 protein
1130	69.5	4.2	425	2	T24111	hypothetical prote	1203	69	4.2	443	2	T14916	mitosis-specific c
1131	69.5	4.2	427	2	T38526	ubiquitin regulato	1204	69	4.2	467	2	T26195	hypothetical prote
1132	69.5	4.2	441	2	C75076	heme biosynthesis	1205	69	4.2	483	2	G86902	dextranucrase (EC
1133	69.5	4.2	450	2	C90608	hypothetical prote	1206	69	4.2	486	2	D64474	hypothetical prote
1134	69.5	4.2	458	2	P86433	protein T17H7.5 [i	1207	69	4.2	490	1	CS7150	NADP-reducing hydr
1135	69.5	4.2	503	1	VNU71B	variant surface gl	1208	69	4.2	495	2	T38959	hypothetical prote
1136	69.5	4.2	514	2	A44100	cell adhesion mole	1209	69	4.2	511	2	I50114	early growth respo
1137	69.5	4.2	514	2	A31643	cell adhesion 80K	1210	69	4.2	513	2	S50915	sin3 protein-bindi
1138	69.5	4.2	519	2	S69989	unspecific monoocy	1211	69	4.2	525	2	A35596	nuclear pore glyco
1139	69.5	4.2	520	2	S14600	E2 glycoprotein pr	1212	69	4.2	538	2	S60645	NADH2 dehydrogenas
1140	69.5	4.2	532	2	C70986	probable coa ligas	1213	69	4.2	555	2	B41492	58K antigen - Rick
1141	69.5	4.2	537	2	B97013	and cellulose-bind	1214	69	4.2	556	2	S06838	gamma-aminobutyric
1142	69.5	4.2	538	2	AG2902	conserved hypotet	1215	69	4.2	556	2	S51892	probable membrane
1143	69.5	4.2	550	2	H97677	hypothetical prote	1216	69	4.2	583	2	T18999	hypothetical prote
1144	69.5	4.2	551	2	G95176	conserved hypotet	1217	69	4.2	610	1	I46001	C4b-binding protei
1145	69.5	4.2	552	2	T25593	hypothetical prote	1218	69	4.2	611	2	A53418	calmagin precursor
1146	69.5	4.2	568	2	A34891	hypothetical prote	1219	69	4.2	647	2	B34457	204 protein - mous
1147	69.5	4.2	574	2	A86365	Ig heavy chain pre	1220	69	4.2	650	2	S22835	alpha-agglutinin -
1148	69.5	4.2	593	2	S55189	probable auxin tra	1221	69	4.2	651	2	T21175	hypothetical prote
1149	69.5	4.2	593	2	T26865	hypothetical prote	1222	69	4.2	652	2	S50210	surface layer prot
1150	69.5	4.2	610	2	S59394	hypothetical prote	1223	69	4.2	658	2	T41309	hypothetical threo
1151	69.5	4.2	611	2	A54086	protein kinase RCK	1224	69	4.2	670	2	F84540	hypothetical prote
1152	69.5	4.2	629	2	S20516	calnexin-t - mouse	1225	69	4.2	677	2	S54561	RNA14 protein - ye
1153	69.5	4.2	640	2	T25367	dnak-type molecula	1226	69	4.2	725	2	E96592	hypothetical prote
1154	69.5	4.2	645	2	S41372	hypothetical prote	1227	69	4.2	739	2	H72364	aspartokinase II -
1155	69.5	4.2	646	2	T19206	hypothetical prote	1228	69	4.2	790	2	T34293	hypothetical prote
1156	69.5	4.2	658	2	JC8011	G protein-coupled	1229	69	4.2	793	1	KXRTF	furin (SC 3.4.21-7
1157	69.5	4.2	675	2	T03744	myoD protein inhib	1230	69	4.2	814	2	T49207	receptor kinase-li
1158	69.5	4.2	719	2	T47727	hypothetical prote	1231	69	4.2	825	2	S26706	transcription fact
1159	69.5	4.2	736	2	T19366	hypothetical prote	1232	69	4.2	836	2	T21631	hypothetical prote
1160	69.5	4.2	782	2	A82940	hypothetical prote	1233	69	4.2	854	1	QRHYLD	LDL receptor precu
1161	69.5	4.2	816	2	A49151	hypothetical prote	1234	69	4.2	871	2	T28706	hypothetical prote
1162	69.5	4.2	833	2	AF2089	fibroblast growth	1235	69	4.2	879	1	QRRTLD	LDL receptor precu
1163	69.5	4.2	844	2	B64678	hypothetical prote	1236	69	4.2	903	1	VGBEK1	glycoprotein B pre
1164	69.5	4.2	850	1	MWUE4	NADH2 dehydrogenas	1237	69	4.2	988	2	A40628	probable transposa
1165	69.5	4.2	852	2	T46091	erythrocyte membra	1238	69	4.2	1007	2	T27327	hypothetical prote
1166	69.5	4.2	862	2	T46289	hypothetical prote	1239	69	4.2	1095	2	JC8066	hypothetical prote
1167	69.5	4.2	871	2	S47518	cadherin - African	1240	69	4.2	1157	2	A55152	138K protein - Tet
1168	69.5	4.2	942	2	T19553	hypothetical prote	1241	69	4.2	1203	2	T04294	PAS1 protein - yea
1169	69.5	4.2	993	2	AE1905	outer membrane sec	1242	69	4.2	1204	2	F81158	hypothetical prote
1170	69.5	4.2	1051	2	JC4091	glycoprotein A - p	1243	69	4.2	1215	2	S60904	hypothetical prote
1171	69.5	4.2	1087	1	QFMGH	neurofilament trip	1244	69	4.2	1360	2	T34302	cell polarity prot
1172	69.5	4.2	1132	2	T43483	translation initia	1245	69	4.2	1385	2	T13415	hypothetical prote
1173	69.5	4.2	1460	2	S48457	nucleoporin RAV7 -	1246	69	4.2	1455	1	A48925	mannose receptor p
1174	69.5	4.2	1502	2	S45429	probable membrane	1247	69	4.2	1624	2	T25592	hypothetical prote
1175	69.5	4.2	1522	2	S48904	protein F20H11.2 [	1248	69	4.2	1633	2	T01879	hypothetical prote
1176	69.5	4.2	1870	2	D88486	myosin-like protei	1249	69	4.2	1680	2	T41628	probable transcrip
1177	69.5	4.2	1875	2	S38173	myosin heavy chain	1250	69	4.2	1758	2	S57015	probable purine nu
1178	69.5	4.2	1957	2	A45627	hypothetical prote	1251	69	4.2	1804	2	H96597	hypothetical prote
1179	69.5	4.2	2894	2	C64474	hypothetical prote	1252	69	4.2	1819	2	D97033	uncharacterized pr
1180	69.5	4.2	4199	2	S76412	hypothetical prote	1253	69	4.2	1963	1	MWKW	myosin heavy chain
1181	69	4.2	171	2	T31478	hypothetical prote	1254	69	4.2	2067	2	A42854	probable spindle p
1182	69	4.2	234	2	T35448	hypothetical prote	1255	69	4.2	2329	2	S44625	C50C3.6 protein -
1183	69	4.2	255	2	T22429	hypothetical prote	1256	69	4.2	2361	2	T25752	hypothetical prote
1184	69	4.2	258	2	S23106	priA protein - shi	1257	69	4.2	2464	1	QRMSPI	microtubule-associ
1185	69	4.2	284	2	T06241	histone H1 (clone	1258	68.5	4.1	168	2	S52994	arabinogalactan-li
1186	69	4.2	299	2	S44554	citrate transport	1259	68.5	4.1	189	1	ERAD75	early B3 20.6K gly
1187	69	4.2	303	2	S29185	sodium channel pro	1260	68.5	4.1	189	2	JX0235	core protein MGC-2
1188	69	4.2	339	2	S08981	malate dehydrogena	1261	68.5	4.1	204	2	S51232	gibberellin-respon
1189	69	4.2	339	2	F97121	probable membrane-	1262	68.5	4.1	218	2	AH1837	hypothetical prote
1190	69	4.2	343	2	G86709	hypothetical prote	1263	68.5	4.1	246	2	S47805	hypothetical 27.4K
1191	69	4.2	344	1	RWRTC2	T-cell surface gly	1264	68.5	4.1	246	2	D91186	probable outer mem
1192	69	4.2	356	2	S73315	protoporphyrin IX	1265	68.5	4.1	246	2	C86033	probable outer mem
1193	69	4.2	371	1	F0MVCS	gag polyprotein -	1266	68.5	4.1	257	2	C84890	hypothetical prote
1194	69	4.2	382	2	S71669	finger protein MIG	1267	68.5	4.1	261	2	D84262	hypothetical prote
1195	69	4.2	387	2	T15462	hypothetical prote	1268	68.5	4.1	280	2	AE2031	gamma-tocopherol m
1196	69	4.2	396	2	T26987	hypothetical prote	1269	68.5	4.1	287	2	S45662	histone H1 - tomat
1197	69	4.2	400	1	A39822	leukosialin precur	1270	68.5	4.1	287	2	D95406	hypothetical prote



1271	68.5	4.1	288	2	T22846	hypothetical prote	1344	68	4.1	208	1	HSRT1T	histone H1t - rat
1272	68.5	4.1	318	2	T20083	hypothetical prote	1345	68	4.1	211	2	H72608	hypothetical prote
1273	68.5	4.1	345	2	T12344	NADH2 dehydrogenas	1346	68	4.1	228	2	T33579	hypothetical prote
1274	68.5	4.1	349	2	T42965	glycoprotein - ate	1347	68	4.1	245	2	D81977	major tail protein
1275	68.5	4.1	359	2	T70814	probable far prote	1348	68	4.1	246	2	H90833	probable tail comp
1276	68.5	4.1	378	2	T35403	probable polypreny	1349	68	4.1	256	2	H85691	hypothetical prote
1277	68.5	4.1	385	2	H97239	polyferredoxin [im	1350	68	4.1	268	2	T32740	hypothetical prote
1278	68.5	4.1	385	2	UC7783	RAD 23B protein -	1351	68	4.1	288	2	T21790	hypothetical prote
1279	68.5	4.1	394	2	G84206	hypothetical prote	1352	68	4.1	295	2	S50316	CIN5 protein - yea
1280	68.5	4.1	408	1	QRHUBE	beta-3-adrenergic	1353	68	4.1	301	2	H97644	hypothetical prote
1281	68.5	4.1	412	1	AJMSRS	argininosuccinate	1354	68	4.1	304	2	G89790	hypothetical prote
1282	68.5	4.1	412	1	AJRTTS	argininosuccinate	1355	68	4.1	333	2	T15367	hypothetical prote
1283	68.5	4.1	413	2	T04520	hypothetical prote	1356	68	4.1	339	2	AH0050	probable periplasm
1284	68.5	4.1	414	1	QRHUB3	beta-3-adrenergic	1357	68	4.1	360	2	S69063	probable membrane
1285	68.5	4.1	414	2	G64091	cell division prot	1358	68	4.1	372	2	T45628	glycerophosphodies
1286	68.5	4.1	420	2	A88962	protein F59A7.1 [i	1359	68	4.1	378	2	S61992	SLG1 protein - yea
1287	68.5	4.1	421	2	S09595	synaptotagmin p65	1360	68	4.1	380	1	S51826	alcohol dehydrogen
1288	68.5	4.1	426	2	A35641	5-aminimidazole r	1361	68	4.1	384	2	H64161	hypothetical prote
1289	68.5	4.1	435	2	C96340	protein F2D10.28 [	1362	68	4.1	387	2	A56275	1,3-propanediol de
1290	68.5	4.1	435	2	T25330	hypothetical prote	1363	68	4.1	388	2	T43019	probable DNA-bindi
1291	68.5	4.1	443	2	F71929	heat shock protein	1364	68	4.1	402	2	T20595	hypothetical prote
1292	68.5	4.1	458	2	AC0121	probable exported	1365	68	4.1	416	2	T19149	hypothetical prote
1293	68.5	4.1	498	1	VGXPLA	surface glycoprote	1366	68	4.1	420	2	T42616	envelope protein -
1294	68.5	4.1	502	2	T21935	hypothetical prote	1367	68	4.1	422	1	BMHUIY	synaptotagmin I -
1295	68.5	4.1	509	2	T48439	cytochrome P450-li	1368	68	4.1	423	2	T14531	S-locus-specific g
1296	68.5	4.1	514	1	A47692	fumarate hydratase	1369	68	4.1	423	2	H84237	Hr13 transducer [
1297	68.5	4.1	527	2	T26732	hypothetical prote	1370	68	4.1	426	2	T48379	gene hb protein -
1298	68.5	4.1	535	2	B84443	hypothetical prote	1371	68	4.1	427	2	JH0413	synaptotagmin o-p6
1299	68.5	4.1	536	2	AG1482	hypothetical prote	1372	68	4.1	452	2	T46147	zinc finger protei
1300	68.5	4.1	553	2	A49364	59 protein, brain	1373	68	4.1	461	2	D96647	hypothetical prote
1301	68.5	4.1	573	2	H96744	probable cytosolic	1374	68	4.1	461	2	T39862	hypothetical prote
1302	68.5	4.1	588	2	JC8021	chitinase (EC 3.2.	1375	68	4.1	479	2	A84588	probable tyrosine
1303	68.5	4.1	592	2	T32402	hypothetical prote	1376	68	4.1	487	1	S07061	glutamate receptor
1304	68.5	4.1	594	2	S51412	hypothetical prote	1377	68	4.1	493	2	D86652	IMP dehydrogenase
1305	68.5	4.1	630	2	A39344	tumor-associated m	1378	68	4.1	500	2	A11913	apolipoprotein N-a
1306	68.5	4.1	637	2	T20981	hypothetical prote	1379	68	4.1	503	2	T51782	hypothetical prote
1307	68.5	4.1	647	2	S26386	transcription fact	1380	68	4.1	514	2	S18449	variant surface gl
1308	68.5	4.1	659	2	T40383	hypothetical prote	1381	68	4.1	515	2	B84406	TRK potassium upta
1309	68.5	4.1	659	2	F64370	ferrous iron trans	1382	68	4.1	516	2	A31270	radial spoke prote
1310	68.5	4.1	670	2	S22293	zinc finger protei	1383	68	4.1	537	1	F0MVW7	gag polyprotein -
1311	68.5	4.1	696	2	G71829	probable outer mem	1384	68	4.1	543	2	A38093	transformation-sen
1312	68.5	4.1	697	2	A86402	protein T22C5.17 [	1385	68	4.1	550	2	T06379	SAR DNA-binding pr
1313	68.5	4.1	699	2	T09483	Cys-rich protein R	1386	68	4.1	562	2	B41035	chitinase (EC 3.2.
1314	68.5	4.1	721	2	E70766	hypothetical prote	1387	68	4.1	562	2	S50371	chitinase (EC 3.2.
1315	68.5	4.1	725	2	T01268	leucine-rich repea	1388	68	4.1	573	2	S50861	hypothetical prote
1316	68.5	4.1	737	2	AG2156	hypothetical prote	1389	68	4.1	576	2	T22455	hypothetical prote
1317	68.5	4.1	751	2	AC2098	hypothetical prote	1390	68	4.1	581	2	T22455	hypothetical prote
1318	68.5	4.1	763	2	S56116	glycoprotein H - e	1391	68	4.1	590	2	S66956	hypothetical prote
1319	68.5	4.1	770	2	G98445	protein C26B6.2 [i	1392	68	4.1	599	1	A54906	afamin precursor -
1320	68.5	4.1	795	2	T20609	hypothetical prote	1393	68	4.1	600	2	S56744	mucin (clone pGM7-
1321	68.5	4.1	798	2	T50514	hypothetical prote	1394	68	4.1	610	2	T22909	hypothetical prote
1322	68.5	4.1	825	1	GLHQ	beta-glucosidase (	1395	68	4.1	621	1	YRNC	monophenol monooxy
1323	68.5	4.1	846	2	S52418	GRP-binding regula	1396	68	4.1	623	2	T28051	hypothetical prote
1324	68.5	4.1	853	2	H70939	probable nirB prot	1397	68	4.1	630	2	S77346	hypothetical prote
1325	68.5	4.1	865	2	AC1966	hypothetical prote	1398	68	4.1	632	2	T48616	hypothetical prote
1326	68.5	4.1	914	2	T25220	hypothetical prote	1399	68	4.1	638	2	S36723	YUN36 protein - ye
1327	68.5	4.1	915	2	T33030	hypothetical prote	1400	68	4.1	645	2	T16078	hypothetical prote
1328	68.5	4.1	925	2	T00781	hypothetical prote	1401	68	4.1	647	2	T39141	hypothetical prote
1329	68.5	4.1	952	2	T18837	hypothetical prote	1402	68	4.1	648	2	T04837	probable serine/th
1330	68.5	4.1	1043	2	T13172	gag-like protein p	1403	68	4.1	655	1	A55726	RNA-binding protei
1331	68.5	4.1	1278	2	A71609	probable secreted	1404	68	4.1	659	2	H81431	methyl-accepting c
1332	68.5	4.1	1285	2	H85041	hypothetical prote	1405	68	4.1	659	2	A98085	hypothetical prote
1333	68.5	4.1	1311	2	A56390	mannosyl-glycoprot	1406	68	4.1	662	2	B81251	probable methyl-ac
1334	68.5	4.1	1435	2	S69632	regulatory protein	1407	68	4.1	668	2	B86831	hypothetical prote
1335	68.5	4.1	1438	2	A38216	neurexin III-alpha	1408	68	4.1	669	2	B70186	translation elonga
1336	68.5	4.1	1444	1	A30588	140K adhesin precu	1409	68	4.1	686	2	S66693	hypothetical prote
1337	68.5	4.1	1541	2	S46686	hypothetical prote	1410	68	4.1	695	2	T51652	long-chain-fatty-a
1338	68.5	4.1	1791	2	T46089	hypothetical prote	1411	68	4.1	698	1	UX0202	disbasic processing
1339	68.5	4.1	2114	2	E36505	hypothetical prote	1412	68	4.1	709	2	S51793	hypothetical prote
1340	68.5	4.1	2292	1	GNNYEB	genome polyprotein	1413	68	4.1	730	2	A75486	probable long-chai
1341	68.5	4.1	2292	1	GNNYEB	genome polyprotein	1414	68	4.1	733	2	T01875	probable long-chai
1342	68.5	4.1	2292	2	S55401	capsid polyprotein	1415	68	4.1	752	2	T34355	hypothetical prote
1343	68	4.1	62	2	S53366	mucin 5AC (clone M	1416	68	4.1	761	2	T03719	probable thyroid r

cell division prot  
cyclin F - human  
gag-kit polyprotei  
probable membrane  
arylesterase/monox  
hypothetical prote  
aluminum resistat  
glutamine receptor  
glutamate receptor  
pol polyprotein -  
hypothetical prote  
glutamate receptor  
T20H2.17 protein -  
hypothetical prote  
starch phosphoryla  
dna exoribonucleas  
hypothetical prote  
conserved hypotet  
zinc finger RNA bi  
microtubule-associ  
probable membrane  
hypothetical prote  
Ca2+-transporting  
DNA repair protein  
related to pathway  
agglutinin-like pr  
hypothetical prote  
hypothetical prote  
hypothetical prote  
protein kinase cek  
hypothetical prote  
gene expanded prot  
multifunctional am  
IgA-specific metal  
IgA-specific metal  
neurexin III-alpha  
1,4-beta-glucanase  
major merozoite su  
myosin heavy chain  
variant-specific s  
hypothetical prote  
hypothetical prote  
laminin alpha-1 ch  
50S ribosomal prot  
hypothetical prote  
conserved domain p  
hypothetical prote  
hypothetical prote  
hypothetical prote  
protein T05A8.6 [i  
early EIA 25K prot  
probable replicati  
probable starch sy  
hypothetical prote  
glycoprotein G - b  
hypothetical prote  
B26r protein - var  
conserved hypotet  
hypothetical prote  
hypothetical prote  
transforming prote  
hypothetical prote  
protein W10G11.5 [i  
MG307 homolog H08  
hypothetical prote  
protein B0454.9 [i  
probable polyA-bin  
hypothetical prote  
leucine-rich repea  
opsin, red-sensiti  
hypothetical prote

1117 68 4.1 784 2 C82679  
1118 68 4.1 786 2 A55501  
1119 68 4.1 790 2 F0MVHZ  
1120 68 4.1 793 2 S65240  
1121 68 4.1 833 2 G75621  
1122 68 4.1 849 2 T20422  
1123 68 4.1 859 2 S66827  
1124 68 4.1 864 2 A43954  
1125 68 4.1 869 2 S35792  
1126 68 4.1 899 2 GNMVMM  
1127 68 4.1 903 2 T00074  
1128 68 4.1 908 2 S19098  
1129 68 4.1 923 2 A86334  
1130 68 4.1 971 2 T10678  
1131 68 4.1 974 2 S34189  
1132 68 4.1 991 2 S43891  
1133 68 4.1 1010 2 T16616  
1134 68 4.1 1018 2 T18249  
1135 68 4.1 1052 2 T14343  
1136 68 4.1 1072 2 A37127  
1137 68 4.1 1117 2 S63399  
1138 68 4.1 1153 2 T21386  
1139 68 4.1 1173 2 S48877  
1140 68 4.1 1196 2 S35994  
1141 68 4.1 1203 2 T51029  
1142 68 4.1 1230 2 T22458  
1143 68 4.1 1260 2 S60896  
1144 68 4.1 1275 2 T33369  
1145 68 4.1 1279 2 T13613  
1146 68 4.1 1280 2 T00365  
1147 68 4.1 1338 2 T40993  
1148 68 4.1 1371 2 T29019  
1149 68 4.1 1429 2 T13720  
1150 68 4.1 1440 2 SYHUQT  
1151 68 4.1 1541 2 A37023  
1152 68 4.1 1545 2 B41859  
1153 68 4.1 1578 2 T48216  
1154 68 4.1 1711 2 T13137  
1155 68 4.1 1772 2 A45532  
1156 68 4.1 1968 2 S05697  
1157 68 4.1 2228 2 T14029  
1158 68 4.1 2810 2 T22298  
1159 68 4.1 3191 2 T22945  
1160 68 4.1 3712 2 S18253  
1161 67.5 4.1 117 2 AB0028  
1162 67.5 4.1 127 2 T30102  
1163 67.5 4.1 137 2 P95239  
1164 67.5 4.1 137 2 H98103  
1165 67.5 4.1 159 2 T31598  
1166 67.5 4.1 180 2 T31974  
1167 67.5 4.1 191 2 S38117  
1168 67.5 4.1 210 2 B88082  
1169 67.5 4.1 232 2 WMA0C2  
1170 67.5 4.1 235 2 T02598  
1171 67.5 4.1 238 2 T07921  
1172 67.5 4.1 240 2 H69932  
1173 67.5 4.1 248 2 P00769  
1174 67.5 4.1 252 2 AG1423  
1175 67.5 4.1 256 2 H36857  
1176 67.5 4.1 297 2 S55063  
1177 67.5 4.1 306 2 AB1156  
1178 67.5 4.1 311 2 T40921  
1179 67.5 4.1 326 2 S15749  
1180 67.5 4.1 327 2 D90530  
1181 67.5 4.1 345 2 E88103  
1182 67.5 4.1 345 2 S73729  
1183 67.5 4.1 346 2 T46916  
1184 67.5 4.1 348 2 C88088  
1185 67.5 4.1 348 2 T40623  
1186 67.5 4.1 355 2 T15526  
1187 67.5 4.1 358 2 T01296  
1188 67.5 4.1 364 1 OOHUR  
1189 67.5 4.1 369 2 A91950

hypothetical prote  
riboflavin bioeynt  
paired box transcr  
hypothetical 44.2K  
probable WRKY-type  
ABC transporter Ar  
protein T12M4.6 [i  
hypothetical prote  
hypothetical prote  
hypothetical prote  
gamma-aminobutyric

1490 67.5 4.1 376 2 D72647  
1491 67.5 4.1 383 2 E96972  
1492 67.5 4.1 391 2 A44063  
1493 67.5 4.1 399 2 T42242  
1494 67.5 4.1 410 2 C84638  
1495 67.5 4.1 426 2 A11920  
1496 67.5 4.1 467 2 B86225  
1497 67.5 4.1 476 2 T27051  
1498 67.5 4.1 482 2 A12094  
1499 67.5 4.1 487 2 T49424  
1500 67.5 4.1 493 2 A34130

## ALIGNMENTS

## RESULT 1

A37009  
CD44 homolog membrane glycoprotein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 09-Jul-2004  
C:Accession: A37009  
R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; Goeddel, D.V.  
J. Immunol. 143, 3390-3395, 1989  
A:Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CAN  
A:Reference number: A37009, MUID:90038499, PMID:2681416  
A:Accession: A37009  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-363 <ZHO>  
A:Cross-references: UNIPROT:P15379; UNIPARC:UPI000002A5F4; GB:M30655; NID:g200332; PIDN  
C:Superfamily: human cell adhesion protein CD44  
C:Keywords: cell adhesion; glycoprotein; membrane protein

Query Match 13.9%; Score 229.5; DB 2; Length 363;

Best Local Similarity 24.9%; Pred. No. 7.7e-11;

Matches 89; Conservative 57; Mismatches 148; Indels 63; Gaps 14;

QY 15 WTTR---LIVQSLRAEELSIQVSCRMIGITLVSKKQNLNFTAKEACRLGLSLACK 71  
DB 6 WHTANGLCLQLSLAHQQLDLNVCYAGVFFVKKNGRYSISRTEAADICQAFNSTLPTM 65  
QY 72 DQVETALKASFETCSYGVWGDGFVVISRISPNPKGKNGVGLIMKVPVSROFAAYCYNS 131  
DB 66 DQMKLALSGFTCYGFI-EGNVVPRHPNACAAHNTGVYILVTSNTHVDTYCFNA 124  
QY 132 SQTWNSCIPETITTKDPIFNQTATQTTFEFIVSOST-YSVASPYST----IPAPT---- 182  
DB 125 SAPPEEDC-----TSVTDLPNFDGFPVITTVNRDGTYSKKGEYRTHQEDIDASNIID 179  
QY 183 -----TTTPPA-PASTSIPRRKCLICVTEVFEMETSTMTST-EPEPFVENKAAPK--- 227  
DB 180 DVSSGSTTEKSTPEGVILHTYLTQPTGDDDSFFIRSTLATRORDSSKSGSRSTVT 239  
QY 228 ---NEAAGFGG-----VPTALLVLALFFGAAAGLGFYVVKRYVKAPF 267  
DB 240 HGSSELHSSANQDSGVTTTSGPMRRPQIPWLIILASL-LALALILAVC-----IAVNS 293  
QY 268 FTNKKQKQKEMI---ETKVVKKEKANDSNPNESKTKDKNPKESKSPSKTTVTCLEAE 321  
DB 294 RRRCGQKKLVGGNGTVEDRKPSLN-GEASKSQEMVHLVYNKBPSETPDQCMTAD 349

## RESULT 2

A30901  
Lymphocyte adhesion receptor precursor - baboon

C:Species: Papio sp. (baboon)

C:Date: 18-Apr-1989 #sequence\_revision 18-Apr-1989 #text\_change 21-Jul-2000

C:Accession: A33935; A30901

R;Idzerda, R.L.; Carter, W.G.; Nottenburg, C.; Wayner, E.A.; Gallatin, W.M.; St. John, H.

Proc. Natl. Acad. Sci. U.S.A. 86, 4659-4663, 1989

A:Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion recep

A:Reference number: A33935, MUID:89282830, PMID:2471974

A;Accession: A33935  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-362 <ID>  
A;Cross-references: UNIPARC:UPI000012736C; GB:M22452; NID:g176576; PID:g176577  
C;Comment: This protein was isolated from the herpes papio induced B cell lymphoma.  
C;Genetics:  
A;Gene: CD44; ECMRII; Hermes-1 antigen  
C;Superfamily: human cell adhesion protein CD44  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-362/Product: lymphocyte adhesion receptor #status predicted <MAT>  
F;21-270/Domain: extracellular #status predicted <EXT>  
F;271-290/Domain: transmembrane #status predicted <TM>  
F;291-362/Domain: intracellular #status predicted <CYT>  
F;25,57,100,110,120,256/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;296/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 13.4%; Score 222.5; DB 2; Length 362;  
Best Local Similarity 25.5%; Pred. No. 2.8e-10;  
Matches 92; Conservative 43; Mismatches 127; Indels 99; Gaps 16;

Qy 20 LVQGSRAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQDVETALK 79  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 14 LVQLSL--AQIDLNITCFEGIIYHVEKNGRYSISRTEADLCFAFNSTLPTMAQEKALS 71  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 80 ASFETCSYGVGDGVFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWNSC 139  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 72 IGFTCRYGFI--EGHVIPRIHPNCAANNTGVYILTNTS-QVDTYCFNASAPGBCD 129  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 140 IPEIITTKDPIFNITQTATQTTEFIVSDST--YSVASPYSTIP-----APT----- 182  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 130 -----TSVTDLPNAPDGPITITIVNRDGRVYKGEYTNEDINPSSPTDDDDVSSGSS 184  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 183 -----TTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAP 226  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 185 ERSSTLGGYIFVNFHSTSPPIDEG-----PWITSDTRTPATDQCAF 229  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 227 K-----NEAAGF-----GG-----VPTALLVALLFFGAAGLGFY 258  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 230 DPSGSGTHTHGSEAGSHSREGGANTTSGPLRTPQIPEWLIILASL-LALALILAVC- 287  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 259 VKRYVKAFFPNKQOKEMIEK---VVEKANDSNPNESKTKD---NPESKSPS 311  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 288 ----IAVNSRRRCQKKLVINGNGAVEDRKSSGLN-GEASKSOEMVHLVKNKSESTPD 342  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 312 K 312  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 343 Q 343

RESULT 3  
A34424  
CD44 membrane glycoprotein precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 01-Dec-2000  
C;Accession: A34424; A34907  
R;Nottenburg, C.; Rees, G.; St. John, T.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989  
A;Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate  
A;Reference number: A34424; MUID:90046829; PMID:2682651  
A;Accession: A34424  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-365 <NOT>  
A;Cross-references: UNIPARC:UPI0000088CD; GB:M27130; NID:g192530; PIDN:AAA37407.1; PID:  
R;Wolfe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.  
J. Biol. Chem. 265, 341-347, 1990  
A;Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antigen  
A;Reference number: A34907; MUID:90094420; PMID:2403559  
A;Accession: A34907  
A;Status: preliminary  
A;Molecule type: mRNA

A;Residues: 8-195, 'G', 197-365 <WOL>  
A;Cross-references: UNIPARC:UPI000016CFB0; GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:  
C;Superfamily: human cell adhesion protein CD44  
C;Keywords: cell adhesion; glycoprotein; membrane protein

Query Match 13.4%; Score 222.5; DB 2; Length 365;  
Best Local Similarity 24.5%; Pred. No. 2.8e-10;  
Matches 88; Conservative 56; Mismatches 150; Indels 65; Gaps 14;

Qy 15 WTTR--LLVQGSIR--AEELSIOVSCRMGITLVSKKANQQLNFTAEKACRLGLSLA 69  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 6 WHTAWGLCLQLSLAHPHQIDLVNITCRYAGVHVEKNGRYSISRTEADLCQAFNSTLP 65  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 70 GKQVETALKASFETCSYGVGDGVFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCY 129  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 66 TMDQMKLALSGFETCRYGFI--EGNVVPIRIHPNCAANHTGVYIILVNTSHDYTCF 124  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 130 NSSDTWNSCIPETITTKDPIENTQTATQTTEFIVSDST--YSVASPYST----- 177  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 125 NASAPPEDC-----TSVTDLPNSFDGPVTITIVNRDGRYSKKGEYRTHQEDIDASNII 179  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 178 ----IPAPTTTPAPAS---TSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAPF- 227  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 180 DDDVSSGSTIEKSTPESYIHLTVLPTQPTGDDDSFFIRSTLATRDSSKDSRGSRT 239  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 228 ----NEAAGFGG-----VPTALLVALLFFGAAGLGFYCVKRVKA 265  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 240 VTHGSELAGHSSANQDSGVTTTSGPMRRPQIPEWLIILASL-LALALILAVC-----IAV 293  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 266 PFPTKNQOKEMI---ETKVVKEEKANDSNPNESKTKDKNPEESKSPSTTVRCLEAE 321  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 294 NSRRRCQKKLVINGNGVIEDRKSELN-GEASKSOEMVHLVKNKEPSEFTPDQCTAD 351  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
RESULT 4  
B38745  
Cell adhesion molecule CD44 precursor, long form (meta-1) - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 09-Jul-2004  
C;Accession: B38745; A38745  
R;Guenther, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; Haubmann, I.; Matzku, S.  
Cell 65, 13-24, 1991  
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcinoma  
A;Reference number: B38745; MUID:91191552; PMID:1707342  
A;Accession: B38745  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-503 <GUE>  
A;Cross-references: UNIPROT:P26051; UNIPARC:UPI000012736D; GB:M61874; NID:g576534; PIDN:  
A;Reference number: B38745  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-223, 386-503 <GU2>  
A;Cross-references: UNIPARC:UPI0000179A9B; GB:M61875  
C;Keywords: cell adhesion

Query Match 13.4%; Score 222; DB 2; Length 503;  
Best Local Similarity 25.7%; Pred. No. 4.6e-10;  
Matches 84; Conservative 40; Mismatches 165; Indels 38; Gaps 11;

Qy 15 WTTLLVQGSIRAEELSIOVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQDV 74  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 10 WGLCLQLSLAQOQIDLVNITCRYAGVHVEKNGRYSISRTEADLCFAFNSTLPTMAQM 69  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 75 ETALKASFETCSYGVGDGVFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDT 134  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 70 ELALRKGFETCRYGFI--EGHVIPRIHPNCAANNTGVYIILASNTSHDYTCFNASAP 128  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 135 WTNSCIPETITTKDPIENTQTATQTTEFIVSDST--YSVASPYST-----IPAP----- 182  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Db 129 LEEDC-----TSVTDLPNSFDGPVTITIVNRDGRYSKKGEYRTHQEDIDASNII 183  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :  
Qy 183 -----TTPPA-PASTSIPRRKKLICVTEVFMETSTMST-ETEPFVENKAAPKNEAAGF 233  
||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : : ||| ||| : : : : :

Db 184 SGSTIEKSTPEGYILHTDLTPTSOPTGDRDDAFFTGSTLATIATTPWVSAHTKONQERTOW 243  
Qy 234 GGV---FTALLVLALLFFGAAGLFCVVKRYK--APPFTNKKQKEMETKVKVEKA 288  
Db 244 NPHISNEVLLQTTTRMTDDIRNSTSAHGENWTOPEPPFNHHEYQDEE-ETPHATSTTW 302  
Qy 289 NDSNPNEESKTKD-----NPEESKSP 310  
Db 303 ADPNSTTEAAATQEKWFENWQGNP 329

RESULT 5  
A35616  
T-cell surface glycoprotein CD44 - hamster  
C;Species: Cricetinae Gen. sp. (hamster)  
C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C;Accession: A35616  
R;Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.  
Cell 61, 1303-1313, 1990  
A;Title: CD44 is the principal cell surface receptor for hyaluronate.  
A;Reference number: A35616; MUID:90304889; PMID:1694723  
A;Accession: A35616  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-362 <ARU>  
A;Cross-references: UNIPROT:P20944; UNIPARC:UPI0000179518  
C;Superfamily: human cell adhesion protein CD44  
C;Keywords: cell adhesion; glycoprotein; transmembrane protein

Query Match 13.1%; Score 217.5; DB 2; Length 362;  
Best Local Similarity 25.4%; Pred. No. 7e-10;  
Matches 88; Conservative 46; Mismatches 149; Indels 63; Gaps 12;

Qy 24 SLRAEELSIQVSCRMGIVTSKANQOLNFTKEAKRLLGLSLAGKQVETALKASPE 83  
Db 18 SLAHEQIDDLNITCRYAGVFFVEKNGRYSISRTEAADLCQAFNSTLPTMDQMVALSKGPE 77

Qy 84 TCSYGWVGDFVVISRISPNPKCGKGVGLVWKVPVSRQFAAYCYNSSDTWNSCIPEI 143  
Db 78 TCYRGFI-EGHVVIPIQPNACIAHNTGVILTSNTS-HDYTCFNASAPLEEDC---- 131

Qy 144 ITTKDPIFNQTATOTTEFIVSDST-YSVASPYST-----IPAPTTTPPAPAS----- 190  
Db 132 -TSVTDLPNSFEQPVITIVNRDGRYSKKGERTHQEDIDASNITDDDDVSSGSSSEKST 190

Qy 191 -----TSIPRKKLICVTEVFMETSTWSTE-----TEPFVEN 222  
Db 191 SGGYVFHTYLTPIHSTADQDDPYFIGSTMATRDQSSMDPRGNSLAVTDGSKLTGHSSGN 250

Qy 223 KAFAKNEAGFG---GVPTALLVLALLFFGAAGLFCVVKRYKAPPTNKKQKEMIE 279  
Db 251 QDSGANTTSRPGKPKQIPPEWLIILASL-LALAILAVC-----IAVNSRRRCQKKGKVI 304

Qy 280 TKVVKEEKANDSNPNEESKTKDNPE-----ESKSPSKTTVRCLEAE 321  
Db 305 NS--GGKVEDRKPSELNGEASKSQEWHLVKNPSETPDQFTAD 348

RESULT 6  
A53286  
cell-surface glycoprotein CD44 precursor - bovine  
N;Alternate names: CD44 protein  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A53286; S22123  
R;Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.  
Mol. Immunol. 28, 1131-1135, 1991  
A;Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.  
A;Reference number: A53286; MUID:92017904; PMID:1922105  
A;Accession: A53286  
A;Molecule type: mRNA  
A;Residues: 1-366 <BOS>

A;Cross-references: UNIPROT:Q29423; UNIPARC:UPI0000127366; EMBL:X62881; NID:g186; PIDN:  
A;Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)  
C;Superfamily: human cell adhesion protein CD44  
C;Keywords: cell adhesion; glycoprotein; transmembrane protein  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>  
F;274-294/Domain: transmembrane #status predicted <TMW>  
F;25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 12.6%; Score 208.5; DB 2; Length 366;  
Best Local Similarity 23.8%; Pred. No. 3.7e-09;  
Matches 81; Conservative 44; Mismatches 142; Indels 73; Gaps 11;

Qy 20 LVQSLRAEELSIQVSCRMGIVTSKANQOLNFTKEAKRLLGLSLAGKQVETALK 79  
Db 14 LVQLSL--AQIDLNTICRYAGVFFVEKNGRYSISRTEAADLCQAFNSTLPTMQMRAARN 71

Qy 80 ASFETCSYGWVGDFVVISRISPNPKCGKGVGLVWKVPVSRQFAAYCYNSSDTWNSC 139  
Db 72 IGPETCRYGFI-EGHVVIPIRIHPNSICAAANTGVILTSNTS-QYDTICFNASAPGEDC 129

Qy 140 IPEIITKDPINFNTQTATOTTEFIVSDST-YSVASPYSTIP-----APTTPPAPAS 190  
Db 130 -----TSVTDLPNAFEGPITITIVNRDGRYTKKGERTNPEDINPSVSPSPDPDEMS 184

Qy 191 TSIPRKKLICVTEVF-----METSTMSTETETEPFVENKAAFK 227  
Db 185 SGSPSRSTSGGYSIFHTHLPTVHPSPRRPMSQRANSTSDTRDYSSHDPSGRSRTYTHA 244

Qy 228 NEAAGFGG-----VPTALLVLALLFFGAAGLFCVVKRYKAPPT 269  
Db 245 SESAGHSGSSEHGANTTSGPMRKPQIPFWLIILASL-LALAILAVC-----IAVNSRR 298

Qy 270 NKNQKEMETKVKVEEKANDSNPNEESKTKDNPEESKS 309  
Db 299 RCQKKGKGVIN-----NGNGTWEEKPSGLNGEASKS 330

RESULT 7  
JH0417  
cell adhesion molecule CD44 - human  
C;Species: Homo sapiens (man)  
C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 31-Dec-2004  
C;Accession: JH0417; A32376; G02251; A32377  
R;Harn, H.J.; Isola, N.; Cooper, D.L.  
Biochem. Biophys. Res. Commun. 178, 1127-1134, 1991  
A;Title: The multispecific cell adhesion molecule CD44 is represented in reticulocyte  
A;Reference number: JH0417; MUID:91337049; PMID:1840487  
A;Accession: JH0417  
A;Molecule type: mRNA  
A;Residues: 1-361 <HAR>  
A;Cross-references: UNIPROT:Q92493; UNIPARC:UPI000016A68F; GB:M59040; NID:g180129; PIDN:  
A;Experimental source: reticulocyte  
A;Note: The authors translated the codon ATG for residues 63, 66 and 239 as Trp and GGA  
R;Stamenkovic, I.; Amiot, M.; Pesando, J.M.; Seed, B.  
Cell 56, 1057-1062, 1989  
A;Title: A lymphocyte molecule implicated in lymph node homing is a member of the cartil  
A;Reference number: A32376; MUID:89168434; PMID:2466575  
A;Accession: A32376  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-238, 'E', 240-361 <STA>  
A;Cross-references: UNIPARC:UPI0000143A5B; GB:M24915; NID:g180196; PIDN:AAA35674.1; PID  
R;Bosch, P.P.; Stevens, J.W.; Buckwalter, J.A.; Midura, R.J.  
submitted to the EMBL Data Library, November 1995  
A;Reference number: H00921  
A;Accession: G02251  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 1-25, 'M', 27-108, 'S', 110-361 <BOS>  
A;Cross-references: UNIPARC:UPI000016A285; EMBL:U40373; NID:g1101785; PID:g1101786  
R;Goldstein, L.A.; Zhou, D.F.H.; Picker, L.J.; Minty, C.N.; Bagatzte, R.F.; Ding, J.F.;  
Cell 56, 1063-1072, 1989



[illegible]



A;Gene: GDB:CD44  
A;Cross-references: GDB:120739; OMIM:107269  
A;Map position: 11pter-11p13  
A;Introns: 257/1  
C;Superfamily: human cell adhesion protein CD44

Query Match 11.9%; Score 198; DB 2; Length 395;  
Best Local Similarity 23.0%; Pred. No. 2.9e-08;  
Matches 85; Conservative 49; Mismatches 145; Indels 90; Gaps 14;

Qy 25 LRAEELSIOVSCRMGITLVSKKANQNLNFTAEKACRLGLSLAGKQDVETALKASFET 84  
Db 17 LSLAQIDLNITCRFAGVHVEKNGRYSISRTEAADLCKAFNSTLPTWQAQMEKALSIGFET 76

Qy 85 CSYGWVGDFVVISRISPNKCGKNGVGLVWKVPVSRQFAAYCYNSSDWTWNSCI---- 140  
Db 77 CRYGFI-EGHVVIPIRHNSICAANNVTGVILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy 141 -----PEIITKDPINPTOTATOTTFEIVSDS--- 167  
Db 135 LPNAPDGPITITVNRDGRVQKGEYRNPEDIPSNPTDDVSSGSSSRSTSGGYI 194

Qy 168 --TYSVASPY-----STIPAPTTTPPAPASTSI-PRRKKLICVTEVFMTSTWST 214  
Db 195 FVTFSTVHPIDEDSPWITDSTRIPATNMDSSHSTTLQPTANPTGLVEDLDRTGPLSM 254

Qy 215 ET-----EPFVENKAAPKNEAGF-----GG-----VPTALLVLALLPFGA 250  
Db 255 TTRDQDTPHPSGGSHTHGSESDGSHSGSGGANTTSGPIRTQP1PEWLIILASL-LAL 313

Qy 251 AAGLFCVVKRYVKAFFPTNKNQKME1ETK--VVKEEKANDSNPNESKKTDK-----N 303  
Db 314 ALILAVC-----IAVNSRRRCQKKVINGNGAVGDRKPSGLN-GEASKSQEMVHLVN 367

Qy 304 PEEKSPSK 312  
Db 368 KESSETPDQ 376

RESULT 13  
137369  
epican - human  
C;Species: Homo sapiens (man)  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 03-Aug-2001  
C;Accession: I37369; S24631  
R;Kugelman, L.C.; Ganguly, S.; Haggerty, J.G.; Weissman, S.M.; Milstone, L.M.  
J. Invest. Dermatol. 99, 866-891, 1992  
A;Title: The core protein of epican, a heparan sulfate proteoglycan on keratinocytes, is  
A;Reference number: I37369; PMID:1281868  
A;Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992  
A;Accession: I37369  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-699 <RES>  
A;Cross-references: UNIPARC:UPI000016A89D; EMBL:X66733; NID:g31190; PID:g31191

Query Match 11.9%; Score 196.5; DB 2; Length 699;  
Best Local Similarity 25.4%; Pred. No. 7.7e-08;  
Matches 60; Conservative 34; Mismatches 93; Indels 49; Gaps 7;

Qy 25 LRAEELSIOVSCRMGITLVSKKANQNLNFTAEKACRLGLSLAGKQDVETALKASFET 84  
Db 17 LSLAQIDLNITCRFAGVHVEKNGRYSISRTEAADLCKAFNSTLPTWQAQMEKALSIGFET 76

Qy 85 CSYGWVGDFVVISRISPNKCGKNGVGLVWKVPVSRQFAAYCYNSSDWTWNSCI---- 140  
Db 77 CRYGFI-EGHVVIPIRHNSICAANNVTGVILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy 141 -----PEIITKDPINPTOTATOTTFEIVSDTYS 170  
Db 135 LPNAPDGPITITVNRDGRVQKGEYRNPEDIPSNPTDDVSSGSSSRSTSGGY- 193

Qy 171 VASPYSTI-PAPTTTPP--APASTSIPRKKLICVTEVFMTSTWSTETETPFVENK 223

Db 194 IFYTFSTVHPIPEDSPWITDSTRIPATS-----TSSNTISAGWEPNEENE 240

RESULT 14  
S24240  
lymphocyte surface antigen CD44 precursor - horse  
C;Species: Equus caballus (domestic horse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: I46245; S24240  
R;Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; Butcl  
Immunogenetics 37, 474-477, 1993  
A;Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.  
A;Reference number: I46245; MUID:93170897; PMID:8436424  
A;Accession: I46245  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-359 <TA2>  
A;Cross-references: UNIPROT:Q05078; UNIPARC:UPI0000127369; EMBL:X66862; NID:g1059; PIDN:  
C;Superfamily: human cell adhesion protein CD44  
C;Keywords: surface antigen; transmembrane protein

Query Match 11.2%; Score 186; DB 2; Length 359;  
Best Local Similarity 24.6%; Pred. No. 2.3e-07;  
Matches 84; Conservative 42; Mismatches 159; Indels 56; Gaps 11;

Qy 25 LRAEELSIOVSCRMGITLVSKKANQNLNFTAEKACRLGLSLAGKQDVETALKASFET 84  
Db 17 LSLAQIDLNITCRVAGVHVEKNGRYSISRTEAADLCKAFNSTLPTWQAQMEKALNIGFET 76

Qy 85 CSYGWVGDFVVISRISPNKCGKNGVGLVWKVPVSRQFAAYCYNSSDWTWNSCI---- 140  
Db 77 CRIGFI-EGHVVIPIRHNSICAANNVTGVILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134

Qy 141 -----PEIIT-----TKDPIFNITQTATQTTEFIVSDTYSVASPYST 177  
Db 135 LPNAPFGPITITVNRDGRVTKKGEYRNPEDINPSTPADDDVSSGSSSRSTSGGYSI 194

Qy 178 IPA--PTTP-----PAPASTSIPIRKKLICVTEVFMTSTWSTETETPFVENK 223  
Db 195 FHTLPTTRPTQDQSSPWSDSPEKPTTKDRASGGRAQTTHGSETSGHSTGSGQ---EGG 251

Qy 224 AAFKNEAAGGGVPTALLVLALLFFGAAGLGCYVKRYKAFPTNKNQKME1ETK-- 281  
Db 252 ASTTSGPIRRPQ1PEWLIILASL-LALALILAVC-----IAVNSRRRCQKKLVINNGN 305

Qy 282 -VVKEEKANDSNPNESKKTDKNPNESKSPSKTTVRCLEAE 321  
Db 306 GAVDDRKASGLN-GEASRSQEMVHLVNKESSETQDQPMPTAD 345

RESULT 15  
I50421  
aggrecan precursor - chicken  
N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein  
C;Species: Gallus gallus (chicken)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072  
R;Li, H.; Schwartz, N.B.; Vertel, B.M.  
J. Biol. Chem. 268, 23504-23511, 1993  
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and  
A;Reference number: A48884; MUID:94043149; PMID:8226878  
A;Accession: I50421  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-2109 <LIX>  
A;Cross-references: UNIPROT:P07898; UNIPARC:UPI000013177E; GB:L21913; NID:g416133; PIDN:  
R;Chandrasekaran, L.; Tanzer, M.L.  
Biochem. J. 296, 885-887, 1993  
A;Reference number: S39796; MUID:94107258; PMID:8280087  
A;Contents: annotation; erratum  
A;Accession: S39796  
A;Molecule type: mRNA

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Query Match          9.0%; Score 148.5; DB 1; Length 2109;
Best Local Similarity 27.0%; Pred. No. 0.0022;
Matches 74; Conservative 27; Mismatches 104; Indels 69; Gaps 13;

QY 50 QQLNFTBEAKCRLLGLSLAGKQVETALKASPTCSYGVYGGDFV--VISRISFNPKCG 107
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 EKTTFQAFPKCHSLGARLATTGELYLAWKDGMDMCSAGWLADRSVYPSIRAREN--CG 315

QY 108 KXNGGVV--LIWKVPV-----SRQFAAYCYNSSDTWTNSCIP-----EITTKDPINF 153

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Search completed: March 20, 2006, 14:09:39  
Job time : 49.4292 secs

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A:Cross-references: UNIPARC:UPI00001712F6; GB:M13993; NID:G211654; PIDN:AAA48720.1; PID:  
A:Experimental source: sternal cartilage  
F:Tanaka, T.; Har-El, R.; Tanzer, M.L.  
J. Biol. Chem. 263, 15831-15835, 1988  
A:Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.  
A:Reference number: A32002; MUID:95008500; PMID:3170613  
A:Accession: A32002  
A:Molecule type: DNA  
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A:Cross-references: UNIPARC:UPI0000173C76  
A:Note: the authors translated the codon TCC for residue 1787 as Phe  
R:Krueger, R.C.  
J. Biol. Chem. 265, 12088-12097, 1990  
A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide s  
A:Reference number: I50216; MUID:90307744; PMID:1694853  
A:Accession: I50216  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 'PA', 1044-1559 <KRU>  
A:Cross-references: UNIPARC:UPI00001712P9; GB:M38187; NID:G211685; PIDN:AAA48731.1; PID:  
R:Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.  
J. Biol. Chem. 265, 12075-12087, 1990  
A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation an  
A:Reference number: A37072; MUID:90307743; PMID:2365711  
A:Accession: A37072  
A:Molecule type: protein  
A:Residues: 998-1015, 'X', 1017-1019, 'X', 1021-1023 <KR2>  
A:Cross-references: UNIPARC:UPI0000173C77  
A:Note: amino end of 86k core peptide CS-A  
A:Accession: B37072  
A:Molecule type: protein  
A:Residues: 1247-1250, 'D', 1252-1272, 'X', 1274-1275 <KR3>  
A:Cross-references: UNIPARC:UPI0000173C78  
A:Note: amino end of 75k core peptide CS-B  
C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG  
C:Keywords: alternative splicing  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-2109/Product: aggrecan #status predicted <MAT>  
F:44-131/Domain: immunoglobulin homology <IMM>  
F:166-243/Domain: link protein repeat homology <LNK1>  
F:264-346/Domain: link protein repeat homology <LNK2>  
F:537-614/Domain: link protein repeat homology <LNK3>  
F:635-716/Domain: link protein repeat homology <LNK4>  
F:1859-1890/Domain: EGF homology <EGF>  
F:1897-2017/Domain: C-type lectin homology <LCH>  
F:2024-2080/Domain: complement factor H repeat homology <FHD>



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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:07:04 ; Search time 22.783 Seconds

(without alignments)

1168.483 Million cell updates/sec

Title: US-10-063-510-6

Perfect score: 1657

Sequence: 1 MARCFSLVLLTSITWTRLL.....NPBESKSPSKTVRCLEAEV 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued\_Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCUTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1657	100.0	322	2	US-09-232-160-21
2	1657	100.0	322	2	US-09-907-794A-201
3	1657	100.0	322	2	US-09-905-125A-201
4	1657	100.0	322	2	US-09-902-775A-201
5	1657	100.0	322	2	US-09-906-700-201
6	1657	100.0	322	2	US-09-903-603A-201
7	1657	100.0	322	2	US-09-904-920A-201
8	1657	100.0	322	2	US-09-909-064-201
9	1657	100.0	322	2	US-09-905-381A-201
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21	224.5	13.5	339	1	US-08-892-880-3
22	222.5	13.4	362	6	5504194-2
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32	161	9.7	90	2	US-09-206-695-3
33	161	9.7	90	2	US-09-799-118-3
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35	145	8.8	259	2	US-09-949-016-10954
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38	145	8.8	277	2	US-09-206-695-2
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43	131.5	7.9	883	2	US-10-195-970-3
44	131	7.9	649	2	US-10-188-495-63
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46	130.5	7.9	883	2	US-10-195-970-6
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73	113.5	6.8	97	2	US-09-206-695-5
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92	101.5	6.1	590	2	US-09-957-187-12
93	101.5	6.1	590	2	US-09-991-053-12
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106	93	5.6	629	2	US-08-265-428-6	Sequence 6, Appli	179	84.5	5.1	1011	2	US-08-836-325-2	Sequence 2, Appli
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112	92	5.6	201	2	US-09-270-767-32397	Sequence 32397, A	185	84	5.1	216	2	US-08-928-361B-27	Sequence 27, Appl
113	92	5.6	201	2	US-09-270-767-47614	Sequence 47614, A	186	84	5.1	216	2	US-08-928-361B-27	Sequence 27, Appl
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115	91.5	5.5	639	2	US-09-823-240A-5	Sequence 5, Appli	188	84	5.1	920	1	US-08-481-206-10	Sequence 10, Appl
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119	90	5.4	1367	2	US-09-487-558B-108	Sequence 108, App	192	84	5.1	1721	2	US-08-700-651-5	Sequence 5, Appli
120	89	5.4	353	1	US-08-073-807A-17	Sequence 17, Appl	193	84	5.1	1721	2	US-08-228-361B-6	Sequence 6, Appli
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123	89	5.4	416	1	US-09-311-784A-26	Sequence 26, Appli	196	83.5	5.0	346	1	US-08-687-702-36	Sequence 36, Appl
124	89	5.4	471	2	US-09-949-016-9525	Sequence 9525, Ap	197	83.5	5.0	393	2	US-09-377-557-14	Sequence 14, Appl
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129	87.5	5.3	334	2	US-09-248-796A-204627	Sequence 204627, A	202	83.5	5.0	879	1	US-08-413-118-2	Sequence 3, Appli
130	87.5	5.3	536	2	US-09-292-225-21	Sequence 21, Appl	203	83.5	5.0	879	1	US-08-413-118-3	Sequence 3, Appli
131	87.5	5.3	555	2	US-09-292-225-15	Sequence 15, Appl	204	83.5	5.0	879	2	US-08-413-118-3	Sequence 3, Appli
132	87.5	5.3	555	2	US-09-292-225-18	Sequence 18, Appl	205	83.5	5.0	879	2	US-08-413-118-3	Sequence 3, Appli
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139	87.5	5.3	1085	2	US-08-353-784-5	Sequence 5, Appli	212	83	5.0	351	2	US-09-248-796A-23675	Sequence 23675, A
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141	87.5	5.3	1085	2	US-08-484-159-5	Sequence 5, Appli	214	83	5.0	409	2	US-09-949-016-6281	Sequence 6281, Ap
142	87	5.3	288	2	US-09-216-393B-341	Sequence 341, App	215	83	5.0	454	2	US-09-949-016-6281	Sequence 11120, A
143	87	5.3	288	2	US-09-216-393B-344	Sequence 344, App	216	83	5.0	605	2	US-03-487-558B-428	Sequence 428, App
144	87	5.3	631	2	US-09-620-412C-325	Sequence 325, App	217	83	5.0	736	2	US-08-457-040B-26	Sequence 26, Appl
145	87	5.3	631	2	US-09-598-419-325	Sequence 325, App	218	82.5	5.0	203	2	US-09-270-767-35040	Sequence 35040, A
146	87	5.3	664	2	US-10-197-220-168	Sequence 168, App	219	82.5	5.0	203	2	US-09-270-767-50257	Sequence 50257, A
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149	87	5.3	849	2	US-08-189-718A-19	Sequence 19, Appl	222	82.5	5.0	447	2	US-09-252-991A-28081	Sequence 28081, A
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151	87	5.3	894	2	US-08-362-525-22	Sequence 22, Appl	224	82.5	5.0	591	2	US-09-991-181-416	Sequence 416, App
152	87	5.3	894	2	US-08-971-692-15	Sequence 15, Appl	225	82.5	5.0	208	2	US-09-990-444-416	Sequence 416, App
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154	87	5.3	905	2	US-08-487-691-2	Sequence 2, Appli	227	82.5	5.0	790	2	US-09-949-016-8169	Sequence 8169, Ap
155	87	5.3	905	2	US-08-666-221B-4	Sequence 4, Appli	228	82.5	5.0	866	1	US-09-949-016-8170	Sequence 8170, Ap
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157	87	5.3	1016	2	US-10-197-220-95	Sequence 95, Appli	230	82	4.9	866	2	US-08-487-691-17	Sequence 17, Appl
158	87	5.3	1537	1	US-08-325-267A-2	Sequence 2, Appli	231	82	4.9	208	2	US-09-991-181-416	Sequence 416, App
159	87	5.3	1537	2	US-08-487-558B-104	Sequence 104, App	232	82	4.9	208	2	US-09-832-129-36	Sequence 36, Appl
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161	86.5	5.2	503	2	US-09-487-558B-424	Sequence 424, App	234	82	4.9	208	2	US-09-992-598-416	Sequence 416, App
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163	86.5	5.2	807	2	US-09-294-663-4	Sequence 4, Appli	236	82	4.9	455	2	US-09-949-016-10520	Sequence 10520, A
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173	85.5	5.2	781	2	US-09-949-016-6959	Sequence 6959, Ap	246	82	4.9	553	2	US-09-430-669-2	Sequence 2, Appli

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252	81.5	4.9	586	1	US-09-005-069-70	Sequence 70, Appl	325	79.5	4.8	461	2	US-10-046-433-6	Sequence 6, Appl
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254	81.5	4.9	586	2	US-09-004-730A-30	Sequence 30, Appl	327	79.5	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
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261	81.5	4.9	1445	1	US-08-446-363-2	Sequence 2, Appl	334	79.5	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
262	81	4.9	49	1	US-08-340-428B-23	Sequence 23, Appl	335	79.5	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
263	81	4.9	49	4	PCT-US93-07306-23	Sequence 23, Appl	336	79.5	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
264	81	4.9	289	2	US-09-466-778-8	Sequence 8, Appl	337	79.5	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
265	81	4.9	413	2	US-08-669-408B-10	Sequence 10, Appl	338	79.5	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
266	81	4.9	531	2	US-09-248-796A-15560	Sequence 15560, A	339	79.5	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
267	81	4.9	855	1	US-08-816-693A-2	Sequence 2, Appl	340	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
268	81	4.9	855	2	US-08-885-291-2	Sequence 2, Appl	341	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
269	81	4.9	855	2	US-09-496-672-2	Sequence 2, Appl	342	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
270	81	4.9	855	2	US-09-618-425-11	Sequence 11, Appl	343	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
271	81	4.9	883	2	US-09-248-796A-18931	Sequence 18931, A	344	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
272	81	4.9	1169	2	US-09-487-558B-106	Sequence 106, App	345	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
273	81	4.9	1322	2	US-09-487-558B-114	Sequence 114, App	346	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
274	80.5	4.9	334	2	US-09-197-970B-7	Sequence 7, Appl	347	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
275	80.5	4.9	478	2	US-09-345-473E-51	Sequence 51, Appl	348	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
276	80.5	4.9	478	2	US-09-862-027-51	Sequence 51, Appl	349	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
277	80.5	4.9	541	2	US-10-039-770B-1	Sequence 1, Appl	350	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
278	80.5	4.9	556	2	US-09-949-016-11052	Sequence 11052, A	351	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
279	80.5	4.9	595	1	US-08-232-087A-2	Sequence 2, Appl	352	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
280	80.5	4.9	595	2	US-09-006-353A-9	Sequence 9, Appl	353	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
281	80.5	4.9	595	2	US-09-573-386-9	Sequence 9, Appl	354	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
282	80.5	4.9	595	2	US-09-949-016-6048	Sequence 6048, App	355	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
283	80.5	4.9	624	2	US-09-877-730-24	Sequence 24, Appl	356	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
284	80.5	4.9	642	2	US-09-949-016-8043	Sequence 8043, App	357	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
285	80.5	4.9	673	2	US-09-949-016-7388	Sequence 7388, App	358	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
286	80.5	4.9	712	2	US-09-877-730-22	Sequence 22, Appl	359	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
287	80.5	4.9	793	2	US-09-877-730-28	Sequence 28, Appl	360	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
288	80.5	4.9	991	2	US-09-877-730-12	Sequence 12, Appl	361	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
289	80.5	4.9	1069	2	US-09-877-730-2	Sequence 2, Appl	362	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
290	80.5	4.9	1072	2	US-09-877-730-18	Sequence 18, Appl	363	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
291	80.5	4.9	1150	2	US-09-877-730-8	Sequence 8, Appl	364	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
292	80	4.8	52	1	US-08-225-477B-10	Sequence 10, Appl	365	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
293	80	4.8	52	4	PCT-US95-04353-10	Sequence 10, Appl	366	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
294	80	4.8	95	2	US-09-252-991A-28504	Sequence 28504, A	367	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
295	80	4.8	251	2	US-09-248-796A-23216	Sequence 23216, A	368	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
296	80	4.8	257	2	US-09-902-540-15102	Sequence 15102, A	369	79	4.8	461	2	US-09-949-016-7840	Sequence 7840, Ap
297	80	4.8	372	2	US-09-248-796A-19896	Sequence 19896, A	370	78.5	4.7	130	2	US-08-928-361B-14	Sequence 14, Appl
298	80	4.8	404	2	US-09-270-767-41751	Sequence 41751, A	371	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
299	80	4.8	423	2	US-09-270-767-44448	Sequence 44448, A	372	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
300	80	4.8	451	1	US-08-287-001A-2	Sequence 2, Appl	373	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
301	80	4.8	451	4	PCT-US95-09941-2	Sequence 2, Appl	374	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
302	80	4.8	468	1	US-08-959-011-3	Sequence 3, Appl	375	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
303	80	4.8	823	2	US-09-248-796A-16699	Sequence 16699, A	376	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
304	80	4.8	893	2	US-08-189-738A-18	Sequence 18, Appl	377	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
305	79.5	4.8	153	2	US-09-252-991A-17880	Sequence 17880, A	378	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
306	79.5	4.8	154	2	US-09-270-767-40476	Sequence 40476, A	379	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
307	79.5	4.8	154	2	US-09-270-767-55692	Sequence 55692, A	380	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
308	79.5	4.8	324	2	US-09-489-039A-8593	Sequence 8593, App	381	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
309	79.5	4.8	374	2	US-09-248-796A-17283	Sequence 17283, A	382	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
310	79.5	4.8	439	2	US-10-360-101-226	Sequence 226, App	383	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
311	79.5	4.8	461	1	US-08-385-229-2	Sequence 2, Appl	384	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
312	79.5	4.8	461	1	US-08-650-000-2	Sequence 2, Appl	385	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
313	79.5	4.8	461	2	US-09-042-785A-7	Sequence 7, Appl	386	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
314	79.5	4.8	461	2	US-08-477-347-3	Sequence 3, Appl	387	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
315	79.5	4.8	461	2	US-09-006-353A-4	Sequence 4, Appl	388	78.5	4.7	130	2	US-09-949-016-7840	Sequence 7840, Ap
316	79.5	4.8	461	2	US-08-476-862-2	Sequence 2, Appl	389	78	4.7	280	2	US-09-949-016-7840	Sequence 7840, Ap
317	79.5	4.8	461	2	US-09-573-986-4	Sequence 4, Appl	390	78	4.7	280	2	US-09-949-016-7840	Sequence 7840, Ap
318	79.5	4.8	461	2	US-08-406-824A-2	Sequence 2, Appl	391	78	4.7	280	2	US-09-949-016-7840	Sequence 7840, Ap
319	79.5	4.8	461	2	US-09-800-909-2	Sequence 2, Appl	392	78	4.7	280	2	US-09-949-016-7840	Sequence 7840, Ap

333	78	4.7	280	2	US-09-903-603A-325	Sequence 325, App	466	76	4.6	386	2	US-09-328-352-4722	Sequence 4722, Ap
334	78	4.7	280	2	US-09-904-920A-325	Sequence 325, App	467	76	4.6	402	2	US-09-270-767-45612	Sequence 45612, A
335	78	4.7	280	2	US-09-806-536A-1	Sequence 1, Appli	468	76	4.6	482	2	US-09-991-181-513	Sequence 513, App
336	78	4.7	280	2	US-09-903-064-325	Sequence 325, App	469	76	4.6	482	2	US-09-990-444-513	Sequence 513, App
337	78	4.7	280	2	US-09-905-311A-325	Sequence 325, App	470	76	4.6	482	2	US-09-997-333-513	Sequence 513, App
338	78	4.7	280	2	US-09-906-618-325	Sequence 325, App	471	76	4.6	482	2	US-09-992-598-513	Sequence 513, App
339	78	4.7	280	2	US-09-906-646-325	Sequence 325, App	472	76	4.6	509	2	US-09-907-794A-315	Sequence 315, App
400	78	4.7	280	2	US-09-904-462-325	Sequence 325, App	473	76	4.6	509	2	US-09-905-125A-315	Sequence 315, App
401	78	4.7	280	2	US-09-902-736A-325	Sequence 325, App	474	76	4.6	509	2	US-09-902-775A-315	Sequence 315, App
402	78	4.7	280	2	US-09-906-722A-325	Sequence 325, App	475	76	4.6	509	2	US-09-906-700-315	Sequence 315, App
403	78	4.7	300	2	US-09-248-796A-16245	Sequence 16245, A	476	76	4.6	509	2	US-09-903-603A-315	Sequence 315, App
404	78	4.7	398	2	US-09-248-796A-14978	Sequence 14978, A	477	76	4.6	509	2	US-09-904-920A-315	Sequence 315, App
405	78	4.7	494	2	US-09-248-796A-16546	Sequence 16546, A	478	76	4.6	509	2	US-09-909-064-315	Sequence 315, App
406	78	4.7	564	2	US-10-063-540A-2	Sequence 2, Appli	479	76	4.6	509	2	US-09-905-381A-315	Sequence 315, App
407	78	4.7	609	2	US-09-198-452A-579	Sequence 579, App	480	76	4.6	509	2	US-09-906-618-315	Sequence 315, App
408	78	4.7	1006	2	US-09-949-016-7897	Sequence 7897, Ap	481	76	4.6	509	2	US-09-906-646-315	Sequence 315, App
409	78	4.7	1442	1	US-08-015-986A-3	Sequence 3, Appli	482	76	4.6	509	2	US-09-904-462-315	Sequence 315, App
410	78	4.7	1442	1	US-08-446-363-3	Sequence 3, Appli	483	76	4.6	509	2	US-09-902-736A-315	Sequence 315, App
411	78	4.7	1744	2	US-09-438-185A-542	Sequence 542, App	484	76	4.6	509	2	US-09-906-722A-315	Sequence 315, App
412	78	4.7	2176	2	US-09-949-016-5923	Sequence 9923, Ap	485	76	4.6	563	2	US-09-949-016-10405	Sequence 10405, A
413	77.5	4.7	497	2	US-09-377-557-10	Sequence 10, Appl	486	76	4.6	687	1	US-08-232-538-6	Sequence 6, Appli
414	77.5	4.7	514	2	US-08-738-168B-15	Sequence 15, Appl	487	76	4.6	687	2	US-08-786-164-6	Sequence 2, Appli
415	77.5	4.7	1262	2	US-09-107-433-5067	Sequence 5067, Ap	488	76	4.6	687	2	US-09-427-353-2	Sequence 2, Appli
416	77.5	4.7	1475	2	US-09-538-092-1160	Sequence 1160, Ap	489	76	4.6	758	1	US-08-874-678-1	Sequence 1, Appli
417	77.5	4.7	3969	2	US-09-538-092-1262	Sequence 1262, Ap	490	76	4.6	758	2	US-08-643-839-1	Sequence 1, Appli
418	77	4.6	162	2	US-09-068-140A-2	Sequence 2, Appli	491	76	4.6	758	2	US-09-051-363-24	Sequence 24, Appl
419	77	4.6	173	2	US-09-068-140A-13	Sequence 13, Appl	492	76	4.6	758	2	US-09-348-886-1	Sequence 1, Appli
420	77	4.6	249	2	US-08-700-651-15	Sequence 15, Appl	493	76	4.6	758	2	US-10-105-901A-1	Sequence 1, Appli
421	77	4.6	249	2	US-08-928-361B-20	Sequence 20, Appl	494	76	4.6	780	1	US-08-232-538-14	Sequence 14, Appl
422	77	4.6	249	2	US-09-588-995A-20	Sequence 20, Appl	495	76	4.6	780	1	US-08-786-164-14	Sequence 14, Appl
423	77	4.6	714	2	US-09-949-016-7038	Sequence 7038, Ap	496	76	4.6	985	2	US-09-248-796A-16090	Sequence 16090, A
424	77	4.6	908	2	US-09-949-016-7580	Sequence 7580, Ap	497	76	4.6	1014	2	US-09-078-347A-3	Sequence 3, Appli
425	77	4.6	1140	2	US-09-538-092-647	Sequence 647, App	498	76	4.6	1014	2	US-09-596-248D-25	Sequence 25, Appl
426	77	4.6	1401	2	US-09-127-670-6	Sequence 6, Appli	499	76	4.6	1014	2	US-09-296-662-35	Sequence 35, Appl
427	77	4.6	2123	2	US-08-968-685A-10	Sequence 10, Appl	500	76	4.6	1063	2	US-09-596-248D-47	Sequence 47, Appl
428	76.5	4.6	134	2	US-09-248-796A-27317	Sequence 27317, A	501	76	4.6	1338	2	US-08-750-141A-3	Sequence 3, Appli
429	76.5	4.6	240	1	US-08-114-555A-8	Sequence 8, Appli	502	76	4.6	1338	2	US-09-119-014D-6	Sequence 6, Appli
430	76.5	4.6	240	2	US-08-559-397A-14	Sequence 14, Appl	503	76	4.6	1401	2	US-08-781-891-206	Sequence 206, App
431	76.5	4.6	303	2	US-09-248-796A-14269	Sequence 14269, A	504	76	4.6	1401	2	US-09-618-166-206	Sequence 206, App
432	76.5	4.6	334	2	US-10-012-231A-41	Sequence 41, Appl	505	76	4.6	1426	2	US-09-136-574A-43	Sequence 43, Appl
433	76.5	4.6	334	2	US-10-015-389A-41	Sequence 41, Appl	506	76	4.6	1645	2	US-09-976-594-769	Sequence 769, App
434	76.5	4.6	334	2	US-10-006-768A-41	Sequence 41, Appl	507	75.5	4.6	258	2	US-08-961-083-90	Sequence 90, Appl
435	76.5	4.6	334	2	US-10-015-671A-41	Sequence 41, Appl	508	75.5	4.6	258	2	US-09-536-784-90	Sequence 90, Appl
436	76.5	4.6	334	2	US-10-015-393A-41	Sequence 41, Appl	509	75.5	4.6	258	2	US-09-765-271-90	Sequence 90, Appl
437	76.5	4.6	334	2	US-10-011-833A-41	Sequence 41, Appl	510	75.5	4.6	258	2	US-09-765-272A-90	Sequence 90, Appl
438	76.5	4.6	334	2	US-10-006-041A-41	Sequence 41, Appl	511	75.5	4.6	348	1	US-08-035-392-2	Sequence 2, Appli
439	76.5	4.6	334	2	US-10-012-064A-41	Sequence 41, Appl	512	75.5	4.6	348	1	US-08-504-511A-2	Sequence 2, Appli
440	76.5	4.6	348	2	US-09-216-295-16	Sequence 16, Appl	513	75.5	4.6	430	1	US-08-035-392-4	Sequence 4, Appli
441	76.5	4.6	348	2	US-09-632-570-16	Sequence 16, Appl	514	75.5	4.6	430	1	US-08-504-511A-4	Sequence 4, Appli
442	76.5	4.6	348	2	US-09-632-575-46	Sequence 46, Appl	515	75.5	4.6	451	2	US-09-134-001C-4461	Sequence 4461, Ap
443	76.5	4.6	382	1	US-08-415-818-7	Sequence 7, Appli	516	75.5	4.6	453	2	US-09-230-225B-4	Sequence 4, Appli
444	76.5	4.6	382	1	US-08-894-236-7	Sequence 7, Appli	517	75.5	4.6	510	2	US-09-270-767-43633	Sequence 43633, A
445	76.5	4.6	382	1	US-08-555-268A-14	Sequence 14, Appl	518	75.5	4.6	511	1	US-08-220-151-17	Sequence 17, Appl
446	76.5	4.6	382	2	US-09-430-775-36	Sequence 36, Appl	519	75.5	4.6	511	1	US-08-413-118-17	Sequence 17, Appl
447	76.5	4.6	382	4	PCT-US96-01444-7	Sequence 7, Appli	520	75.5	4.6	511	2	US-08-473-446-17	Sequence 17, Appl
448	76.5	4.6	397	2	US-09-198-452A-201	Sequence 201, App	521	75.5	4.6	565	2	US-08-961-083-218	Sequence 218, App
449	76.5	4.6	397	2	US-09-438-185A-188	Sequence 188, App	522	75.5	4.6	565	2	US-09-536-784-218	Sequence 218, App
450	76.5	4.6	452	2	US-09-248-796A-16219	Sequence 16219, A	523	75.5	4.6	565	2	US-09-765-271-218	Sequence 218, App
451	76.5	4.6	484	1	US-08-127-499A-26	Sequence 26, Appl	524	75.5	4.6	565	2	US-09-765-272A-218	Sequence 218, App
452	76.5	4.6	484	1	US-08-482-847-26	Sequence 26, Appl	525	75.5	4.6	639	2	US-09-949-016-6812	Sequence 6812, Ap
453	76.5	4.6	653	2	US-09-991-181-229	Sequence 229, App	526	75.5	4.6	641	2	US-10-164-595-46	Sequence 46, Appl
454	76.5	4.6	653	2	US-09-990-444-229	Sequence 229, App	527	75.5	4.6	652	2	US-09-949-016-7323	Sequence 7323, Ap
455	76.5	4.6	653	2	US-09-997-333-229	Sequence 229, App	528	75	4.5	210	2	US-09-270-767-32951	Sequence 32951, A
456	76.5	4.6	653	2	US-09-992-598-329	Sequence 229, App	529	75	4.5	210	2	US-09-270-767-48168	Sequence 48168, A
457	76.5	4.6	1013	2	US-09-248-796A-14747	Sequence 14747, A	530	75	4.5	424	1	US-08-419-414-2	Sequence 2, Appli
458	76.5	4.6	1307	2	US-10-104-047-2438	Sequence 2, Appli	531	75	4.5	425	2	US-09-748-537-14	Sequence 14, Appl
459	76.5	4.6	5037	2	US-09-424-783-4	Sequence 4, Appli	532	75	4.5	554	1	US-08-524-051-2	Sequence 2, Appli
460	76.5	4.6	154	2	US-09-270-767-61124	Sequence 61124, A	533	75	4.5	554	2	US-09-052-778-16	Sequence 16, Appl
461	76	4.6	299	2	US-09-270-767-44350	Sequence 44350, A	534	75	4.5	557	2	US-09-248-796A-26892	Sequence 26892, A
462	76	4.6	321	2	US-09-248-796A-20146	Sequence 20146, A	535	75	4.5	904	2	US-09-198-484-2	Sequence 2, Appli
463	76	4.6	345	2	US-09-543-681A-6150	Sequence 6150, Ap	536	75	4.5	941	2	US-07-757-022B-14	Sequence 14, Appl
464	76	4.6	380	2	US-09-134-001C-4558	Sequence 4558, Ap	537	75	4.5	1022	2	US-07-757-022B-84	Sequence 84, Appl
465	76	4.6	380	2			538	75	4.5	1038	2	US-07-757-022B-74	Sequence 74, Appl

539	75	4.5	1049	2	US-07-757-022B-58	Sequence 58, Appl	612	74	4.5	339	2	US-08-410-614-4	Sequence 4, Appl
540	75	4.5	1140	2	US-07-757-022B-104	Sequence 104, App	613	74	4.5	370	2	US-09-270-767-37418	Sequence 37418, A
541	75	4.5	1151	1	US-08-286-889-37	Sequence 37, Appl	614	74	4.5	370	2	US-09-270-767-52635	Sequence 52635, A
542	75	4.5	1151	1	US-08-485-618-37	Sequence 37, Appl	615	74	4.5	395	2	US-09-949-016-9564	Sequence 9564, Ap
543	75	4.5	1151	1	US-08-362-652-37	Sequence 37, Appl	616	74	4.5	422	2	US-09-949-016-8251	Sequence 8251, Ap
544	75	4.5	1151	1	US-08-603-672-37	Sequence 37, Appl	617	74	4.5	428	2	US-09-134-000C-6457	Sequence 6457, Ap
545	75	4.5	1151	1	US-08-482-293A-37	Sequence 37, Appl	618	74	4.5	472	2	US-09-625-188-6	Sequence 6, Appl
546	75	4.5	1151	1	US-08-943-363-37	Sequence 37, Appl	619	74	4.5	493	2	US-09-248-796A-17819	Sequence 17819, A
547	75	4.5	1151	2	US-09-193-043-37	Sequence 37, Appl	620	74	4.5	681	2	US-09-336-910A-2	Sequence 2, Appl
548	75	4.5	1151	2	US-09-688-307A-37	Sequence 37, Appl	621	74	4.5	681	2	US-09-336-910A-2	Sequence 2, Appl
549	75	4.5	1151	2	US-09-350-259-37	Sequence 37, Appl	622	74	4.5	778	2	US-09-248-796A-16358	Sequence 16358, A
550	75	4.5	1161	2	US-09-193-043-55	Sequence 55, Appl	623	74	4.5	910	2	US-09-270-767-42083	Sequence 42083, A
551	75	4.5	1161	2	US-09-688-307A-55	Sequence 55, Appl	624	74	4.5	1021	2	US-09-902-540-16773	Sequence 16773, A
552	75	4.5	1161	2	US-09-350-259-55	Sequence 55, Appl	625	74	4.5	1693	2	US-08-840-316-1	Sequence 1, Appl
553	75	4.5	1162	1	US-08-728-323A-2	Sequence 2, Appl	626	74	4.5	1693	2	US-08-809-523-1	Sequence 1, Appl
554	75	4.5	1162	2	US-09-298-568-2	Sequence 2, Appl	627	74	4.5	1693	2	US-08-471-971-1	Sequence 1, Appl
555	75	4.5	1162	2	US-09-410-399-2	Sequence 2, Appl	628	74	4.5	1693	2	US-09-402-776-1	Sequence 1, Appl
556	75	4.5	1162	2	US-09-894-273-2	Sequence 2, Appl	629	74	4.5	1693	2	US-08-470-246-1	Sequence 1, Appl
557	75	4.5	1270	2	US-07-757-022B-44	Sequence 44, Appl	630	74	4.5	1693	2	US-08-316-765-1	Sequence 1, Appl
558	75	4.5	1311	2	US-07-757-022B-42	Sequence 42, Appl	631	74	4.5	1693	2	US-09-724-475-1	Sequence 1, Appl
559	75	4.5	1313	2	US-07-757-022B-142	Sequence 142, App	632	74	4.5	1693	4	PCT-US93-08849A-1	Sequence 1, Appl
560	75	4.5	1314	2	US-07-757-022B-50	Sequence 50, Appl	633	74	4.5	1693	4	PCT-US93-08849A-1	Sequence 1, Appl
561	75	4.5	1320	2	US-07-757-022B-46	Sequence 46, Appl	634	74	4.5	1729	2	US-09-134-000C-5675	Sequence 5675, Ap
562	75	4.5	1320	2	US-07-757-022B-60	Sequence 60, Appl	635	74	4.5	2414	1	US-08-227-536-2	Sequence 2, Appl
563	75	4.5	1320	2	US-10-164-595-58	Sequence 58, Appl	636	74	4.5	2414	2	US-09-538-092-1289	Sequence 1289, Ap
564	75	4.5	1354	2	US-07-757-022B-48	Sequence 48, Appl	637	74	4.5	2414	2	PCT-US95-04682-2	Sequence 2, Appl
565	75	4.5	1361	2	US-07-757-022B-40	Sequence 40, Appl	638	73.5	4.4	124	2	US-08-700-651-11	Sequence 11, Appl
566	75	4.5	1363	2	US-07-757-022B-52	Sequence 52, Appl	639	73.5	4.4	124	2	US-08-928-361B-16	Sequence 16, Appl
567	75	4.5	1404	2	US-07-757-022B-2	Sequence 2, Appl	640	73.5	4.4	124	2	US-09-588-995A-16	Sequence 16, Appl
568	75	4.5	1404	2	US-07-757-022B-62	Sequence 62, Appl	641	73.5	4.4	128	2	US-08-700-651-7	Sequence 7, Appl
569	75	4.5	1404	2	US-10-164-595-78	Sequence 78, Appl	642	73.5	4.4	128	2	US-09-928-361B-12	Sequence 12, Appl
570	75	4.5	1404	2	US-09-298-970A-1	Sequence 1, Appl	643	73.5	4.4	128	2	US-09-588-995A-12	Sequence 12, Appl
571	75	4.5	1404	2	US-09-897-188-1	Sequence 1, Appl	644	73.5	4.4	130	2	US-08-700-651-8	Sequence 8, Appl
572	75	4.5	1411	2	US-09-949-016-10827	Sequence 10827, A	645	73.5	4.4	130	2	US-08-928-361B-13	Sequence 13, Appl
573	74.5	4.5	109	2	US-09-107-532A-4999	Sequence 4999, Ap	646	73.5	4.4	130	2	US-09-588-995A-13	Sequence 13, Appl
574	74.5	4.5	145	2	US-08-808-599A-41	Sequence 41, Appl	647	73.5	4.4	138	2	US-08-700-651-10	Sequence 10, Appl
575	74.5	4.5	186	2	US-09-252-991A-20433	Sequence 20433, A	648	73.5	4.4	138	2	US-08-928-361B-15	Sequence 15, Appl
576	74.5	4.5	216	2	US-09-248-796A-25076	Sequence 25076, A	649	73.5	4.4	138	2	US-09-588-995A-15	Sequence 15, Appl
577	74.5	4.5	270	2	US-09-134-000C-3553	Sequence 3553, Ap	650	73.5	4.4	262	2	US-09-248-796A-21451	Sequence 21451, A
578	74.5	4.5	312	2	US-09-248-796A-20143	Sequence 20143, A	651	73.5	4.4	321	2	US-09-107-433-4282	Sequence 4282, Ap
579	74.5	4.5	333	2	US-09-107-532A-6475	Sequence 6475, Ap	652	73.5	4.4	382	2	US-09-248-796A-17276	Sequence 17276, A
580	74.5	4.5	386	2	US-09-270-767-44120	Sequence 44120, A	653	73.5	4.4	397	2	US-08-991-426-4	Sequence 4, Appl
581	74.5	4.5	429	2	US-09-949-016-8183	Sequence 8183, Ap	654	73.5	4.4	397	2	US-09-143-470-4	Sequence 4, Appl
582	74.5	4.5	429	2	US-09-949-016-8184	Sequence 8184, Ap	655	73.5	4.4	397	2	US-08-649-006A-4	Sequence 4, Appl
583	74.5	4.5	478	1	US-08-456-670B-40	Sequence 40, Appl	656	73.5	4.4	397	2	US-09-771-023-4	Sequence 4, Appl
584	74.5	4.5	478	2	US-09-372-036-40	Sequence 40, Appl	657	73.5	4.4	427	1	US-08-262-197C-53	Sequence 53, Appl
585	74.5	4.5	530	2	US-09-912-935-38	Sequence 38, Appl	658	73.5	4.4	499	2	US-09-561-763-2	Sequence 2, Appl
586	74.5	4.5	564	2	US-09-949-016-6898	Sequence 6898, Ap	659	73.5	4.4	499	2	US-09-431-367B-2	Sequence 2, Appl
587	74.5	4.5	565	2	US-09-949-016-6902	Sequence 6902, Ap	660	73.5	4.4	540	2	US-09-583-110-3685	Sequence 3685, Ap
588	74.5	4.5	587	2	US-09-815-923-4	Sequence 4, Appl	661	73.5	4.4	570	2	US-09-565-501A-104	Sequence 104, App
589	74.5	4.5	639	2	US-09-248-796A-20583	Sequence 20583, A	662	73.5	4.4	570	2	US-09-639-206A-104	Sequence 104, App
590	74.5	4.5	758	2	US-09-949-016-8288	Sequence 8288, Ap	663	73.5	4.4	570	2	US-09-874-923-104	Sequence 104, App
591	74.5	4.5	794	2	US-09-252-991A-28569	Sequence 28569, A	664	73.5	4.4	638	1	US-08-463-262A-11	Sequence 11, Appl
592	74.5	4.5	998	1	US-08-449-645A-20	Sequence 20, Appl	665	73.5	4.4	638	1	US-08-463-989-11	Sequence 11, Appl
593	74.5	4.5	998	1	US-08-702-367A-20	Sequence 20, Appl	666	73.5	4.4	638	2	US-09-003-574-11	Sequence 11, Appl
594	74.5	4.5	998	1	PCT-US95-04681-20	Sequence 20, Appl	667	73.5	4.4	638	2	US-09-003-570-11	Sequence 11, Appl
595	74.5	4.5	1638	2	US-09-071-035-258	Sequence 258, App	668	73.5	4.4	638	2	US-09-864-541A-11	Sequence 11, Appl
596	74.5	4.5	1638	2	US-09-071-035-262	Sequence 262, App	669	73.5	4.4	641	2	US-09-613-303-51	Sequence 51, Appl
597	74.5	4.5	1638	2	US-09-071-035-266	Sequence 266, App	670	73.5	4.4	641	2	US-10-267-311-51	Sequence 51, Appl
598	74.5	4.5	1638	2	US-10-206-576-258	Sequence 258, App	671	73.5	4.4	646	2	US-09-502-540-12044	Sequence 12044, A
599	74.5	4.5	1638	2	US-10-206-576-262	Sequence 262, App	672	73.5	4.4	659	2	US-09-543-681A-6013	Sequence 6013, Ap
600	74.5	4.5	1638	2	US-10-206-576-266	Sequence 266, App	673	73.5	4.4	712	2	US-09-949-016-10600	Sequence 10600, A
601	74.5	4.5	1747	2	US-09-134-000C-5999	Sequence 5999, Ap	674	73.5	4.4	713	2	US-08-899-437-2	Sequence 2, Appl
602	74	4.5	197	2	US-09-513-999C-7852	Sequence 7852, Ap	675	73.5	4.4	713	2	US-09-126-121-2	Sequence 2, Appl
603	74	4.5	257	2	US-09-567-458A-2	Sequence 2, Appl	676	73.5	4.4	763	2	US-08-961-083-66	Sequence 66, Appl
604	74	4.5	279	2	US-09-248-796A-16859	Sequence 16859, A	677	73.5	4.4	763	2	US-09-536-784-66	Sequence 66, Appl
605	74	4.5	299	2	US-09-107-433-3811	Sequence 3811, Ap	678	73.5	4.4	763	2	US-09-765-271-66	Sequence 66, Appl
606	74	4.5	323	2	US-09-270-767-44688	Sequence 44688, A	679	73.5	4.4	763	2	US-09-765-272A-66	Sequence 66, Appl
607	74	4.5	339	1	US-08-433-854-4	Sequence 4, Appl	680	73.5	4.4	780	2	US-09-248-796A-16702	Sequence 16702, A
608	74	4.5	339	1	US-08-174-745A-4	Sequence 4, Appl	681	73.5	4.4	795	2	US-09-193-562D-11	Sequence 11, Appl
609	74	4.5	339	1	US-08-195-947-4	Sequence 4, Appl	682	73.5	4.4	795	2	US-10-055-412B-11	Sequence 11, Appl
610	74	4.5	339	1	US-08-433-885-4	Sequence 4, Appl	683	73.5	4.4	819	2	US-09-468-656A-10	Sequence 10, Appl
611	74	4.5	339	1	US-08-433-908B-4	Sequence 4, Appl	684	73.5	4.4	821	2	US-09-193-562D-12	Sequence 12, Appl

685	73.5	4.4	821	2	US-10-055-412B-12	Sequence 12, Appl	758	72.5	4.4	185	2	US-09-248-796A-18311	Sequence 18311, A
686	73.5	4.4	826	2	US-09-769-787-194	Sequence 194, App	759	72.5	4.4	204	2	US-09-902-540-14080	Sequence 14080, A
687	73.5	4.4	905	2	US-09-193-562D-2	Sequence 2, Appli	760	72.5	4.4	206	2	US-09-198-452A-879	Sequence 879, App
688	73.5	4.4	905	2	US-10-055-412B-2	Sequence 2, Appli	761	72.5	4.4	206	2	US-09-438-185A-822	Sequence 822, App
689	73.5	4.4	919	2	US-09-949-016-6954	Sequence 6954, Ap	762	72.5	4.4	293	2	US-09-496-320-5	Sequence 5, Appli
690	73.5	4.4	922	2	US-09-248-796A-16269	Sequence 16269, A	763	72.5	4.4	315	2	US-09-328-352-5948	Sequence 5948, Ap
691	73.5	4.4	1101	2	US-09-561-709B-5	Sequence 5, Appli	764	72.5	4.4	328	2	US-09-489-039A-12803	Sequence 12803, A
692	73.5	4.4	1761	2	US-09-561-709B-1	Sequence 1, Appli	765	72.5	4.4	340	2	US-09-492-709A-262	Sequence 262, App
693	73.5	4.4	1876	2	US-09-418-710-71	Sequence 71, Appl	766	72.5	4.4	368	2	US-09-248-796A-19000	Sequence 19000, A
694	73.5	4.4	1876	2	US-09-839-479-70	Sequence 70, Appl	767	72.5	4.4	378	2	US-09-248-796A-18526	Sequence 18526, A
695	73.5	4.4	1878	2	US-09-418-710-13	Sequence 13, Appl	768	72.5	4.4	445	2	US-09-710-279-1294	Sequence 1294, Ap
696	73.5	4.4	1878	2	US-09-839-479-13	Sequence 13, Appl	769	72.5	4.4	462	6	5171671-2	Patent No. 5171671
697	73	4.4	155	2	US-09-252-991A-22634	Sequence 22634, A	770	72.5	4.4	463	1	US-08-162-402B-9	Sequence 9, Appli
698	73	4.4	162	2	US-08-700-651-13	Sequence 13, Appl	771	72.5	4.4	494	2	US-09-902-540-9960	Sequence 9960, Ap
699	73	4.4	326	2	US-09-248-796A-19891	Sequence 19891, A	772	72.5	4.4	510	2	US-09-211-417-1	Sequence 1, Appli
700	73	4.4	332	2	US-09-313-942-10	Sequence 10, Appl	773	72.5	4.4	608	2	US-09-949-016-11148	Sequence 11148, A
701	73	4.4	332	2	US-10-282-162-10	Sequence 10, Appl	774	72.5	4.4	608	2	US-09-949-016-11149	Sequence 11149, A
702	73	4.4	340	2	US-09-248-796A-24600	Sequence 24600, A	775	72.5	4.4	608	2	US-09-949-016-11150	Sequence 11150, A
703	73	4.4	380	2	US-09-270-767-43987	Sequence 43987, A	776	72.5	4.4	608	2	US-09-949-016-11151	Sequence 11151, A
704	73	4.4	428	2	US-09-489-039A-10901	Sequence 10901, A	777	72.5	4.4	652	2	US-09-310-463-4	Sequence 4, Appli
705	73	4.4	488	1	US-08-599-455B-5	Sequence 5, Appli	778	72.5	4.4	652	2	US-08-842-248A-4	Sequence 4, Appli
706	73	4.4	488	2	US-09-069-781B-5	Sequence 5, Appli	779	72.5	4.4	678	2	US-09-991-181-179	Sequence 179, App
707	73	4.4	488	2	US-09-137-132-5	Sequence 5, Appli	780	72.5	4.4	678	2	US-09-990-444-179	Sequence 179, App
708	73	4.4	488	2	US-08-864-564A-5	Sequence 5, Appli	781	72.5	4.4	678	2	US-09-997-333-179	Sequence 179, App
709	73	4.4	488	2	US-09-094-410-5	Sequence 5, Appli	782	72.5	4.4	678	2	US-09-992-598-179	Sequence 179, App
710	73	4.4	488	2	US-08-708-123D-5	Sequence 5, Appli	783	72.5	4.4	707	2	US-09-228-986-80	Sequence 80, Appl
711	73	4.4	488	2	US-08-583-153A-5	Sequence 5, Appli	784	72.5	4.4	707	2	US-10-101-464A-80	Sequence 80, Appl
712	73	4.4	488	2	US-08-638-524B-5	Sequence 5, Appli	785	72.5	4.4	719	2	US-09-949-016-9669	Sequence 9669, Ap
713	73	4.4	497	2	US-08-956-171E-5234	Sequence 5234, Ap	786	72.5	4.4	743	2	US-10-104-047-2340	Sequence 2340, Ap
714	73	4.4	497	2	US-08-781-986A-5234	Sequence 5234, Ap	787	72.5	4.4	798	2	US-09-270-767-42988	Sequence 42988, A
715	73	4.4	502	2	US-09-248-796A-15481	Sequence 15481, A	788	72.5	4.4	806	1	US-08-270-076A-11	Sequence 11, Appl
716	73	4.4	579	2	US-09-198-452A-918	Sequence 918, App	789	72.5	4.4	827	2	US-09-270-767-46276	Sequence 46276, A
717	73	4.4	606	2	US-09-438-185A-853	Sequence 853, App	790	72.5	4.4	841	2	US-09-949-016-9669	Sequence 9669, Ap
718	73	4.4	645	2	US-09-270-767-42233	Sequence 42233, A	791	72.5	4.4	878	2	US-09-556-706B-2	Sequence 2, Appli
719	73	4.4	650	2	US-08-362-525-2	Sequence 2, Appli	792	72.5	4.4	878	2	US-09-724-418A-2	Sequence 2, Appli
720	73	4.4	658	1	US-08-825-558-4	Sequence 4, Appli	793	72.5	4.4	907	2	US-08-783-774-2	Sequence 2, Appli
721	73	4.4	658	2	US-09-312-611-4	Sequence 4, Appli	794	72.5	4.4	907	2	US-09-328-599A-1	Sequence 1, Appli
722	73	4.4	708	1	US-07-797-556-2	Sequence 2, Appli	795	72.5	4.4	907	4	PCT-US95-04611A-19	Sequence 19, Appl
723	73	4.4	708	1	US-08-308-881-2	Sequence 2, Appli	796	72.5	4.4	1007	2	US-09-155-558-30	Sequence 30, Appl
724	73	4.4	708	1	US-09-058-263-2	Sequence 2, Appli	797	72.5	4.4	1306	2	US-09-134-000C-6670	Sequence 6670, Ap
725	73	4.4	708	1	US-09-059-099-2	Sequence 2, Appli	798	72.5	4.4	2308	1	US-08-015-973-1	Sequence 1, Appli
726	73	4.4	708	1	US-09-058-264-2	Sequence 2, Appli	799	72.5	4.4	2308	1	US-08-448-164-1	Sequence 1, Appli
727	73	4.4	708	2	US-09-455-962-2	Sequence 2, Appli	800	72.5	4.4	2308	2	US-08-081-929-2	Sequence 2, Appli
728	73	4.4	708	4	PCT-US95-06530-2	Sequence 2, Appli	801	72.5	4.4	2308	2	US-10-000-954-2	Sequence 2, Appli
729	73	4.4	830	2	US-09-107-433-4309	Sequence 4309, Ap	802	72.5	4.4	2314	2	US-09-816-703A-2	Sequence 2, Appli
730	73	4.4	851	2	US-09-583-110-3850	Sequence 3850, Ap	803	72.5	4.4	3069	2	US-09-712-363-246	Sequence 246, App
731	73	4.4	852	2	US-09-206-551-19	Sequence 19, Appl	804	72.5	4.4	3256	2	US-09-919-172-98	Sequence 98, Appl
732	73	4.4	859	2	US-09-313-942-7	Sequence 7, Appli	805	72.5	4.4	3256	2	US-09-976-594-22	Sequence 22, Appl
733	73	4.4	859	2	US-10-282-162-7	Sequence 7, Appli	806	72.5	4.4	3256	2	US-09-919-039-21	Sequence 21, Appl
734	73	4.4	918	1	US-08-825-558-6	Sequence 6, Appli	807	72	4.3	248	2	US-09-248-796A-18840	Sequence 18840, A
735	73	4.4	918	2	US-09-312-611-6	Sequence 6, Appli	808	72	4.3	295	2	US-09-270-767-45025	Sequence 45025, A
736	73	4.4	918	2	US-09-853-180B-3	Sequence 3, Appli	809	72	4.3	303	2	US-09-270-767-57613	Sequence 57613, A
737	73	4.4	918	2	US-09-949-002-333	Sequence 333, App	810	72	4.3	308	2	US-10-104-047-3898	Sequence 3898, Ap
738	73	4.4	933	1	US-08-682-847-2	Sequence 2, Appli	811	72	4.3	317	2	US-09-538-092-978	Sequence 978, App
739	73	4.4	937	2	US-09-949-002-536	Sequence 536, App	812	72	4.3	327	2	US-09-270-767-42324	Sequence 42324, A
740	73	4.4	951	2	US-09-313-942-9	Sequence 9, Appli	813	72	4.3	342	2	US-09-949-016-10365	Sequence 10365, A
741	73	4.4	951	2	US-10-282-162-9	Sequence 9, Appli	814	72	4.3	372	2	US-09-489-039A-13193	Sequence 13193, A
742	73	4.4	1158	2	US-09-313-942-26	Sequence 26, Appl	815	72	4.3	456	2	US-09-058-389A-2	Sequence 44680, A
743	73	4.4	1168	2	US-10-282-162-26	Sequence 26, Appl	816	72	4.3	456	2	US-09-058-389A-2	Sequence 2, Appli
744	73	4.4	1168	2	US-09-313-942-24	Sequence 24, Appl	817	72	4.3	457	2	US-09-611-781-2	Sequence 2, Appli
745	73	4.4	1168	2	US-10-282-162-24	Sequence 24, Appl	818	72	4.3	457	2	US-09-949-016-7211	Sequence 7211, Ap
746	73	4.4	1702	2	US-08-296-791-5	Sequence 5, Appli	819	72	4.3	462	1	US-08-865-597A-2	Sequence 2, Appli
747	73	4.4	1702	2	US-09-839-996-5	Sequence 5, Appli	820	72	4.3	489	2	US-09-545-814-29	Sequence 29, Appl
748	73	4.4	1702	2	US-10-080-505-5	Sequence 5, Appli	821	72	4.3	559	2	US-09-545-814-14	Sequence 14, Appl
749	73	4.4	1702	2	US-10-645-655-5	Sequence 5, Appli	822	72	4.3	583	2	US-09-545-814-5	Sequence 5, Appli
750	73	4.4	1702	4	PCT-US95-10661A-5	Sequence 5, Appli	823	72	4.3	583	2	US-09-545-814-2	Sequence 2, Appli
751	73	4.4	2285	2	US-09-308-375-2	Sequence 2, Appli	824	72	4.3	599	1	US-08-910-551B-2	Sequence 2, Appli
752	73	4.4	2285	2	US-09-932-183A-2	Sequence 2, Appli	825	72	4.3	635	2	US-08-545-814-32	Sequence 32, Appl
753	73	4.4	2736	2	US-09-252-991A-30227	Sequence 30227, A	826	72	4.3	785	2	US-08-374-077C-3	Sequence 3, Appli
754	73	4.4	150	2	US-08-928-361B-18	Sequence 18, Appl	827	72	4.3	785	2	US-08-895-590-3	Sequence 3, Appli
755	72.5	4.4	150	2	US-09-588-995A-18	Sequence 18, Appl	828	72	4.3	785	2	US-09-539-879A-3	Sequence 3, Appli
756	72.5	4.4	167	2	US-08-956-171E-5216	Sequence 5216, Ap	829	72	4.3	801	1	US-08-725-012-2	Sequence 2, Appli
757	72.5	4.4	167	2	US-08-781-986A-5216	Sequence 5216, Ap	830	72	4.3	813	2	US-09-964-899-25	Sequence 25, Appl



831	72	4.3	903	2	US-09-193-562D-46	Sequence 46, Appl	904	70.5	4.3	157	2	US-09-270-767-38100	Sequence 38100, A
832	72	4.3	903	2	US-09-623-624-18	Sequence 18, Appl	905	70.5	4.3	157	2	US-09-270-767-53317	Sequence 53317, A
833	72	4.3	903	2	US-10-055-412B-46	Sequence 46, Appl	906	70.5	4.3	173	2	US-09-107-532A-4115	Sequence 4115, Ap
834	72	4.3	903	2	US-10-270-595-18	Sequence 18, Appl	907	70.5	4.3	198	2	US-09-489-039A-9988	Sequence 9988, Ap
835	72	4.3	915	2	US-09-270-767-43656	Sequence 43656, A	908	70.5	4.3	213	2	US-09-244-805-11	Sequence 11, Appl
836	72	4.3	1129	2	US-09-023-905A-2	Sequence 2, Appl	909	70.5	4.3	213	2	US-09-538-092-1255	Sequence 461, App
837	72	4.3	1203	1	US-09-351-200-2	Sequence 2, Appl	910	70.5	4.3	220	2	US-09-198-452A-461	Sequence 461, App
838	72	4.3	1389	1	US-08-619-198-5	Sequence 5, Appl	911	70.5	4.3	220	2	US-09-438-185A-442	Sequence 442, App
839	72	4.3	1512	1	US-09-443-184-48	Sequence 48, Appl	912	70.5	4.3	232	2	US-09-333-809-214	Sequence 214, App
840	72	4.3	2441	1	US-08-194-468-2	Sequence 2, Appl	913	70.5	4.3	232	2	US-09-333-809-215	Sequence 215, App
841	72	4.3	2441	2	US-08-961-739-2	Sequence 2, Appl	914	70.5	4.3	232	2	US-09-333-809-216	Sequence 216, App
842	72	4.3	2441	2	US-09-514-247A-8	Sequence 8, Appl	915	70.5	4.3	232	2	US-09-746-311B-363	Sequence 363, App
843	72	4.3	2441	2	US-09-686-316-2	Sequence 2, Appl	916	70.5	4.3	232	2	US-09-746-311B-364	Sequence 364, App
844	71.5	4.3	135	2	US-09-252-991A-17514	Sequence 17514, A	917	70.5	4.3	232	2	US-09-746-311B-365	Sequence 365, App
845	71.5	4.3	142	2	US-09-107-532A-4430	Sequence 6315, A	918	70.5	4.3	237	2	US-09-248-796A-22928	Sequence 22928, A
846	71.5	4.3	218	2	US-09-605-703B-2490	Sequence 2490, Ap	919	70.5	4.3	244	2	US-09-107-532A-4536	Sequence 4536, Ap
847	71.5	4.3	232	2	US-09-333-809-217	Sequence 217, App	920	70.5	4.3	256	2	US-09-248-796A-14185	Sequence 14185, A
848	71.5	4.3	232	2	US-09-746-311B-366	Sequence 366, App	921	70.5	4.3	267	2	US-09-270-767-60080	Sequence 60080, A
849	71.5	4.3	240	2	US-09-107-532A-4430	Sequence 4430, Ap	922	70.5	4.3	292	1	US-08-852-020-6	Sequence 6, Appl
850	71.5	4.3	326	2	US-09-134-000C-5607	Sequence 5607, Ap	923	70.5	4.3	292	1	US-08-852-020-6	Sequence 6, Appl
851	71.5	4.3	342	2	US-09-605-703B-250	Sequence 250, App	924	70.5	4.3	319	2	US-09-270-767-44343	Sequence 44343, A
852	71.5	4.3	386	2	US-09-248-796A-18312	Sequence 18312, A	925	70.5	4.3	330	2	US-09-248-796A-14853	Sequence 14853, A
853	71.5	4.3	442	1	US-08-363-255-4	Sequence 4, Appl	926	70.5	4.3	401	2	US-09-949-016-7956	Sequence 7956, Ap
854	71.5	4.3	442	1	US-08-363-255-11	Sequence 11, Appl	927	70.5	4.3	432	2	US-09-134-000C-3498	Sequence 3498, Ap
855	71.5	4.3	442	1	US-08-687-559-6	Sequence 6, Appl	928	70.5	4.3	441	2	US-09-248-796A-20171	Sequence 20171, A
856	71.5	4.3	442	1	US-09-401-415-6	Sequence 6, Appl	929	70.5	4.3	445	2	US-09-270-767-44629	Sequence 44629, A
857	71.5	4.3	540	2	US-09-538-092-793	Sequence 793, App	930	70.5	4.3	462	1	US-08-417-330A-16	Sequence 16, Appl
858	71.5	4.3	650	2	US-09-134-000C-5177	Sequence 5177, Ap	931	70.5	4.3	491	2	US-09-248-796A-18483	Sequence 18483, A
859	71.5	4.3	732	2	US-09-134-000C-6359	Sequence 6359, Ap	932	70.5	4.3	497	2	US-10-104-047-3603	Sequence 3603, Ap
860	71.5	4.3	920	2	US-09-538-092-1197	Sequence 1197, Ap	933	70.5	4.3	522	2	US-09-538-092-1096	Sequence 1096, Ap
861	71.5	4.3	1709	2	US-09-949-016-11345	Sequence 11345, A	934	70.5	4.3	526	2	US-09-487-558B-362	Sequence 362, App
862	71.5	4.3	1724	2	US-09-607-510-2	Sequence 2, Appl	935	70.5	4.3	574	2	US-09-248-796A-16162	Sequence 16162, A
863	71.5	4.3	1751	1	US-09-136-574A-44	Sequence 44, Appl	936	70.5	4.3	639	2	US-09-252-991A-24474	Sequence 24474, A
864	71.5	4.3	3174	1	US-08-477-451-3	Sequence 3, Appl	937	70.5	4.3	676	2	US-09-003-574-34	Sequence 34, Appl
865	71	4.3	144	2	US-09-252-991A-23388	Sequence 23388, A	938	70.5	4.3	676	2	US-09-003-574-34	Sequence 34, Appl
866	71	4.3	169	2	US-09-252-991A-32019	Sequence 32019, A	939	70.5	4.3	676	2	US-09-864-541A-34	Sequence 34, Appl
867	71	4.3	188	2	US-09-248-796A-14699	Sequence 14699, A	940	70.5	4.3	793	2	US-09-588-256-10	Sequence 10, Appl
868	71	4.3	189	2	US-09-270-767-39457	Sequence 39457, A	941	70.5	4.3	942	2	US-09-538-092-602	Sequence 602, App
869	71	4.3	189	2	US-09-270-767-54674	Sequence 54674, A	942	70.5	4.3	979	2	US-09-538-092-990	Sequence 990, App
870	71	4.3	230	2	US-09-328-352-7443	Sequence 7443, Ap	943	70.5	4.3	1014	2	US-09-949-016-8229	Sequence 8229, Ap
871	71	4.3	230	2	US-09-248-796A-22910	Sequence 22910, A	944	70.5	4.3	1168	2	US-09-762-311-5	Sequence 5, Appl
872	71	4.3	239	2	US-09-248-796A-16743	Sequence 16743, A	945	70.5	4.3	1187	2	US-09-949-016-6513	Sequence 6513, Ap
873	71	4.3	251	2	US-09-248-796A-20695	Sequence 20695, A	946	70.5	4.3	1591	2	US-09-270-767-45698	Sequence 45698, A
874	71	4.3	272	2	US-09-248-796A-14774	Sequence 14774, A	947	70.5	4.3	1980	2	US-09-914-272A-3	Sequence 3, Appl
875	71	4.3	316	2	US-09-504-358-10	Sequence 10, Appl	948	70.5	4.3	1980	2	US-10-638-333-3	Sequence 3, Appl
876	71	4.3	316	2	US-09-954-314-10	Sequence 10, Appl	949	70.5	4.3	1980	2	US-10-747-133A-3	Sequence 3, Appl
877	71	4.3	316	2	US-10-230-562-10	Sequence 10, Appl	950	70.5	4.3	2169	2	US-09-949-016-6930	Sequence 6930, Ap
878	71	4.3	385	2	US-09-248-796A-23097	Sequence 23097, A	951	70.5	4.3	2442	2	US-09-514-247A-10	Sequence 10, Appl
879	71	4.3	401	6	5252556-1	Patent No. 5252556	952	70.5	4.3	2442	2	US-09-538-092-1370	Sequence 1370, Ap
880	71	4.3	437	2	US-09-353-332-2	Sequence 2, Appl	953	70	4.2	118	2	US-09-252-991A-18728	Sequence 18728, A
881	71	4.3	554	2	US-09-599-360B-78	Sequence 78, Appl	954	70	4.2	135	2	US-09-270-767-35728	Sequence 35728, A
882	71	4.3	610	1	US-07-821-717B-6	Sequence 6, Appl	955	70	4.2	135	2	US-09-270-767-50945	Sequence 50945, A
883	71	4.3	610	1	US-08-119-262B-6	Sequence 6, Appl	956	70	4.2	222	2	US-09-270-767-50945	Sequence 50945, A
884	71	4.3	610	1	US-08-135-929A-11	Sequence 11, Appl	957	70	4.2	234	2	US-09-252-991A-27628	Sequence 27628, A
885	71	4.3	610	1	US-08-234-265A-11	Sequence 11, Appl	958	70	4.2	236	2	US-09-492-709A-350	Sequence 350, App
886	71	4.3	630	2	US-09-485-529-8	Sequence 8, Appl	959	70	4.2	265	2	US-09-270-767-59225	Sequence 59225, A
887	71	4.3	633	2	US-09-485-529-8	Sequence 8, Appl	960	70	4.2	285	2	US-08-918-288-39	Sequence 39, Appl
888	71	4.3	646	2	US-09-248-796A-20407	Sequence 20407, A	961	70	4.2	312	2	US-09-282-357-39	Sequence 39, Appl
889	71	4.3	785	2	US-09-248-796A-16701	Sequence 16701, A	962	70	4.2	317	6	US-10-101-464A-930	Sequence 930, App
890	71	4.3	883	2	US-09-487-558B-348	Sequence 348, App	963	70	4.2	332	2	US-09-413-814-24	Sequence 24, Appl
891	71	4.3	1011	2	US-09-538-092-1320	Sequence 1320, Ap	964	70	4.2	352	2	US-09-902-540-9867	Sequence 9867, Ap
892	71	4.3	1239	2	US-09-602-362E-27	Sequence 27, Appl	965	70	4.2	353	2	US-09-402-540-9867	Sequence 9867, Ap
893	71	4.3	1374	2	US-10-076-622-577	Sequence 577, App	966	70	4.2	355	1	US-08-458-555-2	Sequence 2, Appl
894	71	4.3	1835	2	US-08-836-325-15	Sequence 15, App	967	70	4.2	360	2	US-09-807-933B-5	Sequence 5, Appl
895	71	4.3	1835	2	US-09-457-571-15	Sequence 15, Appl	968	70	4.2	376	2	US-09-248-796A-19334	Sequence 19334, A
896	71	4.3	1841	2	US-09-477-962-99	Sequence 99, Appl	969	70	4.2	410	2	US-09-543-681A-5962	Sequence 5962, Ap
897	71	4.3	1938	2	US-09-949-016-6609	Sequence 6609, Ap	970	70	4.2	413	2	US-09-248-796A-15624	Sequence 15624, A
898	71	4.3	2035	1	US-08-046-585-5	Sequence 5, Appl	971	70	4.2	423	2	US-09-902-540-13157	Sequence 13157, A
899	71	4.3	2035	1	US-08-393-703-5	Sequence 5, Appl	972	70	4.2	461	2	US-09-248-796A-17227	Sequence 17227, A
900	71	4.3	2035	4	PCT-US93-11721-5	Sequence 5, Appl	973	70	4.2	497	2	US-10-290-579A-176	Sequence 176, App
901	71	4.3	2045	2	US-09-949-016-10491	Sequence 5, Appl	974	70	4.2	523	2	US-09-270-767-43823	Sequence 43823, A
902	71	4.3	2090	2	US-09-538-092-1081	Sequence 1081, A	975	70	4.2	552	2	US-09-107-532A-5095	Sequence 5095, Ap
903	71	4.3	2120	2	US-09-949-016-9768	Sequence 9768, Ap	976	70	4.2	594	2	US-09-248-796A-22710	Sequence 22710, A
												US-09-693-746-22	Sequence 22, Appl



977	70	4.2	631	2	US-09-107-532A-4548	Sequence 4548, Ap	1050	69	4.2	265	2	US-08-918-288-3	Sequence 3, Appli
978	70	4.2	692	2	US-09-003-574-31	Sequence 31, Appl	1051	69	4.2	265	2	US-09-282-357-3	Sequence 3, Appli
979	70	4.2	692	2	US-09-003-570-31	Sequence 31, Appl	1052	69	4.2	288	2	US-09-902-540-14377	Sequence 14377, A
980	70	4.2	692	2	US-09-864-541A-31	Sequence 31, Appl	1053	69	4.2	341	2	US-09-902-540-14167	Sequence 14167, A
981	70	4.2	722	2	US-09-252-991A-26452	Sequence 26452, A	1054	69	4.2	342	2	US-09-252-991A-19903	Sequence 19903, A
982	70	4.2	843	2	US-09-252-991A-32668	Sequence 32668, A	1055	69	4.2	347	2	US-09-540-236-3596	Sequence 3596, Ap
983	70	4.2	915	1	US-08-480-917-2	Sequence 2, Appli	1056	69	4.2	382	2	US-09-487-558B-210	Sequence 210, App
984	70	4.2	915	2	US-09-138-736-2	Sequence 2, Appli	1057	69	4.2	423	2	US-09-248-796A-26813	Sequence 26813, A
985	70	4.2	915	2	US-08-988-242-2	Sequence 2, Appli	1058	69	4.2	430	2	US-09-949-016-8782	Sequence 8782, Ap
986	70	4.2	915	2	US-09-138-735-2	Sequence 2, Appli	1059	69	4.2	490	2	US-09-292-225-41	Sequence 41, Appl
987	70	4.2	1004	2	US-09-155-558-29	Sequence 29, Appl	1060	69	4.2	490	2	US-09-248-796A-20112	Sequence 20112, A
988	70	4.2	3892	2	US-09-328-352-5503	Sequence 5503, Ap	1061	69	4.2	509	2	US-09-292-225-35	Sequence 35, Appl
989	69.5	4.2	51	2	US-09-902-540-15148	Sequence 15148, A	1062	69	4.2	509	2	US-09-292-225-38	Sequence 38, Appl
990	69.5	4.2	139	2	US-09-248-796A-14268	Sequence 14268, A	1063	69	4.2	552	2	US-09-540-236-3610	Sequence 2610, Ap
991	69.5	4.2	184	2	US-09-893-737-14	Sequence 14, Appl	1064	69	4.2	556	2	US-09-538-092-712	Sequence 712, App
992	69.5	4.2	219	1	US-08-463-115-91	Sequence 91, Appl	1065	69	4.2	556	2	US-09-487-558B-426	Sequence 426, App
993	69.5	4.2	219	1	US-08-465-388-91	Sequence 91, Appl	1066	69	4.2	642	1	US-08-245-511-48	Sequence 48, Appl
994	69.5	4.2	290	1	US-08-903-801-1	Sequence 1, Appli	1067	69	4.2	642	1	US-08-600-931A-48	Sequence 48, Appl
995	69.5	4.2	290	2	US-09-295-055-1	Sequence 1, Appli	1068	69	4.2	696	2	US-08-899-437-23	Sequence 23, Appl
996	69.5	4.2	291	6	5194600-2	Patent No. 5194600	1069	69	4.2	696	2	US-09-126-121-23	Sequence 23, Appl
997	69.5	4.2	298	2	US-09-152-060-76	Sequence 76, Appl	1070	69	4.2	720	2	US-08-899-437-6	Sequence 6, Appli
998	69.5	4.2	298	2	US-09-852-797-76	Sequence 76, Appl	1071	69	4.2	720	2	US-09-126-121-6	Sequence 6, Appli
999	69.5	4.2	298	2	US-09-853-161-76	Sequence 76, Appl	1072	69	4.2	801	2	US-09-248-796A-18375	Sequence 18375, A
1000	69.5	4.2	298	2	US-10-058-993-76	Sequence 76, Appl	1073	69	4.2	813	2	US-08-836-325-8	Sequence 8, Appli
1001	69.5	4.2	299	2	US-09-712-363-234	Sequence 234, App	1074	69	4.2	813	2	US-09-457-571-8	Sequence 8, Appli
1002	69.5	4.2	312	2	US-09-254-465A-9	Sequence 9, Appli	1075	69	4.2	817	2	US-09-248-796A-20276	Sequence 20276, A
1003	69.5	4.2	312	2	US-09-907-794A-64	Sequence 64, Appl	1076	69	4.2	823	2	US-10-055-364-37	Sequence 37, Appl
1004	69.5	4.2	312	2	US-09-905-125A-64	Sequence 64, Appl	1077	69	4.2	845	2	US-08-804-439A-94	Sequence 94, Appl
1005	69.5	4.2	312	2	US-09-902-775A-64	Sequence 64, Appl	1078	69	4.2	845	2	US-08-720-229-94	Sequence 94, Appl
1006	69.5	4.2	312	2	US-09-906-700-64	Sequence 64, Appl	1079	69	4.2	861	2	US-09-784-316-2	Sequence 2, Appli
1007	69.5	4.2	312	2	US-09-903-603A-64	Sequence 64, Appl	1080	69	4.2	861	2	US-10-229-124-2	Sequence 2, Appli
1008	69.5	4.2	312	2	US-09-904-920A-64	Sequence 64, Appl	1081	69	4.2	882	2	US-09-328-352-5232	Sequence 5232, Ap
1009	69.5	4.2	312	2	US-09-909-064-64	Sequence 64, Appl	1082	69	4.2	903	1	US-08-220-151-8	Sequence 8, Appli
1010	69.5	4.2	312	2	US-09-905-381A-64	Sequence 64, Appl	1083	69	4.2	903	1	US-08-413-118-8	Sequence 8, Appli
1011	69.5	4.2	312	2	US-09-906-618-64	Sequence 64, Appl	1084	69	4.2	903	2	US-08-473-446-8	Sequence 8, Appli
1012	69.5	4.2	312	2	US-09-953-492-9	Sequence 9, Appli	1085	69	4.2	988	1	US-08-286-819A-19	Sequence 19, Appl
1013	69.5	4.2	312	2	US-09-906-646-64	Sequence 64, Appl	1086	69	4.2	988	2	US-08-980-357-19	Sequence 19, Appl
1014	69.5	4.2	312	2	US-09-904-462-64	Sequence 64, Appl	1087	69	4.2	988	2	US-09-357-375-19	Sequence 19, Appl
1015	69.5	4.2	312	2	US-09-902-736A-64	Sequence 64, Appl	1088	69	4.2	1163	2	US-09-949-016-11047	Sequence 11047, A
1016	69.5	4.2	312	2	US-09-906-722A-64	Sequence 64, Appl	1089	69	4.2	1311	1	US-08-340-011-5	Sequence 5, Appli
1017	69.5	4.2	338	2	US-09-538-092-144	Sequence 144, App	1090	69	4.2	1311	2	US-08-901-710-5	Sequence 5, Appli
1018	69.5	4.2	339	1	US-08-431-080-18	Sequence 18, Appl	1091	69	4.2	1311	2	US-09-169-079-5	Sequence 5, Appli
1019	69.5	4.2	339	1	US-08-938-534-18	Sequence 18, Appl	1092	69	4.2	1455	2	US-08-840-062-5	Sequence 5, Appli
1020	69.5	4.2	389	2	US-09-345-294-18	Sequence 18, Appl	1093	69	4.2	1650	2	US-09-252-951A-21798	Sequence 21798, A
1021	69.5	4.2	385	2	US-09-270-767-42966	Sequence 42966, A	1094	69	4.2	2283	2	US-10-172-502-4	Sequence 4, Appli
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1023	69.5	4.2	497	2	US-10-104-047-3773	Sequence 3773, Ap	1096	68.5	4.1	206	2	US-09-949-016-10049	Sequence 10049, A
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## ALIGNMENTS

## RESULT 1

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US-09-232-160-21
; Sequence 21, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232.160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
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; LENGTH: 322
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; OTHER INFORMATION: 3044710
US-09-232-160-21
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Best Local Similarity 100.0%; Pred. No. 2.4e-159;
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## RESULT 2

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US-09-907-794A-201
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; Sequence 201, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; PRIORITY FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
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; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
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; PRIOR FILING DATE: 2000-01-05  
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; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
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; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Fong, Sherman  
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; APPLICANT: Tumas, Daniel  
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905,125A  
; PRIORITY FILING DATE: 2001-07-12  
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;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
;; PRIOR FILING DATE: 1999-11-29  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 201  
;; LENGTH: 322  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic protein  
US-09-905-125A-201

Query Match 100.0%; Score 1657; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.4e-159;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLTSTWTRLLVQGSRAEELSIQVSCRMGITLVSKKANQOLNFTKEA 60  
DB 1 MARCFSLVLLTSTWTRLLVQGSRAEELSIQVSCRMGITLVSKKANQOLNFTKEA 60  
QY 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVWLSRISPNKCKNGVGLIWKVPV 120  
DB 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVWLSRISPNKCKNGVGLIWKVPV 120  
QY 121 SRQPAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVSPYSTIPA 180  
DB 121 SRQPAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVSPYSTIPA 180  
QY 181 PTTTPPAPASTSIPIRKKLICVTEVFNETSTMSTETEPFVENKAAFNKAAAGFGVPTAL 240  
DB 181 PTTTPPAPASTSIPIRKKLICVTEVFNETSTMSTETEPFVENKAAFNKAAAGFGVPTAL 240  
QY 241 LVLALLFPGAAGLFCVVKRYKAPPTTKNQOKEMIETKVVKKEKANDSNPNESKKT 300  
DB 241 LVLALLFPGAAGLFCVVKRYKAPPTTKNQOKEMIETKVVKKEKANDSNPNESKKT 300  
QY 301 DKNPEESKSPKTTVRCLEAEV 322  
DB 301 DKNPEESKSPKTTVRCLEAEV 322

RESULT 4  
US-09-902-775A-201  
; Sequence 201, Application US/09902775A  
; Patent No. 6686451  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi

;; APPLICANT: Botstein, David  
;; APPLICANT: Desnovers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, A.  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, Christopher J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth, J.  
;; APPLICANT: KJavin, Ivar J.  
;; APPLICANT: Mather, Jennie P.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William, I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCES: 10466-14  
;; CURRENT APPLICATION NUMBER: US/09/902,775A  
;; CURRENT FILING DATE: 2001-07-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: 2000-02-22  
;; PRIOR APPLICATION NUMBER: US 60/143,048  
;; PRIOR FILING DATE: 1999-07-07  
;; PRIOR APPLICATION NUMBER: US 60/145,698  
;; PRIOR FILING DATE: 1999-07-26  
;; PRIOR APPLICATION NUMBER: US 60/146,222  
;; PRIOR FILING DATE: 1999-07-28  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/20944  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
;; PRIOR FILING DATE: 1999-11-29  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 201  
;; LENGTH: 322  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic protein  
US-09-902-775A-201

Query Match 100.0%; Score 1657; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.4e-159;

	Matches	322;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MARCFSLVLLLTSTWTRLLVQGSRAEELSIOVSCRMIGITLVSKKANQOQLNFTAE	KEA	60						
Db	1	MARCFSLVLLLTSTWTRLLVQGSRAEELSIOVSCRMIGITLVSKKANQOQLNFTAE	KEA	60						
Qy	61	CRLLGLSLAGKQDVETALKASFETCSYGWGDGFVVISRISPNPKCGKGVGLIWKVPV		120						
Db	61	CRLLGLSLAGKQDVETALKASFETCSYGWGDGFVVISRISPNPKCGKGVGLIWKVPV		120						
Qy	121	SRQFAAYCYNSSDPTWNTNSCIPETITTKDPIENTQTATQTTFEIVSDSTYSVASPYSTI	PA	180						
Db	121	SRQFAAYCYNSSDPTWNTNSCIPETITTKDPIENTQTATQTTFEIVSDSTYSVASPYSTI	PA	180						
Qy	181	PTTTTPPAPASTSIPRRKKLVCVTEVFVETSTMTSETETEPFVENKAAFNQEAAGFGGVP	TAL	240						
Db	181	PTTTTPPAPASTSIPRRKKLVCVTEVFVETSTMTSETETEPFVENKAAFNQEAAGFGGVP	TAL	240						
Qy	241	LVLALLFFGAAGLGFVVKRYVKAFPTTNKNQOKEMETETVKVKEEKANDSNPNNEESKKT		300						
Db	241	LVLALLFFGAAGLGFVVKRYVKAFPTTNKNQOKEMETETVKVKEEKANDSNPNNEESKKT		300						
Qy	301	DKNPEESKSPSKTTVRCLEAEV		322						
Db	301	DKNPEESKSPSKTTVRCLEAEV		322						

RESULT 5  
US-09-906-700-201

US-09-508-700-201  
; Sequence 201, Application US/09906700  
; Patent No. 6723535

; FACCIC NO. 072333  
; GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transcribed  
TITLE OF INVENTION: Acids Encoding  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/90  
CURRENT FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/0  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/2  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/2

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, , PRIOR FILING DATE: 1999-09-13
, , PRIOR APPLICATION NUMBER: PCT/US99/21090
, , PRIOR FILING DATE: 1999-09-15
, , PRIOR APPLICATION NUMBER: PCT/US99/21547
, , PRIOR FILING DATE: 1999-09-15
, , PRIOR APPLICATION NUMBER: PCT/US99/23089
, , PRIOR FILING DATE: 1999-10-05
, , PRIOR APPLICATION NUMBER: PCT/US99/28214
, , PRIOR FILING DATE: 1999-11-29
, , PRIOR APPLICATION NUMBER: PCT/US99/28313
, , PRIOR FILING DATE: 1999-11-30
, , PRIOR APPLICATION NUMBER: PCT/US99/28564
, , PRIOR FILING DATE: 1999-12-02
, , PRIOR APPLICATION NUMBER: PCT/US99/28565
, , PRIOR FILING DATE: 1999-12-02
, , PRIOR APPLICATION NUMBER: PCT/US99/30095
, , PRIOR FILING DATE: 1999-12-16
, , PRIOR APPLICATION NUMBER: PCT/US99/30911
, , PRIOR FILING DATE: 1999-12-20
, , PRIOR APPLICATION NUMBER: PCT/US99/30999
, , PRIOR FILING DATE: 1999-12-20
, , PRIOR APPLICATION NUMBER: PCT/US00/00219
, , PRIOR FILING DATE: 2000-01-05
, , NUMBER OF SEQ ID NOS: 423
, , SEQ ID NO 201
, , LENGTH: 322
, , TYPE: PRT
, , ORGANISM: Artificial sequence
, , FEATURE:
, , OTHER INFORMATION: Synthetic protein
US-09-506-700-201

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Query Match 100.0%; Score 1657; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.4e-159;  
Matches 322; Conservative 0; Mismatches 0; Indels 0

Qy	1	MARCFS	LVLLLT	TS	TWTRLL	VQGS	LRABEL	SIQV	SCRIM	IGIT	LVSK	KANQO	LNFT	FEAKEA	60
Db	1	MARCFS	LVLLLT	TS	TWTRLL	VQGS	LRABEL	SIQV	SCRIM	IGIT	LVSK	KANQO	LNFT	FEAKEA	60
Qy	61	CRLLGL	SLAGK	QDVET	ALKAS	FETCS	YGWGD	GFVW	ISRI	SPNPK	CGKNG	VGLI	KVPV	120	
Db	61	CRLLGL	SLAGK	QDVET	ALKAS	FETCS	YGWGD	GFVW	ISRI	SPNPK	CGKNG	VGLI	KVPV	120	
Qy	121	SROFAA	CYNSSD	FWTNS	CPIE	ITTKD	PINT	QTAT	QTTF	EFIV	SDSY	VASPY	STIPA	180	
Db	121	SROFAA	CYNSSD	FWTNS	CPIE	ITTKD	PINT	QTAT	QTTF	EFIV	SDSY	VASPY	STIPA	180	
Qy	181	PTTTPP	PAPAST	SIPRR	KKLIC	VTVE	FMET	STM	TSET	PTPF	VENK	AAFK	NEAAG	FGGVP	240
Db	181	PTTTPP	PAPAST	SIPRR	KKLIC	VTVE	FMET	STM	TSET	PTPF	VENK	AAFK	NEAAG	FGGVP	240
Qy	241	LVLALL	FFGAAG	FGFCV	VVKRY	VKA	PPTN	KQOK	EMET	ETKV	VKEE	KAND	SNPN	ESKKT	300
Db	241	LVLALL	FFGAAG	FGFCV	VVKRY	VKA	PPTN	KQOK	EMET	ETKV	VKEE	KAND	SNPN	ESKKT	300
Qy	301	DKNPEE	SKSP	SKTTVR	CLEAF	322									
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RESULT 6  
US-09-093-603A-201  
; Sequence 201, Application US/099030603A  
; Patent No. 6767995  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Bottstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen



APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: GNE.1618P2C12  
CURRENT APPLICATION NUMBER: US/09/903,603A  
CURRENT FILING DATE: 2001-07-11  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 201  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic protein  
US-09-903-603A-201  
Query Match 100.0%; Score 1657; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.4e-159;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MARCFSLVLLTTSITWTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTKEA 60  
Db 1 MARCFSLVLLTTSITWTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTKEA 60

Qy 61 CRLGLSLAGKQOVETALKASFETCSYGWVGDFVWISRI SPNPKCGKNGVGLIWKVPV 120  
Db 61 CRLGLSLAGKQOVETALKASFETCSYGWVGDFVWISRI SPNPKCGKNGVGLIWKVPV 120  
Qy 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIPA 180  
Db 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIPA 180  
Qy 181 PTTTPPAPASTSIPRRKKLICVTEVFMEITMTSTETETEPFVENKAAFKNEAAGFGVPTAL 240  
Db 181 PTTTPPAPASTSIPRRKKLICVTEVFMEITMTSTETETEPFVENKAAFKNEAAGFGVPTAL 240  
Qy 241 LVLALLFFGAAGLFCYVKRYKAPFTTNKQOKEMIETKVVKEEKANDSNPNNEESKKT 300  
Db 241 LVLALLFFGAAGLFCYVKRYKAPFTTNKQOKEMIETKVVKEEKANDSNPNNEESKKT 300  
Qy 301 DKNPESKSPSKTTVRCLEAEV 322  
Db 301 DKNPESKSPSKTTVRCLEAEV 322  
RESULT 7  
US-09-904-920A-201  
Sequence 201, Application US/09904920A  
Patent No. 6806352  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,920A  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15



; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-904-920A-201

Query Match 100.0%; Score 1657; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.4e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARCFSLVLLTSTWTTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKEA 60
Db 1 MARCFSLVLLTSTWTTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKEA 60

Qy 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
Db 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120

Qy 121 SRQFAAYCYNSSDWTNSCIPEIITTKDPIFNTQTATQTFEIVSDSTYSVASPYSTIPA 180
Db 121 SRQFAAYCYNSSDWTNSCIPEIITTKDPIFNTQTATQTFEIVSDSTYSVASPYSTIPA 180

Qy 181 PTTTTPAPASTSIPIRKKLICVTEVFMTSTMTSTETEPFVENKAAFPKNEAAGFGVPTAL 240
Db 181 PTTTTPAPASTSIPIRKKLICVTEVFMTSTMTSTETEPFVENKAAFPKNEAAGFGVPTAL 240

Qy 241 LVLLALLFPGAAGLGCYVKRYVKAFFPTNKNQOKEMILETKVVKEEKANDSNPNEESKKT 300
Db 241 LVLLALLFPGAAGLGCYVKRYVKAFFPTNKNQOKEMILETKVVKEEKANDSNPNEESKKT 300

Qy 301 DKNPEESKSPKTTVRCLEAEV 322
Db 301 DKNPEESKSPKTTVRCLEAEV 322

RESULT 8
US-09-909-064-201
; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-909-064-201

Query Match 100.0%; Score 1657; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.4e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARCFSLVLLTSTWTTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKEA 60
Db 1 MARCFSLVLLTSTWTTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKEA 60

Qy 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
Db 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120

QY 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNQATQTTFIVSDSYVASPYSTIPA 180  
DB 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNQATQTTFIVSDSYVASPYSTIPA 180  
QY 181 PTTTPAPASTSIPRRKKLICVTEVFMTSTMTSTETEPVENKAAPKNEAAGFGVPTAL 240  
DB 181 PTTTPAPASTSIPRRKKLICVTEVFMTSTMTSTETEPVENKAAPKNEAAGFGVPTAL 240  
QY 241 LVALLFFGAAAGLFCYVKRYKAFPTNNKQKEMIEKVKVKEEKANDSNPNEESKKT 300  
DB 241 LVALLFFGAAAGLFCYVKRYKAFPTNNKQKEMIEKVKVKEEKANDSNPNEESKKT 300  
QY 301 DKNPEESKSPKTTVRCLEAEV 322  
DB 301 DKNPEESKSPKTTVRCLEAEV 322

RESULT 9

US-09-905-381A-201  
; Sequence 201, Application US/09905381A  
; Patent No. 6818746

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905,381A  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-09-905-381A-201  
Query Match 100.0%; Score 1657; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.4e-159;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARCFSLVLLTSTIWTTRLLVQGLSLRAEELSIQVSCRMIGITLVSKKANQOLNFEAKEA 60  
DB 1 MARCFSLVLLTSTIWTTRLLVQGLSLRAEELSIQVSCRMIGITLVSKKANQOLNFEAKEA 60  
QY 61 CRLGLSLAGKQOVETALKASFETCSYGVGDGFVVISRISPNPKCKGKNGVGLIWKVPV 120  
DB 61 CRLGLSLAGKQOVETALKASFETCSYGVGDGFVVISRISPNPKCKGKNGVGLIWKVPV 120  
QY 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNQATQTTFIVSDSYVASPYSTIPA 180  
DB 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNQATQTTFIVSDSYVASPYSTIPA 180  
QY 181 PTTTPAPASTSIPRRKKLICVTEVFMTSTMTSTETEPVENKAAPKNEAAGFGVPTAL 240  
DB 181 PTTTPAPASTSIPRRKKLICVTEVFMTSTMTSTETEPVENKAAPKNEAAGFGVPTAL 240  
QY 241 LVALLFFGAAAGLFCYVKRYKAFPTNNKQKEMIEKVKVKEEKANDSNPNEESKKT 300  
DB 241 LVALLFFGAAAGLFCYVKRYKAFPTNNKQKEMIEKVKVKEEKANDSNPNEESKKT 300  
QY 301 DKNPEESKSPKTTVRCLEAEV 322  
DB 301 DKNPEESKSPKTTVRCLEAEV 322

RESULT 10

US-09-906-618-201  
; Sequence 201, Application US/09906618  
; Patent No. 6828146  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.



; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-09-906-646-201

Query Match 100.0%; Score 1657; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.4e-159;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MARCFSLVLLTTSIWTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKA 60  
  
Qy 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120  
Db 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120  
  
Qy 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFFIVSDSTYSVASPYSTIPA 180  
Db 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFFIVSDSTYSVASPYSTIPA 180  
  
Qy 181 PTTTPPAPASTSIPIRKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGVPTAL 240  
Db 181 PTTTPPAPASTSIPIRKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGVPTAL 240  
  
Qy 241 LVLLALFFGAAAGLGFCTYKRYKAFPTTNKQKEMLETQVKEEKANDSNPNEESKKT 300  
Db 241 LVLLALFFGAAAGLGFCTYKRYKAFPTTNKQKEMLETQVKEEKANDSNPNEESKKT 300  
  
Qy 301 DKNPEESKPSKTTVRCLEAEV 322  
Db 301 DKNPEESKPSKTTVRCLEAEV 322

RESULT 12  
US-09-904-462-201  
; Sequence 201, Application US/09904462  
; Patent No. 6878807  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, David  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Klijavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/904,462  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/665,350  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-904-462-201

Query Match 100.0%; Score 1657; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.4e-159;  
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Db 1 MARCFSLVLLTTSIWTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKA 60  
  
Qy 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120  
Db 61 CRLGLSLAGKQDVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPV 120  
  
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Db 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFFIVSDSTYSVASPYSTIPA 180  
  
Qy 181 PTTTPPAPASTSIPIRKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGVPTAL 240  
Db 181 PTTTPPAPASTSIPIRKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGVPTAL 240  
  
Qy 241 LVLLALFFGAAAGLGFCTYKRYKAFPTTNKQKEMLETQVKEEKANDSNPNEESKKT 300  
Db 241 LVLLALFFGAAAGLGFCTYKRYKAFPTTNKQKEMLETQVKEEKANDSNPNEESKKT 300



FILE REFERENCE: GNE.1618P2C61  
CURRENT APPLICATION NUMBER: US/09/906,722A  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 201  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic protein  
US-09-906-722A-201

Query Match 100.0%; Score 1657; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.4e-159;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MARCFSLVLLTSTWTRLLVQGSIRAEELSIQVSCRIMGITLVSKKANQQLNFEAKEA 60  
Db 1 MARCFSLVLLTSTWTRLLVQGSIRAEELSIQVSCRIMGITLVSKKANQQLNFEAKEA 60  
Qy 61 CRLGLSLAGKQDVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPV 120  
Db 61 CRLGLSLAGKQDVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPV 120  
Qy 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTTEFIVSDSTYSVASPYSTIPA 180  
Db 121 SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTTEFIVSDSTYSVASPYSTIPA 180  
Qy 181 PTTTPPAPASTSIPIRRKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGVPTAL 240  
Db 181 PTTTPPAPASTSIPIRRKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGVPTAL 240  
Qy 241 LVLALLFFGAAGLGFCCYVKRYVKAFPPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKT 300  
Db 241 LVLALLFFGAAGLGFCCYVKRYVKAFPPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKT 300  
Qy 301 DKNPEESKSPSKTTVRCLEAEV 322  
Db 301 DKNPEESKSPSKTTVRCLEAEV 322

RESULT 15  
US-09-949-016-7765  
Sequence 7765, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7765  
LENGTH: 344  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7765

Query Match 100.0%; Score 1657; DB 2; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2.6e-159;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 23 MARCFSLVLLTSTWTRLLVQGSIRAEELSIQVSCRIMGITLVSKKANQQLNFEAKEA 82  
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Db 203 PTTTPPAPASTSIPIRRKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGVPTAL 262  
Qy 241 LVLALLFFGAAGLGFCCYVKRYVKAFPPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKT 300  
Db 263 LVLALLFFGAAGLGFCCYVKRYVKAFPPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKT 322  
Qy 301 DKNPEESKSPSKTTVRCLEAEV 322  
Db 323 DKNPEESKSPSKTTVRCLEAEV 344

Search completed: March 20, 2006, 14:08:37  
Job time : 38.783 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 14:07:29 ; Search time 9.85849 Seconds  
(without alignments)  
2147.153 Million cell updates/sec

Title: US-10-063-510-6\_COPY\_16\_235

Perfect score: 1136

Sequence: 1 TTRLLVQGSRLRAELSIQVS.....TEPFVENKAAFKNEAAGFGG 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213.5	18.8	503	2 B38745	cell adhesion mole
2	209.5	18.4	363	2 A37009	CD44 homolog membr
3	207	18.2	362	2 A35616	T-cell surface gly
4	203.5	17.9	362	2 A30901	lymphocyte adhesion
5	202	17.8	742	2 A47195	lymphocyte homing
6	199.5	17.6	493	2 S13530	CD44E protein, epi
7	198.5	17.5	365	2 A34424	CD44 membrane gly
8	198.5	17.5	426	2 JH0518	lymphocyte homing
9	197	17.3	361	2 JH0417	cell adhesion mole
10	196.5	17.3	699	2 I37369	epican - human
11	196	17.3	395	2 I77371	CD44R5 - human
12	194	17.1	351	2 S45305	CD44 antigen precu
13	194	17.1	366	2 A53286	cell-surface glyco
14	183.5	16.2	359	2 S24240	lymphocyte surface
15	145.5	12.8	362	2 A47171	chondroitin sulfat
16	145	12.8	277	2 A41735	hyaluronate-bindin
17	144	12.7	275	2 JC6506	tumor necrosis fac
18	143	12.6	2109	1 I50421	aggreacan precursor
19	137	12.1	276	2 A47290	TSG-6 homolog PS4
20	131.5	11.6	2124	2 A28452	proteoglycan core
21	131	11.5	2132	1 A55182	aggreacan precursor
22	130.5	11.5	883	2 S57653	brevican precursor
23	130.5	11.5	2415	1 A39086	aggreacan - bovine
24	128	11.3	2327	2 T42630	aggreacan - bovine
25	127.5	11.2	883	2 S49126	brevican precursor
26	120.5	10.6	912	2 A54423	brevican precursor
27	118	10.4	1340	2 A39808	proteoglycan core
28	116	10.2	2397	1 A55535	versican precursor
29	115	10.1	370	2 S29139	aggreacan - pig (fr

30	115	10.1	1643	2 T14274	versican precursor
31	115	10.1	3381	2 T42389	versican precursor
32	112.5	9.9	340	2 JC7505	brain link protein
33	111	9.8	2409	1 A60979	versican precursor
34	110.5	9.7	1257	2 S28764	neurocan precursor
35	109	9.6	1069	2 T42681	hypothetical prote
36	108	9.5	354	1 LKHU	proteoglycan link
37	107	9.4	355	1 LRCH	proteoglycan link
38	107	9.4	371	2 A53908	brevican precursor
39	107	9.4	408	1 LKRT2	proteoglycan link
40	107	9.4	1268	2 S52781	neurocan - mouse
41	105.5	9.3	113	2 A55885	chondroitin sulfat
42	104.5	9.2	862	2 S43922	versican - pig-tai
43	104	9.2	354	1 S04243	proteoglycan link
44	104	9.2	354	1 S42938	proteoglycan link
45	102	9.0	739	2 T21769	hypothetical prote
46	101.5	8.9	380	2 T28081	hypothetical prote
47	101	8.9	708	2 T19474	hypothetical prote
48	100	8.8	378	2 I46268	brevican precursor
49	97	8.5	390	1 Q08E77	glycoprotein I pre
50	96	8.5	796	2 T21460	hypothetical prote
51	92.5	8.1	851	2 T22696	hypothetical prote
52	92	8.1	846	2 T21700	hypothetical prote
53	91	8.0	645	2 T29818	hypothetical prote
54	91	8.0	747	2 T34329	hypothetical prote
55	90.5	8.0	402	2 S73773	dihydrolipoamide a
56	90	7.9	388	2 S36500	E2 protein - human
57	89.5	7.9	411	2 A33664	96K lysosomal memb
58	89.5	7.9	518	2 T49778	hypothetical prote
59	89	7.8	307	1 GSPF3	salivary glue prot
60	89	7.8	416	1 A31959	lysosome-associate
61	89	7.8	429	1 JC5861	endo-1,4-beta-xyla
62	89	7.8	517	2 T20658	probable zinc meta
63	88.5	7.8	662	2 A45155	mucin FIM-C.1 - Af
64	88.5	7.8	770	2 T22808	hypothetical prote
65	88.5	7.8	1101	2 S15271	endoglucanase C (E
66	88	7.7	456	2 T31483	hypothetical prote
67	88	7.7	602	2 AD2067	hypothetical prote
68	88	7.7	1229	2 T25697	hypothetical prote
69	87.5	7.7	1085	2 S40476	Ca(2+)-sensing rec
70	87	7.7	235	2 PC2022	mucin like protein
71	87	7.7	721	2 B90487	hypothetical prote
72	87	7.7	1506	2 T30886	integumentary muc
73	86.5	7.6	400	1 A28172	spasmolysin precu
74	86.5	7.6	477	2 S53362	mucin SAC (clone J
75	86.5	7.6	768	2 T00073	hypothetical prote
76	86.5	7.6	909	1 QRXL2	LDL receptor 2 pre
77	86.5	7.6	1007	2 T24643	hypothetical prote
78	86.5	7.6	2616	2 A57096	nudel protein prec
79	85.5	7.5	786	2 T16509	hypothetical prote
80	85.5	7.5	895	2 T02597	Mutator-like trans
81	85.5	7.5	1367	1 S48478	glucan 1,4-alpha-g
82	85	7.5	265	2 T33695	hypothetical prote
83	85	7.5	449	2 T33257	hypothetical prote
84	85	7.5	569	2 A11347	hypothetical prote
85	85	7.5	627	2 G86860	serine/threonine p
86	85	7.5	660	2 JH0067	chitinase (EC 3.2.
87	85	7.5	1016	2 H71460	probable outer mem
88	85	7.5	1162	2 T21557	hypothetical prote
89	84.5	7.4	752	2 E72616	hypothetical prote
90	84.5	7.4	1161	2 S57180	probable membrane
91	84	7.4	262	2 S76772	hypothetical prote
92	84	7.4	335	2 H96667	AP2-containing DNA
93	84	7.4	543	2 S35047	mucin JUL7 - human
94	84	7.4	927	2 T24031	hypothetical prote
95	84	7.4	1331	2 A48954	mannan endo-1,4-be
96	84	7.4	1362	2 A75207	amylopullulanase p
97	84	7.4	1779	2 T31085	xylanase - Caldice
98	84	7.4	1832	2 T31113	mucin-like glycop
99	84	7.4	3020	2 A45932	mucin 2 precursor,
100	83.5	7.4	216	2 I51920	mucin - rhesus mac
101	83.5	7.4	279	2 S53363	mucin SAC (clone J
102	83.5	7.4	967	2 S66852	hypothetical prote



103	83.5	7.4	1286	2	A88396	protein M01E10.2 [	176	78	6.9	1091	1	IJCENL	neural cell adhesi
104	83	7.3	409	2	S44346	Rad23 protein homo	177	78	6.9	1723	2	H86557	polymorphic membra
105	83	7.3	605	2	S48940	hypothetical prote	178	78	6.9	1723	2	E72067	polymorphic membra
106	83	7.3	977	2	T16232	hypothetical prote	179	78	6.9	1732	2	C81601	agrin precursor -
107	82.5	7.3	383	1	S15624	E2 protein - human	180	78	6.9	1955	1	AGCH	actinin receptor p
108	82.5	7.3	726	2	S67044	probable membrane	181	77.5	6.8	514	2	JQ1317	hypothetical prote
109	82.5	7.3	825	2	S62042	formin isoform IV	182	77.5	6.8	592	2	T34446	hypothetical prote
110	82.5	7.3	1206	2	S24407	formin isoform IV	183	77.5	6.8	623	2	T18892	hypothetical prote
111	82.5	7.3	1407	2	T18381	latrophilin-2 (spl	184	77.5	6.8	688	2	T18263	s-layer protein -
112	82.5	7.3	1420	2	T18395	latrophilin-2 (spl	185	77.5	6.8	1127	2	H86386	probable mutator-1
113	82.5	7.3	1422	2	T18383	latrophilin-2, spl	186	77.5	6.8	2761	2	T21064	hypothetical prote
114	82.5	7.3	1435	2	T18387	latrophilin-2 (spl	187	77	6.8	350	2	E75341	peptidyl-prolyl ci
115	82.5	7.3	1450	2	T18382	latrophilin-2 (spl	188	77	6.8	433	2	F75206	maltoase-binding pe
116	82.5	7.3	1463	2	T18386	latrophilin-2 (spl	189	77	6.8	598	2	T22610	hypothetical prote
117	82.5	7.3	1465	2	T18384	latrophilin-2 (spl	190	77	6.8	639	2	T33166	hypothetical prote
118	82.5	7.3	1468	2	S11515	formin - mouse	191	77	6.8	771	2	JC7388	M83 protein - huma
119	82.5	7.3	1478	2	T18398	latrophilin-2 (spl	192	77	6.8	1092	1	JN0635	neural cell adhesi
120	82	7.2	389	2	T33340	hypothetical prote	193	77	6.8	1513	2	A54895	mucin 2, intestina
121	82	7.2	463	2	T38444	hypothetical prote	194	77	6.8	2187	2	T30826	nascent polypeptid
122	82	7.2	476	2	T46118	myosin-binding pro	195	76.5	6.7	349	2	T43457	hypothetical prote
123	82	7.2	693	2	T19551	mucin-like protein	196	76.5	6.7	433	2	H84120	methyl-accepting c
124	82	7.2	973	2	A97522	ribonuclease E, RN	197	76.5	6.7	505	2	B46629	mucin 6, gastric (
125	82	7.2	977	2	AC2741	ribonuclease E [im	198	76.5	6.7	542	2	I39540	chitinase (SC 3.2.
126	81.5	7.2	386	2	B97212	protein containing	199	76.5	6.7	658	2	T39500	serine/threonine-s
127	81.5	7.2	584	2	T19061	hypothetical prote	200	76.5	6.7	658	2	S60170	protein kinase Pak
128	81.5	7.2	860	2	AG1612	DNA mismatch repai	201	76.5	6.7	718	2	T29708	hypothetical prote
129	81.5	7.2	1216	2	F88473	protein F40H6.5 [i	202	76.5	6.7	750	2	T42614	probable envelope
130	81.5	7.2	1513	2	T23661	hypothetical prote	203	76.5	6.7	1023	2	JC4013	major acidic nucle
131	81.5	7.2	1777	2	T34369	hypothetical prote	204	76.5	6.7	1672	2	C81675	polymorphic membra
132	81.5	7.2	3175	1	RRMVSV	genome polyprotein	205	76	6.7	167	2	A33532	mucin SMUC-40 - hu
133	81	7.1	221	2	S53649	ribosomal protein	206	76	6.7	243	2	B41710	promastigote surfa
134	81	7.1	1128	2	A49960	bud emergence prot	207	76	6.7	340	2	AH0940	probable ABC trans
135	81	7.1	1251	2	T21389	hypothetical prote	208	76	6.7	368	2	S36564	E2 protein - human
136	81	7.1	1537	2	S53465	flocculation prote	209	76	6.7	382	2	B88561	protein F58A4.7b [
137	81	7.1	1609	2	S25345	probable membrane	210	76	6.7	389	2	E97305	NADH-dependent but
138	80.5	7.1	148	1	S07723	immediate-early se	211	76	6.7	389	2	A47013	butanol dehydrogen
139	80.5	7.1	391	1	S15617	E2 protein - human	212	76	6.7	532	2	T28784	hypothetical prote
140	80.5	7.1	441	2	T31482	hypothetical prote	213	76	6.7	549	2	T49298	hypothetical prote
141	80.5	7.1	742	2	T33514	hypothetical prote	214	76	6.7	569	2	B84470	Mutator-like trans
142	80.5	7.1	798	2	T34248	hypothetical prote	215	76	6.7	576	2	S59829	hypothetical prote
143	80.5	7.1	896	2	T22061	hypothetical prote	216	76	6.7	592	2	T16725	hypothetical prote
144	80.5	7.1	2225	2	T26063	hypothetical prote	217	76	6.7	1016	2	T41720	hypothetical prote
145	80	7.0	725	2	A41258	a-agglutinin core	218	76	6.7	1360	2	T33522	hypothetical prote
146	80	7.0	881	2	S56032	probable membrane	219	76	6.7	1489	2	G71406	probable retroviri
147	79.5	7.0	354	2	T46740	microfilarial shea	220	76	6.7	5376	2	T42215	zonadhesin - mouse
148	79.5	7.0	860	2	AC1250	DNA mismatch repai	221	75.5	6.6	194	2	F72525	hypothetical prote
149	79.5	7.0	3570	2	T45025	mucin MUC5B, trach	222	75.5	6.6	260	1	G69223	molybdate-binding
150	79	7.0	249	2	G84781	hypothetical prote	223	75.5	6.6	273	2	T44657	protein GP80 [impo
151	79	7.0	339	2	T25582	hypothetical prote	224	75.5	6.6	321	2	T26152	hypothetical prote
152	79	7.0	352	2	T51659	myb-related transc	225	75.5	6.6	348	1	B46216	transcription fact
153	79	7.0	359	2	T13478	hypothetical prote	226	75.5	6.6	430	1	A46216	transcription fact
154	79	7.0	410	1	B31959	lysosome-associate	227	75.5	6.6	468	2	A55116	vacuolar ATPase (E
155	79	7.0	410	1	JC4317	lysosome-associate	228	75.5	6.6	496	2	B41322	N-acetylglucosyl-L
156	79	7.0	575	2	T21775	hypothetical prote	229	75.5	6.6	511	1	VGBRFA	glycoprotein C - h
157	78.5	6.9	164	2	I53641	mucin 5AC - human	230	75.5	6.6	609	2	G87496	peptidase, M23/M37
158	78.5	6.9	232	2	A60095	larval glue protei	231	75.5	6.6	665	2	G97213	probable membrane-
159	78.5	6.9	294	2	A37232	mucin, tracheal (A	232	75.5	6.6	737	1	S64767	probable serine/th
160	78.5	6.9	322	2	A53715	apomucin precursor	233	75.5	6.6	780	2	A48143	HF-1 regulatory el
161	78.5	6.9	562	2	A57088	nucleoporin-like p	234	75.5	6.6	1212	2	T13804	shs protein - frui
162	78.5	6.9	577	2	G89430	protein K02E2.3 [i	235	75	6.6	94	2	S53365	mucin 5AC (clone C
163	78.5	6.9	825	2	T29634	hypothetical prote	236	75	6.6	310	1	H71054	hypothetical prote
164	78.5	6.9	1420	2	T17158	Cl2AB protein - ra	237	75	6.6	475	2	B84745	probable splicing
165	78.5	6.9	1435	2	T46611	Cl2BB protein - ra	238	75	6.6	554	2	A56596	chitinase (SC 3.2.
166	78.5	6.9	1452	2	T17157	Cl2AA protein - ra	239	75	6.6	604	2	T37994	probable splicing
167	78.5	6.9	1463	2	T17159	Cl2AC protein - ra	240	75	6.6	651	2	T16450	hypothetical prote
168	78.5	6.9	1467	2	T17160	Cl2BA protein - ra	241	75	6.6	793	2	AH1094	probable peptidogl
169	78.5	6.9	1478	2	T17185	Cl2BC protein - ra	242	75	6.6	796	2	E96854	hypothetical prote
170	78.5	6.9	1487	2	T14324	alpha-latrotoxin r	243	75	6.6	940	2	D89723	protein F39D8.lb [
171	78	6.9	253	2	T67619	hypothetical prote	244	75	6.6	945	2	T21998	hypothetical prote
172	78	6.9	293	2	G87018	probable membrane	245	75	6.6	3375	2	T19821	hypothetical prote
173	78	6.9	434	2	B84694	hypothetical prote	246	74.5	6.6	262	2	T33597	hypothetical prote
174	78	6.9	530	2	A45690	transactivator EBN	247	74.5	6.6	290	2	S66355	lectin-related sto
175	78	6.9	1050	2	T31853	hypothetical prote	248	74.5	6.6	382	2	T25280	hypothetical prote

249	74.5	6.6	388	2	T16861	hypothetical prote	322	73	6.4	2468	2	A83412	hypothetical prote
250	74.5	6.6	407	2	T26938	hypothetical prote	323	72.5	6.4	263	2	I51225	snail1 protein - z
251	74.5	6.6	482	2	T22754	hypothetical prote	324	72.5	6.4	321	2	T26153	hypothetical prote
252	74.5	6.6	575	2	S29315	chaperonin 60 - cu	325	72.5	6.4	382	2	T27058	hypothetical prote
253	74.5	6.6	709	2	T28712	hypothetical prote	326	72.5	6.4	463	1	A36479	milk fat globule m
254	74.5	6.6	860	2	JC4566	chitinase [SC 3.2.	327	72.5	6.4	498	1	VGXPLM	surface glycoprote
255	74.5	6.6	909	1	QRXL11	LDL receptor 1 pre	328	72.5	6.4	560	2	T32661	hypothetical prote
256	74.5	6.6	998	2	S37627	protein-tyrosine k	329	72.5	6.4	575	2	S39484	DNA-binding protei
257	74.5	6.6	1042	2	T48801	hypothetical prote	330	72.5	6.4	648	2	PC4395	mucin 3 - human (f
258	74.5	6.6	1075	2	S48992	flocculation prote	331	72.5	6.4	729	2	G96559	hypothetical prote
259	74.5	6.6	1388	2	A53317	collagen alpha 1(X	332	72.5	6.4	765	1	T44946	transducer protein
260	74.5	6.6	1638	1	CGHUIV	collagen alpha 1(V	333	72.5	6.4	797	1	VGBEX1	glycoprotein X pre
261	74.5	6.6	2688	2	I49477	alpha-A-crystallin	334	72.5	6.4	867	2	T45463	membrane glycoprot
262	74	6.5	147	2	S09762	hypothetical prote	335	72.5	6.4	896	2	S36326	clathrin assembly
263	74	6.5	223	2	T21930	hypothetical prote	336	72.5	6.4	907	1	QQ8E21	membrane antigen 9
264	74	6.5	313	2	AH0734	probable bacteriop	337	72.5	6.4	915	2	S36327	clathrin assembly
265	74	6.5	384	2	T21929	hypothetical prote	338	72.5	6.4	930	2	B72537	hypothetical prote
266	74	6.5	397	2	E97176	N-terminal domain	339	72.5	6.4	1021	2	S64506	protein kinase BUB
267	74	6.5	417	2	T20327	hypothetical prote	340	72.5	6.4	1180	2	E86719	hypothetical prote
268	74	6.5	418	2	T16713	hypothetical prote	341	72.5	6.4	1737	2	A59235	unconventional myo
269	74	6.5	515	2	AD1162	flagellar motor sw	342	72.5	6.4	1965	2	T33216	hypothetical prote
270	74	6.5	518	2	G88961	protein P59A7.8 [i	343	72	6.3	159	2	F72758	hypothetical prote
271	74	6.5	542	2	S64030	probable membrane	344	72	6.3	182	2	T30078	hypothetical prote
272	74	6.5	586	2	S66697	probable membrane	345	72	6.3	199	2	JE0351	OX40 ligand protei
273	74	6.5	600	2	T06292	hypothetical prote	346	72	6.3	236	2	T03041	hypothetical prote
274	74	6.5	906	2	G90281	conserved hypotet	347	72	6.3	246	2	PC4397	mucin 3 T10 - huma
275	74	6.5	1047	2	A55617	masquerade precurs	348	72	6.3	324	2	S36646	integrin-associated
276	74	6.5	2414	2	A54277	transcription adap	349	72	6.3	405	2	A60534	P2B/AMP-1 precurs
277	73.5	6.5	263	2	T38003	hypothetical ser-t	350	72	6.3	448	2	G88639	protein C34H4.2 [i
278	73.5	6.5	358	2	AD2378	hypothetical prote	351	72	6.3	481	2	T38149	pre-mrna splicing
279	73.5	6.5	371	2	S20075	promastigote surfa	352	72	6.3	482	2	A44997	merozoite surface
280	73.5	6.5	435	2	AG1028	prepilin [imported	353	72	6.3	576	2	T38293	hypothetical serin
281	73.5	6.5	447	2	A39321	mucin - rat (fragm	354	72	6.3	592	2	T40863	hypothetical prote
282	73.5	6.5	451	2	S71754	cellular hepatitis	355	72	6.3	1176	2	T49482	hypothetical prote
283	73.5	6.5	484	1	A24994	cellulose 1,4-beta	356	72	6.3	1203	2	T17415	mycelial surface a
284	73.5	6.5	511	1	VGBE1K	glycoprotein C - h	357	72	6.3	1367	2	S51959	hypothetical prote
285	73.5	6.5	542	2	T19952	hypothetical prote	358	72	6.3	1419	2	T30531	agglutinin-like ad
286	73.5	6.5	595	2	A42086	CD30 antigen precu	359	72	6.3	1489	2	T31108	cyst germination s
287	73.5	6.5	601	2	H90270	hypothetical prote	360	72	6.3	2526	2	T20531	hypothetical prote
288	73.5	6.5	626	2	AB1328	probable peptidogl	361	72	6.3	2722	2	T20532	hypothetical prote
289	73.5	6.5	708	2	F87245	penicillin-binding	362	72	6.3	2731	2	E88320	protein F07A11.6 [
290	73.5	6.5	806	2	E69424	hypothetical prote	363	72	6.3	2971	2	T08026	non-structural hyp
291	73.5	6.5	866	2	T45462	membrane glycoprot	364	71.5	6.3	141	2	A38196	hypothetical prote
292	73.5	6.5	901	2	A44925	phosphoprotein, sy	365	71.5	6.3	152	2	T15170	hypothetical prote
293	73.5	6.5	905	2	T02205	Lu-ECAM-1 protein	366	71.5	6.3	162	2	C84948	NADH2 dehydrogenas
294	73.5	6.5	976	2	A87576	peptidase, M16 fam	367	71.5	6.3	152	2	T28759	hypothetical prote
295	73.5	6.5	989	2	T47503	hypothetical prote	368	71.5	6.3	281	2	T49537	hypothetical prote
296	73.5	6.5	998	2	S31735	NAD ADP-ribosyltra	369	71.5	6.3	305	2	AB2149	hypothetical prote
297	73.5	6.5	1004	2	T38074	hypothetical prote	370	71.5	6.3	363	2	T25278	hypothetical prote
298	73.5	6.5	1016	2	T19006	ankyrin related pr	371	71.5	6.3	477	2	T32938	hypothetical prote
299	73.5	6.5	2232	2	T34434	hypothetical prote	372	71.5	6.3	496	2	E90181	hypothetical prote
300	73.5	6.5	3176	2	CGH03A	collagen alpha 3(V	373	71.5	6.3	499	2	A12449	hypothetical prote
301	73	6.4	260	2	I50109	gastrulation prote	374	71.5	6.3	540	2	H98086	chaperonin, 60 kDa
302	73	6.4	327	2	S20074	promastigote surfa	375	71.5	6.3	540	2	G95222	probable transposa
303	73	6.4	461	2	T51044	related to spore c	376	71.5	6.3	675	2	T47378	hypothetical prote
304	73	6.4	486	2	S66097	cell-cycle protein	377	71.5	6.3	755	2	T20950	hypothetical prote
305	73	6.4	492	1	CHBOA3	gamma-aminobutyric	378	71.5	6.3	822	2	JC4076	dextranase (EC 3.2
306	73	6.4	528	2	S69589	hypothetical prote	379	71.5	6.3	882	2	T01168	hypothetical prote
307	73	6.4	550	2	C75557	hypothetical prote	380	71.5	6.3	1166	2	S37692	probable tumor sup
308	73	6.4	600	2	E72027	phosphoenolpyruvat	381	71.5	6.3	1557	2	D41214	protein-tyrosine-p
309	73	6.4	600	2	A86597	phosphoenolpyruvat	382	71.5	6.3	1630	2	C41214	mucin SAC (clone M
310	73	6.4	639	2	T13151	adaptor protein CM	383	71	6.2	98	2	S53367	hypothetical prote
311	73	6.4	681	2	S33316	structural protein	384	71	6.2	240	2	T33698	mucin - rat
312	73	6.4	728	2	T20561	hypothetical prote	385	71	6.2	292	2	S24169	hypothetical prote
313	73	6.4	771	2	T34376	hypothetical prote	386	71	6.2	304	2	T15922	hypothetical prote
314	73	6.4	781	2	T49472	hormone-sensitive	387	71	6.2	343	2	S75435	hypothetical prote
315	73	6.4	814	2	T33140	hypothetical prote	388	71	6.2	349	2	T05857	leukosialin precu
316	73	6.4	825	2	T48431	hypothetical prote	389	71	6.2	378	2	S00842	alcohol dehydrogen
317	73	6.4	884	2	AE3166	ATP-dependent DNA	390	71	6.2	379	1	S71571	promastigote surfa
318	73	6.4	938	2	A36337	membrane glycoprot	391	71	6.2	384	2	A41710	cellulase (EC 3.2.
319	73	6.4	993	2	F97717	hypothetical prote	392	71	6.2	410	1	S68153	lysosomal membrane
320	73	6.4	1235	2	T13710	protein-tyrosine k	393	71	6.2	415	2	A35560	hypothetical prote
321	73	6.4	2179	1	GNNYH4	genome polypeptide	394	71	6.2	416	2	T20448	hypothetical prote

395	71	6.2	534	2	G97703	hypothenical prote	468	69.5	6.1	120	1	W4WL42	E4 protein - human
396	71	6.2	626	1	NSHUA	platelet glycoprot	469	69.5	6.1	124	2	E84613	hypothenical prote
397	71	6.2	727	2	A88131	protein F10G7.9 [i	470	69.5	6.1	150	2	T48611	agp6 protein - Ara
398	71	6.2	738	2	I40719	isocitrate dehydro	471	69.5	6.1	172	2	T21753	hypothenical prote
399	71	6.2	739	1	A34873	transcription fact	472	69.5	6.1	202	2	A82378	hypothenical prote
400	71	6.2	791	2	T39924	hypothenical prote	473	69.5	6.1	299	2	G70784	probable mmpS3 pro
401	71	6.2	1014	1	A29725	NAD ADP-riboyltra	474	69.5	6.1	372	2	T48660	heat shock protein
402	71	6.2	1156	2	T43326	germline RNA helic	475	69.5	6.1	373	2	F81333	chaperone bnaJ Cj1
403	71	6.2	1172	2	T32759	hypothenical prote	476	69.5	6.1	400	2	T32705	hypothenical prote
404	71	6.2	1241	2	S01827	period clock prote	477	69.5	6.1	425	1	F0MVGC	gag polyprotein -
405	71	6.2	1272	2	S26180	neurofascin - chic	478	69.5	6.1	432	2	T08771	hypothenical prote
406	71	6.2	1367	2	T33819	hypothenical prote	479	69.5	6.1	458	2	F86433	protein T17H7.5 [i
407	71	6.2	1595	2	T31082	endo-1.4-beta-xyla	480	69.5	6.1	455	2	S46759	hypothenical prote
408	71	6.2	1993	2	A1450	probable peptidogl	481	69.5	6.1	476	2	E44977	merozoite surface
409	70.5	6.2	118	2	S49913	cryptogein - Phyto	482	69.5	6.1	514	2	A44100	cell adhesion mole
410	70.5	6.2	128	2	A35690	mucin 3 (clone SIB	483	69.5	6.1	514	2	A31643	cell adhesion 80K
411	70.5	6.2	168	2	A31196	prespore-specific	484	69.5	6.1	519	2	F69989	unspecific monoocy
412	70.5	6.2	172	2	F49247	merozoite surface	485	69.5	6.1	540	1	F0MVHL	gag polyprotein -
413	70.5	6.2	174	2	E49247	merozoite surface	486	69.5	6.1	558	2	A98199	translocated intim
414	70.5	6.2	254	2	D88560	protein F58A4.1 [i	487	69.5	6.1	558	2	E86045	probable transloca
415	70.5	6.2	255	2	I46606	MHC SIA-DQ alpha c	488	69.5	6.1	621	2	T20307	hypothenical prote
416	70.5	6.2	275	2	T21933	hypothenical prote	489	69.5	6.1	640	2	T25367	hypothenical prote
417	70.5	6.2	308	2	T29756	hypothenical prote	490	69.5	6.1	672	2	T20310	hypothenical prote
418	70.5	6.2	321	2	T19259	hypothenical prote	491	69.5	6.1	736	2	T19366	hypothenical prote
419	70.5	6.2	330	2	S28102	rlx protein - Strap	492	69.5	6.1	833	2	AF2089	hypothenical prote
420	70.5	6.2	350	2	A10139	URP-hexose-1-phos	493	69.5	6.1	832	2	T46091	hypothenical prote
421	70.5	6.2	385	2	F70591	probable kerB prot	494	69.5	6.1	963	2	T40290	hypothenical prote
422	70.5	6.2	403	1	S35541	transcription fact	495	69.5	6.1	993	2	AE1905	outer membrane sec
423	70.5	6.2	427	2	C88883	protein JCB.10 [im	496	69.5	6.1	1051	2	JC4091	glycoprotein A - P
424	70.5	6.2	431	1	JC2002	transcription fact	497	69.5	6.1	1071	2	T22327	hypothenical prote
425	70.5	6.2	478	2	A32555	major merozoite su	498	69.5	6.1	1118	2	A48292	mucin, tracheobron
426	70.5	6.2	496	2	T30976	hypothenical prote	499	69.5	6.1	1785	2	A45546	major merozoite su
427	70.5	6.2	534	2	T39903	serine-rich protei	500	69.5	6.1	2717	2	A34203	DNA-binding protei
428	70.5	6.2	562	2	A85042	hypothenical prote	501	69	6.1	171	2	T31478	hypothenical prote
429	70.5	6.2	610	2	S35049	mucin JER57 - huma	502	69	6.1	217	2	S01358	salivary glue prot
430	70.5	6.2	616	2	T29234	hypothenical prote	503	69	6.1	255	2	T22429	hypothenical prote
431	70.5	6.2	674	2	S74506	ribonuclease E - S	504	69	6.1	258	2	S23106	pria protein - shi
432	70.5	6.2	802	2	T21315	hypothenical prote	505	69	6.1	286	2	T30919	hypothenical prote
433	70.5	6.2	893	2	T18271	hypothenical prote	506	69	6.1	284	2	T42367	a-agglutinin core
434	70.5	6.2	910	1	S73361	dhaf homolog prote	507	69	6.1	299	2	S44554	citrate transport
435	70.5	6.2	968	2	T00333	hypothenical prote	508	69	6.1	338	2	F69437	hypothenical prote
436	70.5	6.2	1032	2	G89427	protein T08B2.3 [i	509	69	6.1	356	2	S73315	protoporphyrin IX
437	70.5	6.2	1032	2	T18293	guanylate kinase-i	510	69	6.1	382	2	A28067	lysosomal membrane
438	70.5	6.2	1123	2	T18270	hypothenical prote	511	69	6.1	416	2	T34279	hypothenical prote
439	70.5	6.2	1131	2	T15787	hypothenical prote	512	69	6.1	420	2	AB2426	hypothenical prote
440	70.5	6.2	1369	2	S70713	protein-tyrosine k	513	69	6.1	483	2	G86902	dextranucrase (EC
441	70.5	6.2	1742	2	T13256	cellulase (EC 3.2.2	514	69	6.1	511	2	I50114	early growth respo
442	70.5	6.2	1904	2	T13256	tail-host specific	515	69	6.1	530	2	S62439	hypothenical serin
443	70.5	6.2	3054	1	GNBVEV	genome polyprotein	516	69	6.1	608	2	A46312	gag polyprotein -
444	70.5	6.2	3069	2	H70656	fatty-acid synthas	517	69	6.1	652	2	S50210	surface layer prot
445	70	6.2	147	2	JC7938	type II antifreeze	518	69	6.1	658	2	T41309	hypothenical threo
446	70	6.2	209	2	AB2218	hypothenical prote	519	69	6.1	670	2	F84540	hypothenical prote
447	70	6.2	311	2	H96002	probable sugar kin	520	69	6.1	790	2	T34293	hypothenical prote
448	70	6.2	329	2	S38082	pathogenesis-relat	521	69	6.1	814	2	T49207	receptor kinase-li
449	70	6.2	340	2	C90894	probable LACI-type	522	69	6.1	850	1	MMHUE4	erythrocyte membra
450	70	6.2	340	2	F85723	probable LACI-type	523	69	6.1	854	1	QRHYLD	IDL receptor precu
451	70	6.2	340	2	G84905	sugar-binding prot	524	69	6.1	1169	2	S38181	floculation prote
452	70	6.2	357	2	E72245	hydrolase, ama/hip	525	69	6.1	1199	2	A40670	nuclear envelope p
453	70	6.2	358	2	A88082	protein T05A8.7 [i	526	69	6.1	1630	2	A53577	ascites sialoglyco
454	70	6.2	408	2	A46712	glycoprotein Iia -	527	69	6.1	1868	2	S48938	hypothenical prote
455	70	6.2	412	1	AJBORS	argininosuccinate	528	69	6.1	2035	2	A40718	host cell factor C
456	70	6.2	497	2	T51135	hypothenical prote	529	69	6.1	2087	2	A42854	probable spindle p
457	70	6.2	542	2	B47022	chitinase (EC 3.2.2	530	69	6.1	2282	2	T42717	DNA-binding protei
458	70	6.2	589	2	A10684	hypothenical prote	531	69	6.1	2481	2	D90011	FmtB protein limpo
459	70	6.2	613	2	B90294	hypothenical prote	532	69	6.1	26926	1	S13834	titin, cardiac mus
460	70	6.2	767	1	JU0474	glucan 1.4-alpha-g	533	68.5	6.0	204	2	S51232	gibberellin-respon
461	70	6.2	775	1	WNBEJ9	ribonucleoside-dip	534	68.5	6.0	213	2	A86228	hypothenical prote
462	70	6.2	778	1	ALBYG	glucan 1.4-alpha-g	535	68.5	6.0	218	2	AH1837	hypothenical prote
463	70	6.2	835	2	JC6140	cell surface-assoc	536	68.5	6.0	246	2	S47805	hypothenical 27.4K
464	70	6.2	1048	1	S61388	dotA protein - leg	537	68.5	6.0	246	2	D91186	probable outer mem
465	70	6.2	1213	2	A41724	limb deformity (ld	538	68.5	6.0	246	2	C86033	probable outer mem
466	70	6.2	1726	2	A39401	merozoite surface	539	68.5	6.0	257	2	C84890	hypothenical prote
467	70	6.2	3507	2	T34513	hypothenical prote	540	68.5	6.0	261	2	T30170	hypothenical prote

541	68.5	6.0	280	2	AB2031	gamma-tocopherol m	614	68	6.0	1401	2	T30247	Werner syndrome pr
542	68.5	6.0	294	1	AI2016	hypothetical prote	615	68	6.0	1578	2	I48216	neurexin III-alpha
543	68.5	6.0	310	1	YAZQ31	300K antigen Ag231	616	68	6.0	1711	2	T33337	1,4-beta-glucanase
544	68.5	6.0	318	2	T20063	hypothetical prote	617	68	6.0	2440	2	S39162	transcription coac
545	68.5	6.0	359	2	G70814	probable far prote	618	68	6.0	2441	2	S39161	CREB-binding prote
546	68.5	6.0	369	2	T01196	transcription fact	619	68	6.0	3191	2	T22945	hypothetical prote
547	68.5	6.0	385	2	H97239	polyferredoxin [im	620	68	6.0	3712	2	S18253	laminin alpha-1 ch
548	68.5	6.0	420	2	A88962	protein F59A7.1 [i	621	67.5	5.9	150	2	T52587	probable arabinoga
549	68.5	6.0	426	2	A35641	5-aminoimidazole r	622	67.5	5.9	159	2	T31598	hypothetical prote
550	68.5	6.0	435	2	C86340	protein F2D10.28 [	623	67.5	5.9	191	2	S38117	hypothetical prote
551	68.5	6.0	435	1	VXZPXA	hypothetical prote	624	67.5	5.9	210	2	B88082	hypothetical prote
552	68.5	6.0	490	1	660929	surface glycoprote	625	67.5	5.9	256	2	H36857	protein T05A8.6 [i
553	68.5	6.0	507	2	S05542	probable aldehyde	626	67.5	5.9	297	2	S55063	B26R protein - var
554	68.5	6.0	509	2	T48459	hypothetical prote	627	67.5	5.9	338	2	S28004	conserved hypothet
555	68.5	6.0	514	1	A47692	cytochrome P450-1i	628	67.5	5.9	345	2	E88103	probable cell surf
556	68.5	6.0	535	2	B84443	fumurate hydratase	629	67.5	5.9	346	2	T46916	protein W10G11.5 [
557	68.5	6.0	553	2	A49364	hypothetical prote	630	67.5	5.9	376	2	S52137	hypothetical prote
558	68.5	6.0	553	2	S63395	S9 protein, brain	631	67.5	5.9	387	2	A86302	MID2 protein - yea
559	68.5	6.0	607	2	T33044	probable membrane	632	67.5	5.9	391	2	A44063	paired box transcr
560	68.5	6.0	654	2	T33044	hypothetical prote	633	67.5	5.9	399	2	T42242	hypothetical 44.2K
561	68.5	6.0	659	2	T09483	hypothetical prote	634	67.5	5.9	431	2	G85277	Fi41i7.11 protein
562	68.5	6.0	699	2	T40383	Cys-rich protein R	635	67.5	5.9	433	2	S37790	probable serine/th
563	68.5	6.0	700	2	A54641	interspersed repea	636	67.5	5.9	476	2	T32032	hypothetical prote
564	68.5	6.0	721	2	E70766	hypothetical prote	637	67.5	5.9	476	2	T27051	hypothetical prote
565	68.5	6.0	737	2	AG2156	hypothetical prote	638	67.5	5.9	493	2	A34130	gamma-aminobutyric
566	68.5	6.0	795	2	T20609	hypothetical prote	639	67.5	5.9	527	2	T28878	hypothetical prote
567	68.5	6.0	865	2	AC1966	hypothetical prote	640	67.5	5.9	530	2	T32812	hypothetical prote
568	68.5	6.0	942	2	T19553	hypothetical prote	641	67.5	5.9	538	2	S65764	hypothetical prote
569	68.5	6.0	1200	1	SNP80	ice nucleation pro	642	67.5	5.9	601	2	S56144	SH3 domain binding
570	68.5	6.0	1379	2	T45119	FIM protein [impor	643	67.5	5.9	642	2	T39607	fork head protein
571	68.5	6.0	1438	2	A48216	neurexin III-alpha	644	67.5	5.9	642	2	H75141	oligopeptide-bindi
572	68.5	6.0	1471	2	B48218	neurexin III-alpha	645	67.5	5.9	651	2	T21175	hypothetical prote
573	68.5	6.0	1541	2	S46686	hypothetical prote	646	67.5	5.9	656	1	A43358	RNA-binding protei
574	68.5	6.0	3122	2	T17202	DNA-directed DNA p	647	67.5	5.9	670	2	T49510	fibroin-3 related
575	68	6.0	62	2	S53366	mucin SAC (clone M	648	67.5	5.9	710	2	A99486	ABC transporter, b
576	68	6.0	211	2	H72608	hypothetical prote	649	67.5	5.9	736	2	T41259	hypothetical prote
577	68	6.0	248	2	AF1314	carbon dioxide con	650	67.5	5.9	749	2	T50397	probable serine/th
578	68	6.0	295	2	S50316	CIN5 protein - yea	651	67.5	5.9	792	2	S70305	hypothetical prote
579	68	6.0	301	2	H70644	hypothetical prote	652	67.5	5.9	835	2	C84287	hypothetical prote
580	68	6.0	303	2	S40973	hypothetical prote	653	67.5	5.9	839	2	T41826	P95 orf83 - Bombyx
581	68	6.0	333	2	T15367	hypothetical prote	654	67.5	5.9	872	2	JH0561	metabotropic gluta
582	68	6.0	339	2	AH0050	probable periplasm	655	67.5	5.9	882	2	T23807	hypothetical prote
583	68	6.0	372	2	S61992	glycerophosphodie	656	67.5	5.9	886	2	S29605	glycoprotein 350/2
584	68	6.0	378	2	S61992	SttG1 protein - yea	657	67.5	5.9	971	2	F88448	protein C45G9.10 [
585	68	6.0	380	1	S51826	alcohol dehydrogen	658	67.5	5.9	1051	2	T51904	hypothetical prote
586	68	6.0	387	2	A56275	1,3-propanediol de	659	67.5	5.9	1203	2	T04294	hypothetical prote
587	68	6.0	388	2	T43019	probable DNA-bindi	660	67.5	5.9	1348	2	S27812	probable epidermal
588	68	6.0	423	2	T14531	S-locus-specific g	661	67.5	5.9	1348	2	A43917	probable epidermal
589	68	6.0	426	2	I48379	gene hb protein -	662	67.5	5.9	1633	2	T01879	hypothetical prote
590	68	6.0	452	2	T46147	zinc finger protei	663	67.5	5.9	1751	2	A45604	major blood-stage
591	68	6.0	456	2	T38221	hypothetical aerin	664	67.5	5.9	1784	2	T10532	gag-pol polyprotei
592	68	6.0	479	2	A84588	probable tyrosine	665	67.5	5.9	1896	2	B72175	D15R protein - var
593	68	6.0	500	2	A11913	apolipoprotein N-a	666	67.5	5.9	1897	2	T28621	hypothetical prote
594	68	6.0	502	2	T21935	hypothetical prote	667	67.5	5.9	3345	2	T13423	hypothetical prote
595	68	6.0	515	2	B84406	TRK potassium upta	668	67.5	5.9	148	2	S50653	hypothetical prote
596	68	6.0	537	1	F0MVW7	gag polyprotein -	669	67	5.9	149	2	S12913	cystatin - fruit f
597	68	6.0	600	2	S56744	mucin (clone pGM7-	670	67	5.9	153	2	S67294	hypothetical prote
598	68	6.0	655	1	A55726	RNA-binding protei	671	67	5.9	201	1	WMBEHL	D15R protein - huma
599	68	6.0	655	2	B70186	translation elonga	672	67	5.9	214	2	A46629	mucin 6, gastric (
600	68	6.0	679	2	S64258	hypothetical prote	673	67	5.9	232	1	WNADC2	early B1A 25K prot
601	68	6.0	709	2	S51793	ribasic processing	674	67	5.9	233	2	T22977	hypothetical prote
602	68	6.0	730	2	A75486	hypothetical prote	675	67	5.9	264	2	A49149	mesoderm developme
603	68	6.0	749	2	B86403	probable mutator-1	676	67	5.9	276	2	T51685	myb-related trans
604	68	6.0	816	2	S64439	hypothetical prote	677	67	5.9	305	2	T24283	hypothetical prote
605	68	6.0	871	2	T43427	hypothetical prote	678	67	5.9	308	1	B48008	electron transfer
606	68	6.0	916	2	T20909	pob1 protein - fis	679	67	5.9	319	2	T43040	hypothetical prote
607	68	6.0	1016	1	J50428	NAD ADP-ribosyltra	680	67	5.9	398	2	A80975	probable racamase
608	68	6.0	1098	2	T08599	probable transcrip	681	67	5.9	402	2	E86185	hypothetical prote
609	68	6.0	1131	2	T41144	hypothetical serin	682	67	5.9	412	2	E86736	protein F33D4.6a [
610	68	6.0	1203	2	T51029	related to bonchway	683	67	5.9	426	2	F75394	hypothetical prote
611	68	6.0	1204	2	F81158	exodeoxyribonuclea	684	67	5.9	433	2	T14329	dermal glycoprotei
612	68	6.0	1275	2	T33369	hypothetical prote	685	67	5.9	438	1	S70602	cellulose 1,4-beta
613	68	6.0	1390	2	T18883	hypothetical prote	686	67	5.9	441	2	C75076	heme biosynthesis

687	67	5.9	443	2	T14916	mitosis-specific c	760	66.5	5.9	542	2	S32106	groEL protein - La
688	67	5.9	466	2	S45419	hypothetical prote	761	66.5	5.9	562	2	B41035	chitinase (EC 3.2.
689	67	5.9	476	2	C39481	serum response fac	762	66.5	5.9	582	2	S50371	chitinase (EC 3.2.
690	67	5.9	486	2	B39481	serum response fac	763	66.5	5.9	571	2	H97070	membrane associate
691	67	5.9	494	1	A29079	lymphocyte surface	764	66.5	5.9	575	2	S29316	chaperonin 60 - cu
692	67	5.9	514	2	H70699	probable ppp prote	765	66.5	5.9	615	2	T47395	hypothetical prote
693	67	5.9	536	2	H71563	hypothetical prote	766	66.5	5.9	637	2	T20981	hypothetical prote
694	67	5.9	549	2	S04845	Ig heavy chain, pre	767	66.5	5.9	648	2	T43337	polo-like kinase-1
695	67	5.9	558	2	S57953	C4BP protein alpha	768	66.5	5.9	650	2	L49523	tumor necrosis fac
696	67	5.9	579	2	D84137	methyl-accepting c	769	66.5	5.9	681	2	A45705	type I transmembra
697	67	5.9	581	2	S86408	F3H9.11 protein -	770	66.5	5.9	710	2	S67098	probable membrane
698	67	5.9	588	2	B70618	probable PG protei	771	66.5	5.9	719	2	T33170	hypothetical prote
699	67	5.9	610	1	L46001	C4b-binding protei	772	66.5	5.9	739	2	I56187	transcription fact
700	67	5.9	617	2	T15408	hypothetical prote	773	66.5	5.9	811	2	A41054	fascilin II, tran
701	67	5.9	620	2	A70525	hypothetical prote	774	66.5	5.9	843	2	S44868	kinesin heavy chai
702	67	5.9	634	2	T49415	hypothetical prote	775	66.5	5.9	880	2	S44833	F54H12.5 protein -
703	67	5.9	636	2	S63131	hypothetical prote	776	66.5	5.9	913	2	D82885	multiple banded an
704	67	5.9	644	2	F81411	probable membrane	777	66.5	5.9	919	2	T16693	hypothetical prote
705	67	5.9	650	2	S22835	alpha-agglutinin -	778	66.5	5.9	948	2	C75265	hexagonally packed
706	67	5.9	672	2	T32557	hypothetical prote	779	66.5	5.9	996	2	JE0237	apolipoprotein E r
707	67	5.9	698	1	JX0202	long-chain-fatty-a	780	66.5	5.9	1059	2	T22545	hypothetical prote
708	67	5.9	710	2	T21339	hypothetical prote	781	66.5	5.9	1219	2	H84464	hypothetical prote
709	67	5.9	723	2	H85092	hypothetical prote	782	66.5	5.9	1221	2	A10193	hypothetical prote
710	67	5.9	732	2	T25937	hypothetical prote	783	66.5	5.9	1655	2	T32633	ribonuclease E (EC
711	67	5.9	784	2	S26638	SPR-1 protein - hu	784	66	5.8	162	2	T02072	hypothetical prote
712	67	5.9	824	2	T23923	hypothetical prote	785	66	5.8	169	2	A49247	probable glycine c
713	67	5.9	826	2	G30283	hypothetical prote	786	66	5.8	193	2	D72843	merozoite surface
714	67	5.9	850	2	S56015	gastric mucin MUC5	787	66	5.8	253	2	T27279	hypothetical prote
715	67	5.9	855	2	T19405	hypothetical prote	788	66	5.8	255	2	B75309	hypothetical prote
716	67	5.9	910	2	C69456	subtilisin sendai	789	66	5.8	256	2	JC2398	PMS3 homolog misa
717	67	5.9	948	2	T11678	hypothetical prote	790	66	5.8	259	2	B82029	methionyl aminopep
718	67	5.9	1060	2	T31763	hypothetical prote	791	66	5.8	282	2	B90313	conserved hypothet
719	67	5.9	1140	2	D88690	protein F4IH0.3 [	792	66	5.8	335	2	S74357	hypothetical prote
720	67	5.9	1140	2	S73786	hypothetical prote	793	66	5.8	329	2	T43012	conserved hypotnet
721	67	5.9	1228	2	C98219	proline dehydrogen	794	66	5.8	360	2	T33835	hypothetical prote
722	67	5.9	1228	2	AG3067	Werner syndrome pr	795	66	5.8	367	1	W2WL11	E2 protein - human
723	67	5.9	1401	2	T17452	hypothetical prote	796	66	5.8	369	2	A11079	conserved hypotnet
724	67	5.9	1804	2	H96597	hypothetical prote	797	66	5.8	375	2	S36547	E2 protein - human
725	67	5.9	1819	2	T32008	hypothetical prote	798	66	5.8	380	1	S00912	alcohol dehydrogen
726	67	5.9	1900	2	S45530	hypothetical prote	799	66	5.8	383	2	E96972	riboflavin biosynt
727	67	5.9	2476	2	T34032	probable 1-phospha	800	66	5.8	393	1	HVRKC1	Ig mu chain C regi
728	67	5.9	4377	2	A55575	zonadhesin - pig	801	66	5.8	407	2	A30200	120K lysosomal mem
729	66.5	5.9	128	2	T05635	ankyrin 3, long sp	802	66	5.8	426	2	B53580	neurexin III beta
730	66.5	5.9	149	2	E71227	hypothetical prote	803	66	5.8	459	2	T17364	NADH2 dehydrogenas
731	66.5	5.9	175	2	T50094	hypothetical prote	804	66	5.8	463	1	P2WL13	L2 protein - human
732	66.5	5.9	217	2	S45446	hypothetical prote	805	66	5.8	471	1	A38979	cellulose 1,4-beta
733	66.5	5.9	238	2	T07921	hypothetical prote	806	66	5.8	471	1	A26160	cellulose 1,4-beta
734	66.5	5.9	240	2	S31573	probable starch sy	807	66	5.8	482	2	S76376	hypothetical prote
735	66.5	5.9	263	2	S01360	hypothetical prote	808	66	5.8	584	2	JC7809	sulfakinin recepto
736	66.5	5.9	319	1	A35163	salivary glue prot	809	66	5.8	599	2	G71481	probable phosphoen
737	66.5	5.9	327	2	H82554	carbonate dehydrat	810	66	5.8	611	2	T04510	hypothetical prote
738	66.5	5.9	345	2	AH0457	conserved hypotnet	811	66	5.8	614	2	A43390	gamma-aminobutyric
739	66.5	5.9	348	1	B37760	UDP-N-acetylurama	812	66	5.8	619	2	T15969	hypothetical prote
740	66.5	5.9	348	1	A30594	UTP-hexose-1-phosp	813	66	5.8	627	2	T27123	hypothetical prote
741	66.5	5.9	359	2	S42787	galactose-1-phosph	814	66	5.8	643	2	H84305	Htr8 transducer [i
742	66.5	5.9	369	2	E84291	serine/threonine-r	815	66	5.8	645	2	T16078	hypothetical prote
743	66.5	5.9	371	1	AJMSQ3	iron (III) ABC tra	816	66	5.8	655	2	AD2422	DNA polymerase III
744	66.5	5.9	371	1	F0MVCS	glutamate-ammonia	817	66	5.8	657	2	E96812	protein F3F9.10 [i
745	66.5	5.9	373	1	AJHUQ	gag polyprotein -	818	66	5.8	657	2	H71422	hypothetical prote
746	66.5	5.9	385	2	T38113	glutamate-ammonia	819	66	5.8	674	2	A49636	soluble oxidoredu
747	66.5	5.9	397	2	T22932	hypothetical serin	820	66	5.8	687	2	A49636	probable vascular e
748	66.5	5.9	413	2	S48756	hypothetical prote	821	66	5.8	730	2	A53064	folded gastrulatio
749	66.5	5.9	452	2	T26827	transcription fact	822	66	5.8	733	2	T01875	probable long-chai
750	66.5	5.9	458	2	T31631	hypothetical prote	823	66	5.8	786	1	A47547	serine proteinase
751	66.5	5.9	461	2	D72414	hypothetical prote	824	66	5.8	816	2	A49151	fibroblast growth
752	66.5	5.9	506	2	AG1864	anthranilate synth	825	66	5.8	897	2	S50550	SINI-associated pr
753	66.5	5.9	507	2	T50398	hypothetical prote	826	66	5.8	978	1	RGBY13	regulatory protein
754	66.5	5.9	507	2	T23375	hypothetical serin	827	66	5.8	994	1	MNVVM	nonstructural prot
755	66.5	5.9	516	2	A31270	hypothetical prote	828	66	5.8	1039	2	T09883	hypothetical prote
756	66.5	5.9	521	2	S69559	radial spoke prote	829	66	5.8	1041	2	S5862	probable membrane
757	66.5	5.9	521	2	C87474	hypothetical prote	830	66	5.8	1273	2	S58782	SSC31 protein - ye
758	66.5	5.9	527	2	T16022	hypothetical prote	831	66	5.8	1338	2	S09982	protein-tyrosine k
759	66.5	5.9	542	2	JN0661	heat shock protein	832	66	5.8	1422	2	T42636	protein-tyrosine-p

833	66	5.8	1711	2	AB1283	peptidoglycan link	906	65	5.7	393	2	A49008	paired box transcr
834	66	5.8	1829	2	T24583	hypothetical prote	907	65	5.7	402	2	T20595	hypothetical prote
835	66	5.8	2271	2	F90073	hypothetical prote	908	65	5.7	427	2	E83711	hypothetical prote
836	66	5.8	2405	2	T08164	dynein alpha heavy	909	65	5.7	434	2	S62168	hypothetical prote
837	65.5	5.8	157	2	JP0075	lectin CEL-IV, C-t	910	65	5.7	459	2	T17358	NADH2 dehydrogenas
838	65.5	5.8	198	2	A40709	ecdysone receptor	911	65	5.7	465	2	T34984	probable integral
839	65.5	5.8	211	1	MOKAD	lysozyme (EC 3.2.1	912	65	5.7	473	2	G90401	flagella-related p
840	65.5	5.8	248	2	T40149	hypothetical prote	913	65	5.7	503	2	S63257	probable membrane
841	65.5	5.8	282	2	T21222	hypothetical prote	914	65	5.7	506	2	A86169	hypothetical prote
842	65.5	5.8	287	2	S65765	chitinase (EC 3.2.	915	65	5.7	516	2	JE0134	mannan endo-1,4-be
843	65.5	5.8	290	2	A43897	spicule matrix pro	916	65	5.7	585	2	JC5013	2,4-chlorocatechol
844	65.5	5.8	314	2	D96703	hypothetical prote	917	65	5.7	593	2	S49525	glycoprotein G - s
845	65.5	5.8	316	2	G86333	hypothetical prote	918	65	5.7	608	2	S05341	probable reverse t
846	65.5	5.8	328	2	S69715	hypothetical prote	919	65	5.7	609	2	S36569	B1 protein - human
847	65.5	5.8	356	2	D86382	hypothetical prote	920	65	5.7	611	2	S86388	probable chaperoni
848	65.5	5.8	365	2	T26564	hypothetical prote	921	65	5.7	618	2	AI0171	probable exported
849	65.5	5.8	377	2	A48018	mucin 7 precursor,	922	65	5.7	619	2	A43361	Bts-related transc
850	65.5	5.8	443	2	C88427	protein R07E5.6 [i	923	65	5.7	627	2	S37954	RNA polymerase I t
851	65.5	5.8	459	2	G84752	En/Spm-like transp	924	65	5.7	633	2	T04835	probable serine/th
852	65.5	5.8	460	2	T23955	hypothetical prote	925	65	5.7	648	2	T04837	probable serine/th
853	65.5	5.8	461	2	T39862	hypothetical prote	926	65	5.7	674	2	T15524	hypothetical prote
854	65.5	5.8	463	2	T15416	hypothetical prote	927	65	5.7	706	2	S33761	transferrin precur
855	65.5	5.8	493	2	JC5486	membrane glycoprot	928	65	5.7	708	2	T29669	hypothetical prote
856	65.5	5.8	497	2	D81123	conserved hypotet	929	65	5.7	742	2	AH2166	hypothetical prote
857	65.5	5.8	516	2	T24644	hypothetical prote	930	65	5.7	770	2	G88445	protein C26E6.2 [i
858	65.5	5.8	526	2	C84552	hypothetical prote	931	65	5.7	786	2	A55501	cyclin F - human
859	65.5	5.8	540	2	T19956	hypothetical prote	932	65	5.7	792	2	F90566	conserved hypotet
860	65.5	5.8	541	2	T44725	chaperonin 60K [im	933	65	5.7	817	2	P86742	ribonuclease [impo
861	65.5	5.8	575	2	T34280	hypothetical prote	934	65	5.7	859	2	T29630	hypothetical prote
862	65.5	5.8	588	2	A25902	65K antigen - Myco	935	65	5.7	874	2	AI0281	probable insectici
863	65.5	5.8	592	2	S43597	coiled-coil protei	936	65	5.7	876	2	T05943	probable lipoxigen
864	65.5	5.8	594	2	S62529	hypothetical prote	937	65	5.7	921	2	A45183	TBP-associated fac
865	65.5	5.8	608	2	F84219	glucan 1,4-alpha-g	938	65	5.7	921	2	A48184	transcription init
866	65.5	5.8	628	2	T32761	Rtr16 transducer [	939	65	5.7	955	2	P84914	hypothetical prote
867	65.5	5.8	631	2	T44253	hypothetical prote	940	65	5.7	973	2	E86547	polymorphic outer
868	65.5	5.8	642	1	T44253	transducer protein	941	65	5.7	973	2	F72076	polymorphic membra
869	65.5	5.8	649	2	JQ0103	hypothetical 70K p	942	65	5.7	995	2	C81593	neural cell adhesi
870	65.5	5.8	667	2	T15710	hypothetical prote	943	65	5.7	1088	1	IJX114	SKC2D5 protein -
871	65.5	5.8	679	2	T19703	hypothetical prote	944	65	5.7	1095	2	PC1114	protein F14N23.29
872	65.5	5.8	713	2	T44447	enhancer-of-zeste	945	65	5.7	1096	2	H86237	hypothetical prote
873	65.5	5.8	746	2	G02838	DK1 protein [impor	946	65	5.7	1097	2	T49187	hypothetical prote
874	65.5	5.8	759	2	T44142	hypothetical prote	947	65	5.7	1124	2	F71719	cytadherence-acces
875	65.5	5.8	784	2	AH2560	gag-kit polyprotei	948	65	5.7	1139	1	E64234	hypothetical prote
876	65.5	5.8	790	1	F0MVHZ	dihydropterolate sy	949	65	5.7	1146	2	S46837	hypothetical prote
877	65.5	5.8	815	2	H84199	eps8 protein - mou	950	65	5.7	1216	2	B90580	hypothetical prote
878	65.5	5.8	821	2	S39983	hypothetical prote	951	65	5.7	1314	2	H86327	protein F18O14.25
879	65.5	5.8	826	2	T46060	hypothetical prote	952	65	5.7	1459	2	T32271	hypothetical prote
880	65.5	5.8	841	2	B71212	hypothetical prote	953	65	5.7	1566	2	T20058	hypothetical prote
881	65.5	5.8	877	2	F90070	Clumping factor B	954	65	5.7	1605	2	T31435	DNA-directed RNA p
882	65.5	5.8	894	2	T13029	beta-adaptin homol	955	65	5.7	1634	2	T26517	hypothetical prote
883	65.5	5.8	895	2	T29908	hypothetical prote	956	65	5.7	1642	2	T19130	hypothetical prote
884	65.5	5.8	1011	1	JH0581	NAD ADP-ribosyltra	957	65	5.7	1895	2	T15881	hypothetical prote
885	65.5	5.8	1043	2	F97302	hypothetical prote	958	65	5.7	1970	2	T03284	myoblast city prot
886	65.5	5.8	1161	2	A27069	lethal (2) giant 1	959	65	5.7	2311	1	TVCHSR	kinase-related pro
887	65.5	5.8	1306	2	S25370	MSB2 protein - yea	960	64.5	5.7	69	2	AB0028	actin rearrangemen
888	65.5	5.8	1442	1	B48148	protein-tyrosine-p	961	64.5	5.7	117	2	T24968	50S ribosomal prot
889	65.5	5.8	1524	2	S68553	surface layer prot	962	64.5	5.7	134	2	T67295	hypothetical prote
890	65.5	5.8	1650	2	S28721	hypothetical prote	963	64.5	5.7	204	2	S67295	probable membrane
891	65.5	5.8	3124	2	A40020	collagen alpha 1(X	964	64.5	5.7	220	2	I50588	fibroblast growth
892	65.5	5.8	7576	2	T17428	FK506 polyketide s	965	64.5	5.7	224	2	G83392	hypothetical prote
893	65	5.7	179	2	T26929	hypothetical prote	966	64.5	5.7	226	2	T28268	hypothetical prote
894	65	5.7	194	2	B72642	hypothetical prote	967	64.5	5.7	227	2	T50033	capsular polysacch
895	65	5.7	244	2	D90783	probable outer mem	968	64.5	5.7	231	2	F84311	hypothetical prote
896	65	5.7	244	2	F85643	outer membrane pre	969	64.5	5.7	292	2	JC4741	mosquitocidal toxi
897	65	5.7	271	2	B96773	hypothetical prote	970	64.5	5.7	313	2	A34677	secretory pathway
898	65	5.7	275	2	T48436	hypothetical prote	971	64.5	5.7	319	2	S12104	lipase 1 - Moraxel
899	65	5.7	282	2	T26397	hypothetical prote	972	64.5	5.7	322	2	AH2192	hypothetical prote
900	65	5.7	284	2	A97203	2-oxoacid ferredox	973	64.5	5.7	328	2	S67570	hypothetical prote
901	65	5.7	332	2	T31928	hypothetical prote	974	64.5	5.7	336	2	T15837	hypothetical prote
902	65	5.7	348	2	AD3264	electron transfer	975	64.5	5.7	341	2	C83578	hypothetical prote
903	65	5.7	373	2	AG3191	amide hydrolase [i	976	64.5	5.7	345	2	T12344	NADH2 dehydrogenas
904	65	5.7	380	1	S53307	alcohol dehydrogen	977	64.5	5.7	349	2	T42965	glycoprotein - ate
905	65	5.7	392	2	T49471	mucin (muc3) relat	978	64.5	5.7	354	2	S59521	mucin 5ac - mouse

979	64.5	5.7	378	2	A33271	manganese peroxidase	1052	64	5.6	364	1	EDBSP	immediate-early pr
980	64.5	5.7	385	2	AC2857	conserved hypothet	1053	64	5.6	376	2	AG0455	thiamin biosynthes
981	64.5	5.7	385	2	A97634	hypothetical prote	1054	64	5.6	384	2	S36529	E2 protein - human
982	64.5	5.7	397	2	B69378	probable acyl-CoA	1055	64	5.6	393	2	S62335	171-7 protein - fr
983	64.5	5.7	402	2	D69530	probable acyl-CoA	1056	64	5.6	394	2	T20778	hypothetical prote
984	64.5	5.7	412	1	ATMSRS	argininosuccinate	1057	64	5.6	395	2	H75457	hypothetical prote
985	64.5	5.7	412	1	AJRTKS	argininosuccinate	1058	64	5.6	413	2	AG0632	glucose-1-phosphat
986	64.5	5.7	416	2	S65110	chitinase (EC 3.2.	1059	64	5.6	416	2	S68822	neurotensin recept
987	64.5	5.7	420	1	AJBYRS	argininosuccinate	1060	64	5.6	417	2	S76588	hypothetical prote
988	64.5	5.7	424	1	VGBE39	glycoprotein gp63	1061	64	5.6	417	2	T24618	hypothetical prote
989	64.5	5.7	425	1	A26431	nerve growth fact3	1062	64	5.6	428	2	D86003	hypothetical prote
990	64.5	5.7	445	2	T07907	hydroxyproline-ric	1063	64	5.6	428	2	F91157	probable membrane
991	64.5	5.7	471	2	T15155	hypothetical prote	1064	64	5.6	438	1	HVRKCS	Ig mu chain C regi
992	64.5	5.7	485	2	T37550	hypothetical colle	1065	64	5.6	461	1	HVRKCS	Ig mu chain C regi
993	64.5	5.7	491	2	G86297	hypothetical prote	1066	64	5.6	461	2	D96647	hypothetical prote
994	64.5	5.7	512	2	S59437	F309.8 protein - A	1067	64	5.6	471	2	S46739	hypothetical prote
995	64.5	5.7	519	1	S69988	F02569.2 protein [	1068	64	5.6	473	2	T45954	hypothetical prote
996	64.5	5.7	532	2	B35621	unspecific monooxy	1069	64	5.6	519	2	T45764	hypothetical prote
997	64.5	5.7	532	2	B35621	spore germination	1070	64	5.6	543	1	QFMSL	neurofilament trip
998	64.5	5.7	549	2	F71219	probable thermophi	1071	64	5.6	554	2	T45840	GTPase activating-
999	64.5	5.7	568	2	A34891	Ig heavy chain pre	1072	64	5.6	560	2	S50392	hypothetical prote
1000	64.5	5.7	570	2	H97244	gene DMR-N9 protei	1073	64	5.6	561	2	T41097	hypothetical prote
1001	64.5	5.7	574	2	B82282	membrane associate	1074	64	5.6	562	2	S69055	RNA binding protei
1002	64.5	5.7	577	2	A60501	probable chitinase	1075	64	5.6	562	2	T49386	TTAGGG repeat-bind
1003	64.5	5.7	587	2	S21139	thrombomodulin pre	1076	64	5.6	580	2	T20716	hypothetical prote
1004	64.5	5.7	590	2	S66936	amine oxidase (cop	1077	64	5.6	583	2	S67571	hypothetical prote
1005	64.5	5.7	623	2	A48123	hypothetical prote	1078	64	5.6	586	2	S44850	hypothetical prote
1006	64.5	5.7	631	2	H70754	cell cycle regulat	1079	64	5.6	646	2	JCS583	K12H4.1 protein -
1007	64.5	5.7	648	2	A32576	probable abc trans	1080	64	5.6	664	2	T48258	85K SH3 domain-con
1008	64.5	5.7	680	2	S26764	beta-glucuronidase	1081	64	5.6	716	2	G01627	kinesin-like prote
1009	64.5	5.7	680	2	T19939	major coat protein	1082	64	5.6	745	2	T03119	androgen receptor
1010	64.5	5.7	690	2	H86464	hypothetical prote	1083	64	5.6	750	2	T10864	hypothetical prote
1011	64.5	5.7	757	2	P36518	hypothetical prote	1084	64	5.6	756	2	T27642	transcription acti
1012	64.5	5.7	760	1	S07896	protein T2E6.10 [i	1085	64	5.6	768	2	A29066	hypothetical prote
1013	64.5	5.7	770	1	S30293	transcription fact	1086	64	5.6	801	2	A37353	DNA ligase (ATP) (
1014	64.5	5.7	802	2	T32448	hypothetical prote	1087	64	5.6	825	1	GLHO	membrane protein 4
1015	64.5	5.7	833	2	G75621	hypothetical prote	1088	64	5.6	894	2	B96557	beta-glucosidase (
1016	64.5	5.7	854	1	WMBP12	arylesterase/monox	1089	64	5.6	982	2	T43676	probable receptor
1017	64.5	5.7	932	1	PKX2P	gene 12 protein -	1090	64	5.6	1104	2	S59310	hunchback-related
1018	64.5	5.7	1032	2	S65341	H4-exporting ATPas	1091	64	5.6	1115	2	S64101	probable membrane
1019	64.5	5.7	1033	2	T37715	probable membrane	1092	64	5.6	1132	2	B82538	PAN2 protein - yea
1020	64.5	5.7	1079	2	A86220	actin-interacting	1093	64	5.6	1217	2	T25894	ribonuclease E XF2
1021	64.5	5.7	1117	2	S63399	protein F22013.29	1094	64	5.6	1280	2	E95031	hypothetical prote
1022	64.5	5.7	1125	2	B41206	probable membrane	1095	64	5.6	1282	2	JE0120	alkaline amylopull
1023	64.5	5.7	1133	2	T30302	microtubule-associ	1096	64	5.6	1328	2	T43060	glycoprotein A - m
1024	64.5	5.7	1152	2	AC1347	P-type ATPase - Te	1097	64	5.6	1445	1	A48148	agrin - electric r
1025	64.5	5.7	1160	2	A27868	probable peptidogl	1098	64	5.6	1469	2	T19168	protein-tyrosine-p
1026	64.5	5.7	1191	2	T13850	lethal (2) giant 1	1099	64	5.6	1547	2	T28657	hypothetical prote
1027	64.5	5.7	1200	2	T17404	gene u-shaped prot	1100	64	5.6	1607	2	T02837	blackjack protein,
1028	64.5	5.7	1205	2	S84819	hyalin - sea urchi	1101	64	5.6	1671	2	S71828	long chain fatty a
1029	64.5	5.7	1249	2	A56511	probable membrane	1102	64	5.6	1859	1	A34092	sensory transducti
1030	64.5	5.7	1277	2	S70306	myosin I myoA - Em	1103	64	5.6	1862	2	T29959	DNA-directed RNA p
1031	64.5	5.7	1477	2	AG3009	hypothetical prote	1104	64	5.6	1870	2	D88486	DNA-directed RNA p
1032	64.5	5.7	1489	2	G98274	polyketide synthet	1105	64	5.6	1975	2	B81192	protein F20H11.2 [
1033	64.5	5.7	1501	2	C94512	hypothetical prote	1106	64	5.6	1995	2	G81044	hemagglutinin/hemo
1034	64.5	5.7	1505	2	S26785	probable retroelem	1107	64	5.6	2055	2	T30259	hemagglutinin/hemo
1035	64.5	5.7	1842	2	T43409	genome polyprotein	1108	64	5.6	2274	2	T30258	multiple PDZ domai
1036	64.5	5.7	1842	2	T338781	probable fatty-acid	1109	64	5.6	2292	1	GNNYEB	adenomatous polypo
1037	64.5	5.7	2570	2	T17451	fatty acid synthas	1110	64	5.6	2292	1	GNNYEB	genome polyprotein
1038	64	5.6	131	2	T25705	fimbriae-associate	1111	64	5.6	2292	2	S55401	genome polyprotein
1039	64	5.6	171	2	H86413	hypothetical prote	1112	64	5.6	2292	2	S20901	capsid polyprotein
1040	64	5.6	230	2	T33364	hypothetical prote	1113	64	5.6	6805	2	S20901	titin - rabbit (fr
1041	64	5.6	234	2	E72456	hypothetical prote	1114	63.5	5.6	101	2	E72458	hypothetical prote
1042	64	5.6	259	2	C81008	methionine aminope	1115	63.5	5.6	149	2	A71074	probable mechymal
1043	64	5.6	268	2	S63630	acid proteinase (E	1116	63.5	5.6	166	2	B85869	NADH2 dehydrogenas
1044	64	5.6	279	2	E82689	conserved hypothet	1117	63.5	5.6	166	2	A91025	NADH dehydrogenase
1045	64	5.6	298	2	D55354	probable epimerase	1118	63.5	5.6	185	2	S20593	alcohol dehydrogen
1046	64	5.6	309	2	A00144	hypothetical prote	1119	63.5	5.6	197	2	T19892	hypothetical prote
1047	64	5.6	309	2	S40749	hypothetical prote	1120	63.5	5.6	197	2	C49247	merozoite surface
1048	64	5.6	314	1	HNZYVW	hemagglutinin prec	1121	63.5	5.6	205	2	S55670	hypothetical prote
1049	64	5.6	314	1	JQ1793	hemagglutinin prec	1122	63.5	5.6	255	2	I47093	MHC OVAR-DQ-ALPHA-
1050	64	5.6	354	2	F65092	hypothetical prote	1123	63.5	5.6	275	2	S09774	hypothetical prote
1051	64	5.6	360	2	S12850	protein TPX - Ther	1124	63.5	5.6	284	2	T28018	hypothetical prote



1125	63.5	5.6	289	2	T41305	hypothetical prote	1198	63.5	5.6	1324	2	S06187	RNA2 polyprotein -
1126	63.5	5.6	296	2	I40258	outer surface prot	1199	63.5	5.6	1326	2	B56395	secretory phosphol
1127	63.5	5.6	296	2	I40267	outer surface prot	1200	63.5	5.6	1332	2	T23024	hypothetical prote
1128	63.5	5.6	296	2	I40256	outer surface prot	1201	63.5	5.6	1382	2	S70310	hypothetical prote
1129	63.5	5.6	296	2	I40250	outer surface prot	1202	63.5	5.6	1460	2	T00095	hypothetical prote
1130	63.5	5.6	296	2	I40260	outer surface prot	1203	63.5	5.6	1465	2	A56395	secretory phosphol
1131	63.5	5.6	313	2	D71363	hypothetical prote	1204	63.5	5.6	1466	2	T17138	CL1AA protein - ra
1132	63.5	5.6	322	2	B82505	conserved hypothet	1205	63.5	5.6	1467	2	T18411	latrophilin-1, bra
1133	63.5	5.6	327	2	I55459	Fra-2 - rat	1206	63.5	5.6	1471	2	T17149	CL1BA protein - ra
1134	63.5	5.6	341	2	F71042	hypothetical prote	1207	63.5	5.6	1472	2	T18413	latrophilin-1, bra
1135	63.5	5.6	357	2	A37440	red-sensitive visu	1208	63.5	5.6	1475	2	S42718	nuclear pore compl
1136	63.5	5.6	366	2	T27312	hypothetical prote	1209	63.5	5.6	1510	2	T17145	CL1AB protein - ra
1137	63.5	5.6	373	1	AJMSQ	glutamate-ammonia	1210	63.5	5.6	1515	2	T17156	CL1BB protein - ra
1138	63.5	5.6	378	2	A12180	hypothetical prote	1211	63.5	5.6	1544	2	T29482	hypothetical prote
1139	63.5	5.6	423	2	T01559	hypothetical prote	1212	63.5	5.6	1624	2	T25592	hypothetical prote
1140	63.5	5.6	427	2	T00465	probable WRKY-type	1213	63.5	5.6	1729	2	T18396	erythrocyte membra
1141	63.5	5.6	432	2	T25471	hypothetical prote	1214	63.5	5.6	1796	2	S65004	probable membrane
1142	63.5	5.6	445	2	I38521	inwardly rectifyin	1215	63.5	5.6	1854	2	S36859	cIPa protein - Clo
1143	63.5	5.6	445	2	S45713	potassium channel	1216	63.5	5.6	2145	2	JC4747	adenylate cyclase
1144	63.5	5.6	446	2	S66268	inward rectifier p	1217	63.5	5.6	2211	1	KFB05	coagulation factor
1145	63.5	5.6	451	2	F97230	probable maltodex	1218	63.5	5.6	2512	1	XYCHEA	enoyl-lacetyl-carrie
1146	63.5	5.6	462	2	S05050	retinoic acid nucl	1219	63.5	5.6	2512	1	D88450	protein F2H11.2 l
1147	63.5	5.6	484	2	T20451	hypothetical prote	1220	63.5	5.6	2700	2	JQ1917	polyprotein - pars
1148	63.5	5.6	498	2	H85040	hypothetical prote	1221	63	5.5	125	2	S24703	Ig heavy chain V6
1149	63.5	5.6	509	2	A35016	cystathionine gamm	1222	63	5.5	126	2	S14131	hypothetical prote
1150	63.5	5.6	512	2	S21171	activin receptor S	1223	63	5.5	135	2	T49996	AtAGP4 - Arabidops
1151	63.5	5.6	532	2	G70986	probable coA ligas	1224	63	5.5	139	2	T05847	hypothetical prote
1152	63.5	5.6	541	2	S40245	heat shock protein	1225	63	5.5	154	2	C71162	hypothetical prote
1153	63.5	5.6	542	2	B86574	60 KD chaperonin l	1226	63	5.5	190	2	T28357	hypothetical prote
1154	63.5	5.6	546	2	H89780	hypothetical prote	1227	63	5.5	204	2	AG2437	hypothetical prote
1155	63.5	5.6	560	2	D83759	methyl-accepting c	1228	63	5.5	204	2	S49031	cadmium-induced pr
1156	63.5	5.6	630	2	A39344	tumor-associated m	1229	63	5.5	259	2	T09317	glycoprotein - hum
1157	63.5	5.6	631	2	I52257	episialin - mouse	1230	63	5.5	291	2	B81407	hypothetical prote
1158	63.5	5.6	649	2	T04606	protein kinase hom	1231	63	5.5	292	2	B89807	exotoxin 9 limport
1159	63.5	5.6	651	2	C56853	membrane glycoprot	1232	63	5.5	309	2	E70319	phosphoribosylanth
1160	63.5	5.6	653	2	A13404	transposase BME12	1233	63	5.5	309	2	T17557	procyclin homolog
1161	63.5	5.6	675	2	D85065	receptor protein k	1234	63	5.5	321	2	T50966	hypothetical prote
1162	63.5	5.6	688	2	T23108	hypothetical prote	1235	63	5.5	326	2	S15749	transforming prote
1163	63.5	5.6	694	2	S68442	Grb2-associated bi	1236	63	5.5	326	2	I48351	fos-related antige
1164	63.5	5.6	699	2	C43674	US4 protein - huma	1237	63	5.5	326	2	G63366	homoserine dehydro
1165	63.5	5.6	702	2	E69498	hypothetical prote	1238	63	5.5	346	2	H84512	hypothetical prote
1166	63.5	5.6	708	2	H64631	outer membrane pro	1239	63	5.5	348	2	D87097	conserved hypothet
1167	63.5	5.6	713	2	B86315	F2H15.20 protein -	1240	63	5.5	348	2	JQ0431	hypothetical 35.5K
1168	63.5	5.6	733	1	S33643	transforming prote	1241	63	5.5	361	2	T19395	hypothetical prote
1169	63.5	5.6	756	2	JC5886	signaling mediator	1242	63	5.5	371	1	TVXLT1	transforming prote
1170	63.5	5.6	761	2	T00940	hypothetical prote	1243	63	5.5	375	2	T33797	hypothetical prote
1171	63.5	5.6	761	2	T03719	probable thyroid r	1244	63	5.5	376	2	S71558	probable cell wall
1172	63.5	5.6	764	2	A84328	Htr2 transducer [i	1245	63	5.5	380	2	T32944	hypothetical prote
1173	63.5	5.6	767	1	WMBEP6	ribonucleoside-dip	1246	63	5.5	382	1	WZV216	I6 43.5K protein -
1174	63.5	5.6	774	2	T22309	hypothetical prote	1247	63	5.5	396	1	C64907	chloramphenicol re
1175	63.5	5.6	777	2	C86454	hypothetical prote	1248	63	5.5	396	2	H85721	probable resistanc
1176	63.5	5.6	782	2	S04047	finger protein zfy	1249	63	5.5	396	2	G90895	hypothetical prote
1177	63.5	5.6	789	2	H71255	probable cell divi	1250	63	5.5	402	2	S42367	lag-2 protein - Ca
1178	63.5	5.6	808	2	T23129	hypothetical prote	1251	63	5.5	412	1	AJHURS	argininosuccinate
1179	63.5	5.6	826	2	T46061	hypothetical prote	1252	63	5.5	426	2	T04985	probable transamin
1180	63.5	5.6	854	1	WMBP22	gene 12 protein -	1253	63	5.5	443	2	E82046	proteinase Hs1VU,
1181	63.5	5.6	861	2	S77409	hypothetical prote	1254	63	5.5	451	2	T15718	hypothetical prote
1182	63.5	5.6	865	2	A47282	calcium-binding pr	1255	63	5.5	453	2	S59436	hypothetical prote
1183	63.5	5.6	880	2	D89756	protein T23E7.2b l	1256	63	5.5	482	2	A12094	hypothetical prote
1184	63.5	5.6	890	2	T21000	hypothetical prote	1257	63	5.5	486	2	AF1575	hypothetical prote
1185	63.5	5.6	926	2	T38198	COP1 coated vesic	1258	63	5.5	486	2	AC1222	acetaldehyde dehyd
1186	63.5	5.6	937	2	A56517	nucleoporin Nup98	1259	63	5.5	487	2	S40820	probable permease
1187	63.5	5.6	977	2	S49004	tyrosine kinase Mp	1260	63	5.5	519	2	A49367	transducin homolog
1188	63.5	5.6	988	2	I50611	protein-tyrosine k	1261	63	5.5	535	2	S18606	phosphoenolpyruvat
1189	63.5	5.6	1009	2	S60248	protein-tyrosine k	1262	63	5.5	535	2	T38244	hypothetical prote
1190	63.5	5.6	1013	1	S04200	NAD ADP-ribosyltra	1263	63	5.5	537	2	B97013	and cellulose-bind
1191	63.5	5.6	1043	2	T13172	gag-like protein p	1264	63	5.5	539	2	I46470	estrogen depend
1192	63.5	5.6	1067	2	T33061	hypothetical prote	1265	63	5.5	544	1	S41389	penton protein (II
1193	63.5	5.6	1138	2	S64484	phosphatidylserine	1266	63	5.5	547	2	S44841	K0647.1 protein -
1194	63.5	5.6	1199	2	T15826	hypothetical prote	1267	63	5.5	559	1	WMBES1	71K upper matrix p
1195	63.5	5.6	1208	2	T27822	hypothetical prote	1268	63	5.5	564	2	T12550	hypothetical prote
1196	63.5	5.6	1218	2	AC3580	1-pyrroline-5-carb	1269	63	5.5	595	2	B82203	methyl-accepting c
1197	63.5	5.6	1262	2	T25168	hypothetical prote	1270	63	5.5	609	2	S36481	E1 protein - human



1271	63	5.5	609	2	T34371	hypothetical prote	1344	62.5	5.5	343	2	F95915	probable sugar ABC
1272	63	5.5	610	1	A49082	calcium-dependent	1345	62.5	5.5	348	2	B90727	galactose-1-phosph
1273	63	5.5	611	2	S76211	hypothetical prote	1346	62.5	5.5	348	2	C85578	galactose-1-phosph
1274	63	5.5	623	2	H69435	indolepyruvate fer	1347	62.5	5.5	356	2	A32945	GTP-binding protei
1275	63	5.5	630	2	A34041	dnAK-type molecula	1348	62.5	5.5	359	2	T31821	hypothetical prote
1276	63	5.5	632	2	C98264	5'-nucleotidase pr	1349	62.5	5.5	364	2	T16837	hypothetical prote
1277	63	5.5	635	2	T37239	serotonin receptor	1350	62.5	5.5	372	2	T23880	hypothetical prote
1278	63	5.5	636	2	AF3020	S-nucleotidase [i	1351	62.5	5.5	385	2	JC7783	RAD 23B protein -
1279	63	5.5	638	2	S36723	FUN36 protein - ye	1352	62.5	5.5	389	2	A38302	pepsin [EC 3.4.23.
1280	63	5.5	640	2	T75114	hypothetical prote	1353	62.5	5.5	391	2	JC6193	tumor suppressor p
1281	63	5.5	672	2	T43716	dnAK-type molecula	1354	62.5	5.5	393	2	T33103	lin-1 protein - Ca
1282	63	5.5	672	2	T43723	dnAK-type molecula	1355	62.5	5.5	396	2	S54999	ubiquinol-cytochro
1283	63	5.5	677	2	T39590	hypothetical prote	1356	62.5	5.5	396	2	W4236	trans-cinnamate 4-
1284	63	5.5	683	2	T37240	serotonin receptor	1357	62.5	5.5	398	1	W2WL42	E2 protein - human
1285	63	5.5	714	2	AF2479	ABC transporter AT	1358	62.5	5.5	412	2	A57468	P-selectin glycopr
1286	63	5.5	719	2	T47727	hypothetical prote	1359	62.5	5.5	426	2	T50944	hypothetical prote
1287	63	5.5	722	2	E71403	hypothetical prote	1360	62.5	5.5	428	1	O4ECAD	damX protein (arob
1288	63	5.5	729	2	T15076	hypothetical prote	1361	62.5	5.5	433	2	T49675	origin recognition
1289	63	5.5	763	2	T22843	hypothetical prote	1362	62.5	5.5	438	1	MHRB	Ig mu chain C regi
1290	63	5.5	776	2	A55448	An receptor nuclea	1363	62.5	5.5	462	1	A29491	retinoic acid rece
1291	63	5.5	779	2	A57177	NIMA-like protein	1364	62.5	5.5	479	1	MHRBM	Ig mu chain C regi
1292	63	5.5	813	2	A72203	cellobiose-phospho	1365	62.5	5.5	493	2	S73752	hypothetical prote
1293	63	5.5	838	2	G81444	molybdopterin-cont	1366	62.5	5.5	503	2	T37119	probable membrane-
1294	63	5.5	843	2	T01438	hypothetical prote	1367	62.5	5.5	513	2	S11439	cellulose 1,4-beta
1295	63	5.5	862	2	S51493	major nitrogen reg	1368	62.5	5.5	513	2	S50915	SN3 protein-bindi
1296	63	5.5	865	2	B96538	probable protein k	1369	62.5	5.5	518	2	T33196	hypothetical prote
1297	63	5.5	918	1	PXBYP	H <sub>2</sub> -exporting ATPas	1370	62.5	5.5	521	2	C82922	methionyl-tRNA syn
1298	63	5.5	986	2	T33135	hypothetical prote	1371	62.5	5.5	538	2	AG2902	conserved hypothet
1299	63	5.5	1002	2	T19226	hypothetical prote	1372	62.5	5.5	545	2	T10662	aromatic amino-aci
1300	63	5.5	1028	2	E85089	probable transposo	1373	62.5	5.5	550	2	H97677	hypothetical prote
1301	63	5.5	1028	2	C98384	protein Cl384.1 [i	1374	62.5	5.5	557	2	JC5487	cellulase [EC 3.2.
1302	63	5.5	1036	2	B69368	hypothetical prote	1375	62.5	5.5	585	1	B70747	probable serine/th
1303	63	5.5	1065	2	S19482	hypothetical prote	1376	62.5	5.5	586	2	D84710	hypothetical prote
1304	63	5.5	1106	2	T18739	hypothetical prote	1377	62.5	5.5	596	2	S61146	probable membrane
1305	63	5.5	1215	2	T43916	chitinase A [impor	1378	62.5	5.5	601	2	T34396	hypothetical prote
1306	63	5.5	1279	2	T13613	hypothetical prote	1379	62.5	5.5	609	2	F87237	phosphoenolpyruvat
1307	63	5.5	1320	1	S66279	proline dehydrogen	1380	62.5	5.5	617	2	A90644	probable membrane
1308	63	5.5	1320	2	A50633	proline dehydrogen	1381	62.5	5.5	617	2	A85495	probable membrane
1309	63	5.5	1636	2	S60403	probable membrane	1382	62.5	5.5	621	1	YRNC	monophenol monooxy
1310	63	5.5	1817	2	T34249	hypothetical prote	1383	62.5	5.5	626	2	S53871	Pmel 17 protein -
1311	63	5.5	1820	2	S71853	genome polyprotein	1384	62.5	5.5	647	2	S26386	transcription fact
1312	63	5.5	1902	2	C97702	cell surface antig	1385	62.5	5.5	653	2	E86787	hypothetical prote
1313	63	5.5	1972	2	S68176	TOG protein - huma	1386	62.5	5.5	671	1	VCWCE	env polyprotein -
1314	63	5.5	2628	2	T28651	hemagglutinin A -	1387	62.5	5.5	697	2	E96752	hypothetical prote
1315	63	5.5	2697	2	T25444	genome polyprotein	1388	62.5	5.5	706	2	T49700	related to AP-1-li
1316	63	5.5	3066	1	JQ1662	genome polyprotein	1389	62.5	5.5	722	2	T37970	probable G2-specif
1317	63	5.5	3163	1	JQ1895	polyketide synthas	1390	62.5	5.5	725	2	JC1300	endo-beta-1,4-gluc
1318	63	5.5	6420	2	T30283	hypothetical prote	1391	62.5	5.5	728	2	F72693	probable phosphoes
1319	62.5	5.5	123	2	B75546	hypothetical prote	1392	62.5	5.5	761	2	A96810	probable Mutator-1
1320	62.5	5.5	130	2	T12478	hypothetical prote	1393	62.5	5.5	761	2	A81985	plus secretin NMA
1321	62.5	5.5	139	2	G98226	hypothetical prote	1394	62.5	5.5	823	2	G90848	probable exonuclea
1322	62.5	5.5	139	2	A13059	hypothetical prote	1395	62.5	5.5	823	2	F90914	hypothetical prote
1323	62.5	5.5	142	2	G84194	hypothetical prote	1396	62.5	5.5	823	2	B85706	probable exonuclea
1324	62.5	5.5	147	2	T34803	hypothetical prote	1397	62.5	5.5	853	2	H70939	probable niB prot
1325	62.5	5.5	157	2	S36784	mucin - rat (fragm	1398	62.5	5.5	873	2	B41054	fasciclin II Pi-li
1326	62.5	5.5	177	2	G75285	hypothetical prote	1399	62.5	5.5	874	2	AC2287	hypothetical prote
1327	62.5	5.5	198	2	S48994	hypothetical prote	1400	62.5	5.5	887	2	G88484	protein F23P12.8 [
1328	62.5	5.5	210	2	S53300	self-incompatibili	1401	62.5	5.5	893	2	A47550	bride of sevenless
1329	62.5	5.5	219	2	G65018	hypothetical prote	1402	62.5	5.5	899	2	C84765	hypothetical prote
1330	62.5	5.5	220	2	AC2961	thiamin-phosphate	1403	62.5	5.5	903	2	T00074	hypothetical prote
1331	62.5	5.5	234	2	T35448	hypothetical prote	1404	62.5	5.5	907	2	T04820	aconitate hydratase
1332	62.5	5.5	238	2	C98322	probable thiamin b	1405	62.5	5.5	929	2	JC6124	diacylglycerol kin
1333	62.5	5.5	245	2	S43565	RoH10.4 protein (	1406	62.5	5.5	955	4	C40045	probable transcrip
1334	62.5	5.5	252	2	T04739	hypothetical prote	1407	62.5	5.5	968	2	S46992	protein p130 - rat
1335	62.5	5.5	277	2	H97266	mind family ATPase	1408	62.5	5.5	988	1	S35362	protein kinase C (
1336	62.5	5.5	287	2	S45662	histone H1 - tomat	1409	62.5	5.5	1018	2	T40253	hypothetical prote
1337	62.5	5.5	289	2	T52354	hypothetical prote	1410	62.5	5.5	1033	2	T48775	Smcx protein (eeca
1338	62.5	5.5	290	2	T44550	hypothetical prote	1411	62.5	5.5	1117	2	T19727	hypothetical prote
1339	62.5	5.5	290	2	T70974	probable dehydroge	1412	62.5	5.5	1197	2	D86317	protein F15H18.21
1340	62.5	5.5	299	2	F84810	hypothetical prote	1413	62.5	5.5	1203	2	H87687	helicase, UvrD/Rep
1341	62.5	5.5	304	2	H68332	T20H2.26 protein -	1414	62.5	5.5	1302	2	T23236	hypothetical prote
1342	62.5	5.5	306	2	T48715	hypothetical prote	1415	62.5	5.5	1309	1	BVBVD9	RAD9 protein - yea
1343	62.5	5.5	314	2	B75588	FraH-related prote	1416	62.5	5.5	1337	2	T30291	dextranase - Strep





SL13530  
CD44E protein, epithelial - human  
C/Species: Homo sapiens (man)  
C/Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
C/Accession: SL13530  
R/Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.  
EMBO J. 10, 343-348, 1991  
A/Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with d  
A/Reference number: SL13530; MUID:91122041; PMID:1991450  
A/Accession: SL13530  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-493 <STA>  
A/Cross-references: UNIPARC:UPI0000159271; EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PID  
C/Keywords: transmembrane protein

Query Match 17.6%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 9.4e-10;  
Matches 66; Conservative 39; Mismatches 100; Indels 75; Gaps 8;  
QY 10 LRABELSIQVSCRMIGITLVSKKANQOLNFTAEKACRLGLSLAGKQOVETALKASFET 69  
DB 17 LSLAQIDLNITCRAGVHVKEKNGRYSISRTAEADLCKAFNSTLPTWAQKEKALSIGFET 76  
QY 70 CSYGVGDFVVISRIISPKNPKCGKNGVGLIWKVPSRQFAAYCYNSSDTWTNSCI---- 125  
DB 77 CRYGFI-EGHVVIPRIHPNSICAANNVGVIILTYNTS-QYDITYCFNASAPPEEDCTSVTD 134  
QY 126 -----VSDST-----YSVASPYSTIPAPTTPPAPASTSIPRKKLIC 186  
DB 135 LFNAFDGPITITIVNRDGRYVQKGYRTNPEDIPSNPTDDDDVSSGSSRSSTSGYI 194  
QY 149 -----VSDST-----YSVASPYSTIPAPTTPPAPASTSIPRKKLIC 186  
DB 195 FYTSTVHPIDPDESPIWTSTDRIPRTWDSSTLTQTAPNTGLVEDLRTGPLSM 254  
QY 187 VTEVFMETSTWSTETFPVENK-----AAFKNEAAG 217  
DB 255 TTQQ-SNSQSFSTSHGLEEDKDHPTTSTLTSSNRNDVTG 293

RESULT 7  
A34424  
CD44 membrane glycoprotein precursor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 01-Dec-2000  
C/Accession: A34424; A34907  
R/Nottenburg, C.; Rees, G.; St. John, T.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989  
A/Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate  
A/Reference number: A34424; MUID:90046829; PMID:2682651  
A/Accession: A34424  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-365 <NOT>  
A/Cross-references: UNIPARC:UPI00000888CD; GB:M27130; NID:g192530; PIDN:AAA37407.1; PID:  
R/Wolfe, E.J.; Gause, W.C.; Palfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.  
J. Biol. Chem. 265, 341-347, 1990  
A/Title: The cDNA sequence of mouse Egp-1 and homology to human CD44 cell surface antige  
A/Reference number: A34907; MUID:90094420; PMID:2403559  
A/Accession: A34907  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 8-195, 'G', 197-365 <WOI>  
A/Cross-references: UNIPARC:UPI000016CFB0; GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:  
C/Superfamily: human cell adhesion protein CD44  
C/Keywords: cell adhesion; glycoprotein; membrane protein

Query Match 17.5%; Score 198.5; DB 2; Length 365;  
Best Local Similarity 31.8%; Pred. No. 7.9e-10;  
Matches 48; Conservative 24; Mismatches 72; Indels 7; Gaps 3;  
QY 13 EELSIQVSCRMIGITLVSKKANQOLNFTAEKACRLGLSLAGKQOVETALKASFETCSY 72

DB 24 QQIDLNVTCRYAGVHVKEKNGRYSISRTAEADLCOAFNSTLPTMDQWKLALSKGFETCRY 83  
QY 73 GWVGDFVVISRIISPKNPKCGKNGVGLIWKVPSRQFAAYCYNSSDTWTNSCIPEITTK 132  
DB 84 GFI-EGHVVIPRIHPNAICAANNHTGVVILVTSNTSHYDITYCFNASAPPEEDC-----TSV 137  
QY 133 DPFNTQTATQTTEFTVSDST-YSVASPYST 162  
DB 138 TDLPSFDPGPTTIVNRDGRYSKKGVT 168

RESULT 8  
JH0518  
lymphocyte homing receptor CD44, splice form CD44R1 - human  
N/Alternate names: cell adhesion molecule core protein CD44E, keratinocyte, cell surfac  
N/Contains: lymphocyte homing receptor CD44, splice form CD44R1; lymphocyte homing rece  
C/Species: Homo sapiens (man)  
C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 31-Dec-2004  
C/Accession: JH0518; JH0519; PH0859; A39209; A42402; A53029; S16147  
R/Dougherty, G.J.; Lanasdorf, P.M.; Cooper, D.L.; Humphries, R.K.  
J. Exp. Med. 174, 1-5, 1991  
A/Title: Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the human CD44  
A/Reference number: JH0518; MUID:91277598; PMID:2056274  
A/Accession: JH0518  
A/Molecule type: mRNA  
A/Residues: 1-426 <DOU>  
A/Cross-references: UNIPROT:Q9UCB0; UNIPARC:UPI0000179519  
A/Experimental source: lymphocytes, cell line KGLa  
A/Accession: JH0519  
A/Molecule type: mRNA  
A/Residues: 1-223, 288-426 <DO>  
A/Cross-references: UNIPARC:UPI000017951A  
R/Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta  
Biochem. Biophys. Res. Commun. 182, 569-578, 1992  
A/Title: The complex CD44 transcriptional unit: alternative splicing of three internal  
A/Reference number: PH0859; MUID:92134271; PMID:1734871  
A/Accession: PH0859  
A/Molecule type: DNA  
A/Residues: 223-357 <COO>  
A/Cross-references: UNIPARC:UPI000017951B  
R/Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G.  
J. Cell Biol. 113, 207-221, 1991  
A/Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfa  
A/Reference number: A39209; MUID:91177958; PMID:2007624  
A/Accession: A39209  
A/Molecule type: mRNA  
A/Residues: 184-376 <BRO>  
A/Cross-references: UNIPARC:UPI000016A690; GB:X55938; NID:g29802; PIDN:CAA39404.1; PID:  
R/Jackson, D.G.; Buckley, J.; Bell, J.I.  
J. Biol. Chem. 267, 4732-4739, 1992  
A/Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by in  
A/Reference number: A42402; MUID:92165834; PMID:1537855  
A/Accession: A42402  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 217-223, 288-359 <JAC>  
A/Cross-references: UNIPARC:UPI000017951C  
A/Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)  
A/Note: variant B  
A/Accession: C42402  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 217-320 <JAC2>  
A/Cross-references: UNIPARC:UPI000017951D  
A/Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)  
A/Note: variant D  
R/Shepley, M.P.; Racaniello, V.R.  
J. Virol. 68, 1301-1308, 1994  
A/Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphoc;  
A/Reference number: A53029; MUID:94149816; PMID:7508992  
A/Accession: A53029



R;Tanabe, K.K.; Nishi, T.; Saya, H.  
Mol. Carcinog. 7, 213-220, 1993  
A;Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44 a  
A;Reference number: 157483; MUID:93356912; PMID:8352881  
A;Accession: I77371  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-395 <RES>  
A;Cross-references: UNIPARC:UPI000016B3F6; GB:S66400; NID:G435697; PID: AAB27919.1; PID:  
C;Genetics:  
A;Gene: GDB:CD44  
A;Cross-references: GDB:120739; OMIM:107269  
A;Map position: lipter-llp13  
A;Introns: 257/1  
C;Superfamily: human cell adhesion protein CD44

Query Match	17.3%;	Score 196;	DB 2;	Length 395;
Best Local Similarity	30.9%;	Pred. No. 1.4e-09;		
Matches	54;	Conservative 23;	Mismatches 84;	Indels 14; Gaps 5

  

Qy	10	LRAEELSIQVSCRINGITLVSKKANQQLNFTAEKACRLGLSLAGKQDVETALKASPT 69
		: : :     : : :     : : :     : : :     : : :
Db	17	LSLAQIDLNITCRPAVGHVKEKNGRYSISRTEAADLCKAFNLTPTMAQMEKALSIGFT 76
		: : :     : : :     : : :     : : :     : : :
Qy	70	CSYGWGDCGFVVISRISPNPKGNGVGLVTKVPVSRQFAAYCNSSDWTWNSCIPETI 129
		: : :     : : :     : : :     : : :     : : :
Db	77	CRYGFI-EGHVVIPIRHNSICANNVTGVILTSNTS-QYDTVCFNASAPPEEDC----- 129
		: : :     : : :     : : :     : : :     : : :
Qy	130	TTKQPIFNQTATQTTFEIVSDST-YSVASPYSTIPA-----PTTTPPAPASTS 177
		: : :     : : :     : : :     : : :     : : :
Db	130	TSVTLDPNADFQPIITTVNEDGTRYVQKGYRTNPEDIVPSNPTDDDDVSSGSSS 184
		: : :     : : :     : : :     : : :     : : :

RESULT 12  
S45305  
CD44 antigen precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:/Date: 20-Oct-1994 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:/Accession: S45305  
R:Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.  
Biochim. Biophys. Acta 1218, 112-114, 1994  
A:/Title: Molecular cloning of the canine CD44 antigen cDNA.  
A:/Reference number: S45305; MUID:94250687; PMID:7514890  
A:/Accession: S45305  
A:/Status: preliminary  
A:/Molecule type: mRNA  
A:/Residues: 1-351 <MIL>  
A:/Cross-references: UNIPROT:Q28284; UNIPARC:UPI0000127367; EMBL:Z27115; NID:G473226; PTD  
C:/Superfamily: human cell adhesion protein CD44

Query Match	17.1%;	Score 194;	DB 2;	Length 351;
Best Local Similarity	30.3%;	Pred. No. 1.9e-09;		
Matches	53;	Conservative 25;	Mismatches 83;	Indels 14; Gaps 5;
Qy	10	LRAELSIQVSRIMGITLVSRRANQQLNTEAKACRLGLSLAGKQDQVETALKASFET	69	
Db	10	LSLAQIDLNITCRYAGVFHVKNGRYSISRATAADLCKAFNSTLPTTWAQERALSVMGFET	69	
Qy	70	CSYGWGDGFWIISRIPNPKCGKNGGVGLIKWVPVSRQFAAYCVNSSDTWTNSCIPRII	129	
Db	70	CRYGPT-EGHVPIRPIOPNAICAAHNTGVY-LISNTSQIDTYCFNASAPPEEDC-----	122	
Qy	130	TTKDPINFNTQATQTTFEIVSDST-YSVASPYSTIPA-----PTTTTPAPASTS	177	
Db	123	TSVTHLPNAPDGPITITIVNRDGRYSOKGEYRNPEDINPSNPTDDDVSSGSSS	177	

RESULT 13  
A53286  
cell-surface glycoprotein CD44 precursor - bovine  
N:Alternate names: CD44 protein  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 02-May-1994 #sequence revision 18-Nov-1994 #text change 09-Jul-2004

C/Accession: A53286; S22123  
R/Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.  
Mol. Immunol. 28, 1131-1135, 1991  
A/Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.  
A/Reference number: A53286; MUID:92017904; PMID:1922105  
A/Accession: A53286  
A/Molecule type: mRNA  
A/Residues: 1-366 <BOS>  
A/Cross-references: UNIPROT:Q9423; UNIPARC:UPI0000127366; EMBL:X62881; NID:g186; PIDN:"  
A/Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBI:P:63419)  
C/Superfamily: human cell adhesion protein CD44  
C/Keywords: cell adhesion; glycoprotein; transmembrane protein  
F/1-20/Domain: signal sequence #status predicted <SIG>  
F/21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>  
F/274-294/Domain: transmembrane #status predicted <TMW>

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Query Match          17.1%; Score 194; DB 2; Length 366;
Best Local Similarity 29.9%; Pred. No. 2e-09;
Matches 56; Conservative 27; Mismatches 86; Indels 18; Gaps 6;

Qy      5  LVQGSRLABELSIQVSCRMGITVLVKCANQOQLNPTFEAKERLLGLSLAGKQDVETALK 64
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      14  LVQLSL--AQIDLNITCRVAGVPHVEKNGYSISKTEAADLCKAFNSTLPTMAQMEARN 71
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy      65  ASFETCSYGVWGDFVFIISRI SPNPKGRNGVGLVWKVPVSRQFAAYCYNSSDWTNNSC 124
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      72  IGPETCRYGFI-EGHVVIIPRIHPNSICAAANTGVVILTSNTS-QYDTICFNASAPPGEDC 129
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy      125  IPBIIITKDPINFNTQTATQTTFIVSDST-YSVASPYSTIP-----APTTTTPAPAS 175
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      130  -----TSVDLDPNAFEGPTITIVNRDGRYTKKGERTNPEDINPSVVSPPSPPODEMS 194
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

```

QY      176 TSIPRK 182
      :
Db      185 SGSPSR 191

RESULT 14
S24240
lymphocyte surface antigen CD44 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: I46245; S24240
R;Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; But
Immunogenetics 37, 474-477, 1993
A;Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.
A;Reference number: I46245; MUID:93170897; PMID:8436424
A;Accession: I46245
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-359 <TA2>
A;Cross-references: UNIPROT:Q05078; UNIPARC:UPI0000127369; EMBL:X66862; NID:g1059; PIDN
C;Superfamily: human cell adhesion protein CD44
C;Keywords: surface antigen; transmembrane protein

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Query Match	16.2%;	Score 183.5;	DB 2;	Length 359;
Best Local Similarity	29.4%;	Pred. No. 1.6e-08;		
Matches	50;	Conservative 24;	Mismatches 87;	Indels 9; Gaps 5;
QY	10	LRAEELSIQVSRIMGIIIVLSKKANQQLNFTAEACRLGLSLACKQDVEITALKASPET	69	
DB	17	LSLAQIDMLNITCRYAGVFHVERKNGRYSISRTAEADLCKAFNSTLPTMAQMKALNIGFET	76	
QY	70	CSYGVWGDGFVVISIRISPNPKCGKGGVGLIKWVPVSROFAAYCYNSSSTWTNSCIPEII	129	
DB	77	CRIGFI-EGHVVIPIHPNSICAANNVGYILTSNTS-QYDYTCFNASAPPEDC-----	129	
QY	130	TKYKDIPIENTQATQTQTEFIVDSGT-YSVASPYSTIPAPTTTPPAPASTSI	178	
DB	130	TSVTOLPNPAFEGPIRTITIVNRDGTRYTKKGEYRNP-EDINPSTPADDDV	178	





GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:08:48 ; Search time 47.4764 Seconds  
(without alignments)  
3269.333 Million cell updates/sec

Title: US-10-063-510-6\_COPY\_16\_235  
Perfect score: 1136  
Sequence: 1 TTRLLVQSLRABELSIQVS.....TEPFVENKAAPNEAAGFGG 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1136	100.0	322	2	Q9UNF4_HUMAN
2	1122	98.8	322	2	O8TC18_HUMAN
3	1117	98.3	322	2	Q9Y5V7_HUMAN
4	730	64.3	322	2	O6UC88_BOVIN
5	680	59.9	318	2	O8BRC0_MOUSE
6	680	59.9	318	2	Q9N8E4_MOUSE
7	526.5	46.3	201	2	Q7Y822_PIG
8	245	21.6	392	2	O58R15_XENLA
9	241	21.2	441	2	O6GM56_XENLA
10	226	19.9	437	2	O6P8A2_XENTR
11	213.5	18.8	503	1	CD44_RAT
12	213.5	18.8	780	2	O08779_RAT
13	211.5	18.6	364	2	Q70509_RAT
14	211	18.6	265	2	Q98SR5_ANAPL
15	209.5	18.4	398	2	Q90ZL8_ANAPL
16	209.5	18.4	778	1	CD44_MOUSE
17	207	18.2	362	1	CD44_CRIGR
18	205	18.0	431	1	CD44_MESAU
19	203.5	17.9	362	1	CD44_PAPHA
20	203	17.9	742	2	Q9UQ36_HUMAN
21	202	17.8	742	1	CD44_HUMAN
22	200.5	17.6	580	2	O80X37_MOUSE
23	198.5	17.5	168	2	Q90ZL6_ANAPL
24	198.5	17.5	493	2	O86227_HUMAN
25	198.5	17.5	493	2	O9R9V4_PONPY
26	197	17.3	396	2	O9W6S4_CHICK
27	197	17.3	719	2	Q9H5A5_HUMAN
28	196	17.3	294	2	Q92493_HUMAN
29	196	17.3	361	2	O86T72_HUMAN
30	196	17.3	361	2	O8N694_HUMAN
31	195	17.2	364	2	O97569_CERSI

351	1	CD44_CANFA	Q28284	canis fami
366	1	Q9H5A7_BOVIN	Q29423	bos taurus
676	2	Q9H5A7_HUMAN	Q9H5A7	homo sapien
371	2	Q9H5A3_HUMAN	Q9H5A3	homo sapien
338	2	Q9H5A4_HUMAN	Q9H5A4	homo sapien
470	2	Q9H5A6_HUMAN	Q9H5A6	homo sapien
359	1	CD44_HORSE	Q05078	equus cabal
153	2	Q4SI95_TETNG	Q4SI95	tetraodon n
537	1	PGCA_PIG	Q29011	sus scrofa
494	2	Q9BGH3_PIG	Q9BGH3	sus scrofa
3562	1	CSPG2_CHICK	Q90953	gallus gall
277	1	TSG6_HUMAN	P98066	homo sapien
277	2	Q33T17_HUMAN	Q53I17	homo sapien
275	1	TSG6_MOUSE	O08859	mus musculu
280	2	Q5W1C4_BOVIN	O5W1C4	bos taurus
2109	1	PGCA_CHICK	P07898	gallus gall
243	2	Q4S9S8_TETNG	Q4S9S8	tetraodon n
2571	1	STAB1_MOUSE	Q814Y4	mus musculu
2333	1	PGCA_CANFA	Q28343	canis fami
2109	2	P79787_CHICK	P79787	gallus gall
276	1	TSG6_RABIT	P98065	oryctolagus
514	2	Q629I3_RAT	Q629I3	rattus norv
721	2	Q6PID9_HUMAN	Q6PID9	homo sapien
1046	2	Q4SIV9_TETNG	Q4SIV9	tetraodon n
2124	1	PGCA_RAT	P07897	rattus norv
314	2	Q4SE78_TETNG	Q4SE78	tetraodon n
2132	1	PGCA_MOUSE	O61282	mus musculu
883	1	PGCB_MOUSE	O61361	mus musculu
883	2	Q80WT7_MOUSE	Q80WT7	mus musculu
2415	1	PGCA_HUMAN	P16112	homo sapien
1431	1	STAB2_RAT	O8CFM6	rattus norv
2149	2	Q6XL68_BOVIN	Q6XL68	bos taurus
2327	2	Q6XL66_BOVIN	Q6XL66	bos taurus
2364	1	PGCA_BOVIN	P13608	bos taurus
2365	2	Q6XL67_BOVIN	Q6XL67	bos taurus
671	2	Q5T3I5_HUMAN	O5T3I5	homo sapien
850	2	Q59F90_HUMAN	Q59F90	homo sapien
883	1	PGCB_RAT	P55068	rattus norv
911	1	PGCB_HUMAN	Q96GW7	homo sapien
911	2	Q5SZI0_HUMAN	Q5SZI0	homo sapien
266	2	Q5I051_XENLA	Q5I051	xenopus lae
536	2	Q5RG03_BRARE	Q5RG03	brachydanio
845	2	Q4RV64_TETNG	Q4RV64	tetraodon n
1515	2	Q4T6A4_TETNG	Q4T6A4	tetraodon n
2586	2	Q4RUP1_TETNG	Q4RUP1	tetraodon n
386	2	Q4S472_TETNG	Q4S472	tetraodon n
2760	2	Q4T8G9_TETNG	Q4T8G9	tetraodon n
2570	1	STAB1_HUMAN	Q9NY15	homo sapien
383	2	Q5BJ60_XENTR	Q5BJ60	xenopus tro
394	1	PGCA_RABIT	Q28670	oryctolagus
360	1	HPLN3_HUMAN	Q96A86	homo sapien
516	2	Q81WX2_HUMAN	Q81WX2	homo sapien
1091	2	Q4SE77_TETNG	Q4SE77	tetraodon n
1152	2	Q90WM2_XENLA	Q90WM2	xenopus lae
912	1	PGCB_BOVIN	Q28062	bos taurus
1570	2	Q7SZI3_BRARE	Q7SZI3	brachydanio
2559	1	STAB2_MOUSE	Q84RU0	mus musculu
313	2	Q4SHL9_TETNG	Q4SHL9	tetraodon n
359	2	Q7ZX17_XENLA	Q7ZX17	xenopus lae
3396	1	CSPG2_HUMAN	P13611	homo sapien
3410	2	Q59FG9_HUMAN	Q59FG9	homo sapien
368	2	Q8BS97_MOUSE	Q8BS97	mus musculu
368	2	Q4VA91_MOUSE	Q4VA91	mus musculu
2738	1	CSPG2_RAT	Q9ERB4	rattus norv
3358	1	CSPG2_MOUSE	Q62059	mus musculu
744	2	Q4RLD6_TETNG	Q4RLD6	tetraodon n
370	2	Q7M2W7_PIG	Q7M2W7	sus scrofa
394	2	O6DCI6_XENLA	O6DCI6	xenopus lae
3381	1	CSPG2_BOVIN	P81282	bos taurus
1039	2	Q4S473_TETNG	Q4S473	tetraodon n
341	1	HPLN2_MOUSE	Q9EM83	mus musculu
340	1	HPLN2_HUMAN	Q9G9V7	homo sapien
340	2	Q5T3J0_HUMAN	Q5T3J0	homo sapien



105	112.5	9.9	417	1	PCCB_FELCA	P41725 felis silve	178	93	8.2	1155	2	Q4JA20_SULAC	Q4ja20 sulfolobus
106	112	9.9	210	2	Q8C9U7_MOUSE	Q8c9u7 mus musculus	179	92.5	8.1	215	2	Q61413_CAEBR	Q61413 caenorhabdi
107	112	9.9	2551	1	STAB2_HUMAN	Q8wwq8 h stabilin-	180	92.5	8.1	232	2	Q4V322_DROME	Q4v322 drosophila
108	111	9.8	354	2	Q86W61_HUMAN	Q86w61 homo sapien	181	92.5	8.1	236	2	Q4V400_DROME	Q4v400 drosophila
109	111	9.8	359	2	Q5R1X6_RAT	Q5rlx6 rattus norv	182	92.5	8.1	247	2	Q8MKY7_DROME	Q8mk7 drosophila
110	111	9.8	537	2	Q4IQU7_GIBZE	Q4iqu7 gibberella	183	92.5	8.1	276	2	Q54NG3_DICDI	Q54ng3 dictyosteli
111	110.5	9.7	1257	1	CSFG3_RAT	P55067 rattus norv	184	92.5	8.1	289	2	Q60T22_CAEBR	Q60t22 caenorhabdi
112	110	9.7	363	2	Q6NV41_BRARE	Q6nv41 brachydanio	185	92.5	8.1	400	1	HPLN4_MOUSE	Q80wm4 mus musculu
113	110	9.7	1290	2	Q9W6E1_CHICK	Q9w6e1 gallus gall	186	92.5	8.1	448	2	Q61C01_CAEBR	Q61c01 caenorhabdi
114	109	9.6	1321	1	CSFG3_HUMAN	Q44594 homo sapien	187	92.5	8.1	1034	2	Q613E9_CAEBR	Q613e9 caenorhabdi
115	109	9.6	1335	2	Q4LE67_HUMAN	Q4le67 homo sapien	188	92.5	8.1	1491	2	Q4QDK4_LEIMA	Q4qdk4 leishmania
116	108.5	9.6	341	1	HPLN2_RAT	Q8eem2 rattus norv	189	92	8.1	347	2	Q8SYW5_DROME	Q8syw5 drosophila
117	108.5	9.6	1441	2	Q4S3C4_TETNG	Q4s3c4 tetradodon n	190	92	8.1	500	2	Q864U4_BOVIN	Q864u4 bos taurus
118	108	9.5	354	1	HPLN1_HUMAN	P10915 homo sapien	191	92	8.1	504	2	Q54FD8_DICDI	Q54fd8 dictyosteli
119	108	9.5	359	1	HPLN3_MOUSE	Q80wm5 mus musculus	192	92	8.1	738	2	Q5WN81_CAEBR	Q5wn81 caenorhabdi
120	107	9.4	354	1	HPLN1_RAT	P03994 rattus norv	193	92	8.1	846	2	Q01699_CAEBL	Q01699 caenorhabdi
121	107	9.4	355	1	HPLN1_CHICK	P07354 gallus gall	194	92	8.1	989	2	Q83U76_CHLTR	Q83u76 chlamydia t
122	107	9.4	356	1	HPLN1_MOUSE	Q8qup5 mus musculus	195	92	8.1	989	2	Q84F09_CHLTR	Q84f09 chlamydia t
123	107	9.4	862	2	Q8UPF8_HUMAN	Q8uf98 homo sapien	196	92	8.1	1121	2	Q59YM6_CANAL	Q59ym6 candida alb
124	107	9.4	1268	1	CSFG3_MOUSE	P55066 mus musculus	197	92	8.1	1121	2	Q7Z884_CANAL	Q7z884 candida alb
125	107	9.4	1321	1	CSFG3_PANTR	Q5is41 pan troglod	198	92	8.1	1879	2	Q4VZL0_CUCSA	Q4vz10 cucumis sat
126	106.5	9.4	816	2	Q7O474_RAT	Q7o474 rattus norv	199	91.5	8.1	288	2	Q6QPC9_9ADEN	Q6qpc9 simian aden
127	106	9.3	1059	2	Q5ISN4_MACPA	Q5isn4 macaca fasc	200	91.5	8.1	651	2	Q61VZ5_CAEBR	Q61vz5 caenorhabdi
128	105	9.2	354	1	HPLN1_BOVIN	P55252 bos taurus	201	91.5	8.1	860	2	Q7RZK3_NEUCR	Q7rzk3 neurospora
129	104.5	9.2	862	1	CSFG3_MAGNE	Q28858 macaca neme	202	91.5	8.1	1126	2	Q9VGK5_DROME	Q9vgk5 drosophila
130	104	9.2	139	2	Q9S370_HUMAN	Q9s370 homo sapien	203	91	8.0	174	2	Q7YTP1_CAEBL	Q7ytp1 caenorhabdi
131	104	9.2	354	1	HPLN1_HORSE	Q28381 equus cabal	204	91	8.0	213	2	Q5T317_HUMAN	Q5t317 homo sapien
132	104	9.2	354	1	HPLN1_PIGE	P10859 sus scrofa	205	91	8.0	488	2	Q09586_CAEBL	Q09586 caenorhabdi
133	103.5	9.1	1197	2	Q5IS86_9PRIM	Q5is86 saimiri bol	206	91	8.0	576	2	Q61MD1_CAEBR	Q61md1 caenorhabdi
134	103	9.1	80	2	Q86U21_HUMAN	Q86u21 homo sapien	207	91	8.0	624	2	Q19780_CAEBL	Q19780 caenorhabdi
135	103	9.1	231	2	Q5T316_HUMAN	Q5t316 homo sapien	208	91	8.0	644	2	Q54D31_DICDI	Q54d31 dictyosteli
136	102	9.0	739	2	Q02360_CAEBL	Q02360 caenorhabdi	209	91	8.0	698	2	Q61SH2_CAEBR	Q61sh2 caenorhabdi
137	101.5	8.9	380	2	Q02343_CAEBL	Q02343 caenorhabdi	210	91	8.0	876	2	Q619L5_CAEBR	Q619l5 caenorhabdi
138	101.5	8.9	411	2	Q7O2X4_HRV1	Q7o2x4 human herpe	211	90.5	8.0	278	2	Q4WIP3_ASPFU	Q4wip3 aspergillus
139	101.5	8.9	1853	2	Q7KT96_DROME	Q7kt96 drosophila	212	90.5	8.0	402	1	ODP2_MYCPN	P75332 mycoplasma
140	101.5	8.9	1893	2	Q8NKC9_DROME	Q8nkc9 drosophila	213	90.5	8.0	411	2	Q6P6W1_RAT	Q6p6w1 rattus norv
141	101	8.9	708	2	Q18175_CAEBL	Q18175 caenorhabdi	214	90.5	8.0	497	2	Q8QVC4_9REOV	Q8qvc4 eyach virus
142	101	8.9	2535	2	Q755B8_ASHGO	Q755b8 ashbya goss	215	90.5	8.0	699	2	Q8QVE9_9REOV	Q8qve9 eyach virus
143	100.5	8.8	402	1	HPLN4_HUMAN	Q86uw8 homo sapien	216	90.5	8.0	952	2	Q86AH0_DICDI	Q86ah0 dictyosteli
144	100	8.8	319	2	Q4S1V7_TETNG	Q4s1v7 tetradodon n	217	90.5	8.0	972	2	Q60Q42_CAEBR	Q60q42 caenorhabdi
145	99.5	8.8	335	2	Q60H44_BRARE	Q60h44 brachydanio	218	90.5	8.0	1165	2	Q60NC3_CAEBR	Q60nc3 caenorhabdi
146	99.5	8.8	397	2	Q7O2X3_HRV1	Q7o2x3 human herpe	219	90.5	8.0	1175	2	Q9VRL7_DROME	Q9vrl7 drosophila
147	99.5	8.8	577	2	Q52GY0_CAEBL	Q52gy0 caenorhabdi	220	90.5	8.0	1976	2	Q9V9I8_DROME	Q9v9i8 drosophila
148	99	8.7	388	2	Q4H2F0_HPV27	Q4h2f0 human papil	221	90	7.9	388	1	VE2_HPV27	P36789 human papil
149	98.5	8.7	441	2	Q5BA48_EMENI	Q5ba48 aspergillus	222	90	7.9	812	2	Q61KES_CAEBR	Q61kes caenorhabdi
150	98.5	8.7	573	2	Q8CJD9_RAT	Q8cjd9 rattus norv	223	90	7.9	948	2	Q86AV9_DICDI	Q86av9 d phosphati
151	98.5	8.7	4370	2	Q4Q1Q2_LEIMA	Q4q1q2 leishmania	224	90	7.9	1167	2	Q7RWQ7_NEUCR	Q7rwg7 neurospora
152	98	8.6	527	2	Q54VQ0_DICDI	Q54vq0 dictyosteli	225	89.5	7.9	411	1	LAMP2_RAT	P17046 rattus norv
153	98	8.6	2112	2	Q3VEL9_DROME	Q3vel9 drosophila	226	89.5	7.9	440	2	Q9P566_NEUCR	Q9p566 neurospora
154	97.5	8.6	297	2	Q7PR85_ANOGA	Q7pr85 anopheles g	227	89.5	7.9	471	2	Q9VMG7_DROME	Q9vmg7 drosophila
155	97	8.5	390	1	VGLI_HRV11	P06487 human herpe	228	89.5	7.9	558	2	Q4JK70_DERPT	Q4jk70 dermatophag
156	97	8.5	390	2	Q7O2X7_HRV1	Q7o2x7 human herpe	229	89.5	7.9	560	2	Q54LP6_DICDI	Q54lp6 dictyosteli
157	97	8.5	889	2	Q4RUP0_TETNG	Q4rup0 tetradodon n	230	89.5	7.9	917	2	Q7QJ16_ANOGA	Q7qj16 anopheles g
158	97	8.5	1604	2	Q4SNJ3_TETNG	Q4sna3 tetradodon n	231	89.5	7.9	1349	2	Q8WQ4_HUMAN	Q8wq4 homo sapien
159	96	8.5	173	2	Q4KTX2_CEREL	Q4ktx2 cervus elap	232	89	7.9	232	2	Q5BDD1_EMENI	Q5bdd1 aspergillus
160	96	8.5	3178	1	Y589_CAEBL	Q9624 caenorhabdi	233	89	7.8	307	1	SGS3_DROME	P02840 drosophila
161	95.5	8.4	481	2	Q9XUF4_CAEBL	Q9xuf4 caenorhabdi	234	89	7.8	316	2	Q9U970_TOXCA	Q9u970 toxocara ca
162	95.5	8.4	732	2	Q54FJ3_DICDI	Q54fj3 dictyosteli	235	89	7.8	359	2	Q5KCB0_CRYNE	Q5kcb0 cryptococcu
163	95	8.4	294	2	Q54FY4_DICDI	Q54fy4 dictyosteli	236	89	7.8	392	2	Q59F20_HUMAN	Q59f20 homo sapien
164	95	8.4	424	2	Q3FGW0_BRATH	Q3fgw0 arabidopsis	237	89	7.8	416	1	LAMP1_HUMAN	P11279 homo sapien
165	94.5	8.3	182	2	Q91O08_DROME	Q91o08 drosophila	238	89	7.8	417	2	Q8WU33_HUMAN	Q8wu33 homo sapien
166	94.5	8.3	183	2	Q9VT37_DROME	Q9vt37 drosophila	239	89	7.8	429	2	P79046_9ASCO	P79046 humicola gr
167	94.5	8.3	281	2	Q4KS19_9ADEN	Q4ks19 human adeno	240	89	7.8	482	2	Q6BSZ9_DEBHA	Q6bsz9 debaryomyce
168	94.5	8.3	407	2	Q564S9_CAEBL	Q564s9 caenorhabdi	241	89	7.8	503	1	NAS14_CAEBL	Q19269 caenorhabdi
169	94.5	8.3	519	2	Q7YTR7_CAEBL	Q7ytr7 caenorhabdi	242	89	7.8	603	2	Q6CB49_YARLI	Q6ceb9 yarrowia li
170	94.5	8.3	1079	2	Q8N4S7_CAEBL	Q8n4s7 caenorhabdi	243	89	7.8	648	2	Q4QGJ2_LEIMA	Q4qgj2 leishmania
171	94.5	8.3	1748	2	Q54FL9_DICDI	Q54fl9 dictyosteli	244	89	7.8	860	2	Q5WNQ1_CAEBR	Q5wnq1 caenorhabdi
172	94.5	8.3	1795	2	Q76894_DROME	Q76894 drosophila	245	89	7.8	1521	2	Q7Q1W8_ANOGA	Q7q1w8 anopheles g
173	94	8.3	1117	2	Q54S26_DICDI	Q54s26 dictyosteli	246	89	7.8	1569	2	Q54DM4_DICDI	Q54dm4 dictyosteli
174	93.5	8.2	397	2	Q7O2X6_HRV1	Q7o2x6 human herpe	247	89	7.8	1708	2	Q7XWZ9_ORYSA	Q7xwz9 oryza sativ
175	93	8.2	405	2	Q66H22_BRARE	Q66h22 brachydanio	248	88.5	7.8	389	2	Q61129_CAEBR	Q61129 caenorhabdi
176	93	8.2	478	2	Q7YX15_CAEBL	Q7yx15 caenorhabdi	249	88.5	7.8	582	2	Q8IR74_DROME	Q8ir74 drosophila
177	93	8.2	916	2	Q7YZ10_MONBE	Q7yz10 monosiga br	250	88.5	7.8	662	1	MUC1_XENLA	Q05049 xenopus lae

251	88.5	7.8	764	2	Q4WY10 ASPERGILLUS	Q4WY10 ASPERGILLUS	324	85.5	7.5	786	2	Q21027 CAEBEL	Q21027 caenorhabdi
252	88.5	7.8	901	2	Q9H195 HUMAN	Q9h195 homo sapien	325	85.5	7.5	841	2	Q6R8J4 BRARE	Q6r8j4 brachydanio
253	88.5	7.8	956	2	Q60MG7 CAEBER	Q60mg7 caenorhabdi	326	85.5	7.5	866	2	Q4PDE9 USTWA	Q4pde9 ustilago ma
254	88.5	7.8	1038	2	Q4T3K8 TETNG	Q4t3k8 tetraodon n	327	85.5	7.5	895	2	Q80973 ARATH	Q80973 arabidopsis
255	88.5	7.8	1101	1	GUNC_CELFI	PI4090 cellulomona	328	85.5	7.5	908	2	Q59PF9 CANAL	Q59pf9 candida alb
256	88.5	7.8	1148	2	Q6CBJ2 YARLI	Q6cbj2 yarrowia li	329	85.5	7.5	935	2	Q6R8J3 BRARE	Q6r8j3 brachydanio
257	88.5	7.8	2273	2	Q63HU2 BURPS	Q63hu2 burkholderi	330	85.5	7.5	951	2	Q9FVX8 ORYSA	Q9fvx8 oryza sativ
258	88	7.7	103	2	Q9TTB3 FIG	Q9ttb3 sus scrofa	331	85.5	7.5	977	2	Q6R8J2 BRARE	Q6r8j2 brachydanio
259	88	7.7	239	2	Q55G69 DICDI	Q55c69 dictyosteli	332	85.5	7.5	1209	2	Q4SFS8 TETNG	Q4sfs8 tetraodon n
260	88	7.7	302	2	Q55XK5 CRYNE	Q55xk5 cryptococcu	333	85.5	7.5	1367	1	MUCL_YEAST	Q4sfs8 tetraodon n
261	88	7.7	302	2	Q5KWC9 CRYNE	Q5kmc9 cryptococcu	334	85.5	7.5	1367	1	MUCL_YEAST	Q4sfs8 tetraodon n
262	88	7.7	359	2	Q5CUB9 CRYNE	Q5cub9 cryptococcu	335	85.5	7.5	1367	1	MUCL_YEAST	Q4sfs8 tetraodon n
263	88	7.7	382	2	Q6C971 YARLI	Q6c971 yarrowia li	336	85.5	7.5	2448	2	Q8WQ5 HUMAN	Q8wq5 homo sapien
264	88	7.7	456	2	Q9U2W2 CAEBEL	Q9u2w2 caenorhabdi	337	85.5	7.5	4862	2	Q5R127 BRARE	Q5r127 brachydanio
265	88	7.7	487	2	Q4U479 ANOAG	Q4u479 anopheles g	338	85	7.5	6995	2	Q9GRK2 HUMAN	Q9grk2 homo sapien
266	88	7.7	602	2	Q8YV91 ANASP	Q8yv91 anabaena sp	339	85	7.5	172	2	Q8VC95 MOUSE	Q8vc95 mus musculu
267	88	7.7	616	2	Q8R0X0 MOUSE	Q8r0x0 mus musculu	340	85	7.5	265	2	Q9GZE5 CAEBEL	Q9gze5 caenorhabdi
268	88	7.7	656	2	Q8BUE7 MOUSE	Q8bue7 mus musculu	341	85	7.5	345	2	Q691Y8 ANOSA	Q691y8 anolis sagr
269	88	7.7	716	2	Q9NYE4 HUMAN	Q9nye4 homo sapien	342	85	7.5	429	2	Q76430 CAEBEL	Q76430 caenorhabdi
270	88	7.7	730	2	Q86A28 DICDI	Q86a28 dictyosteli	343	85	7.5	449	2	Q71UN8 CAEBEL	Q71un8 caenorhabdi
271	88	7.7	931	2	Q51LJ1 MAGGR	Q51lj1 magnaporthe	344	85	7.5	569	2	Q9KGV9 LISMO	Q9kgv9 listeria mo
272	88	7.7	1007	2	Q5P0B5 AZOSE	Q5p0b5 azoarcus sp	345	85	7.5	612	2	Q622S9 CAEBR	Q622s9 caenorhabdi
273	88	7.7	1051	2	Q6C1J9 YARLI	Q6c1j9 yarrowia li	346	85	7.5	626	2	Q9NDD1 LEITR	Q9ndd1 leishmania
274	88	7.7	1254	2	Q418T5 CAEBEL	Q418t5 caenorhabdi	347	85	7.5	627	1	PKNB_LACLA	Q9c6t5 lactococcus
275	87.5	7.7	299	2	Q5H2T1 XANOR	Q5h2t1 xanthomonas	348	85	7.5	852	2	Q6CIA5 YARLI	Q6cia5 yarrowia li
276	87.5	7.7	555	2	Q9U6R7 DERPA	Q9u6r7 dermatophag	349	85	7.5	879	2	Q4IC17 GIBZE	Q4ic17 gibberella
277	87.5	7.7	653	2	Q59VC5 CANAL	Q59vc5 candida alb	350	85	7.5	961	2	Q5ATY9 EMENI	Q5aty9 aspergillus
278	87.5	7.7	653	2	Q8NK55 CANAL	Q8nk55 candida alb	351	85	7.5	961	2	Q92223 EMENI	Q92223 emericella
279	87.5	7.7	752	2	Q52CR1 MAGGR	Q52cr1 magnaporthe	352	85	7.5	991	2	Q83UW2 CHLTR	Q83uw2 chlamydia t
280	87.5	7.7	997	1	VGNM_APMV	F38485 andean pota	353	85	7.5	991	2	Q84FV0 CHLTR	Q84fv0 chlamydia t
281	87.5	7.7	1085	1	CASR_BOVIN	F35384 bos taurus	354	85	7.5	1016	1	PMPH_CHLOR	Q84880 chlamydia t
282	87	7.7	235	2	Q63349 RAT	Q63349 rattus norv	355	85	7.5	1025	2	Q62609 CAEBR	Q626g9 caenorhabdi
283	87	7.7	264	2	Q80XS5 MOUSE	Q80xs5 mus musculu	356	85	7.5	1049	2	Q960E6 DROME	Q960e6 drosophila
284	87	7.7	391	2	Q753G3 ASHGO	Q753g3 ashbya goss	357	85	7.5	1049	2	Q9V6L1 DROME	Q9v6l1 drosophila
285	87	7.7	433	2	Q5A3K1 CANAL	Q5a3k1 candida alb	358	85	7.5	1153	2	Q4IAN9 GIBZE	Q4ian9 gibberella
286	87	7.7	532	2	Q4JK69 DERPT	Q4jk69 dermatophag	359	85	7.5	1170	2	Q95011 CAEBEL	Q95011 caenorhabdi
287	87	7.7	567	2	Q60X66 CAEBR	Q60x66 caenorhabdi	360	85	7.5	1286	2	Q9VR49 DROME	Q9vr49 drosophila
288	87	7.7	612	2	Q7QJB6 ANOAG	Q7qjb6 anopheles g	361	84.5	7.4	220	2	Q9EQG0 MOUSE	Q9eqg0 mus musculu
289	87	7.7	661	2	Q13444 CLAFU	Q13444 cladosporiu	362	84.5	7.4	245	2	Q564Z3 CAEBEL	Q564z3 caenorhabdi
290	87	7.7	701	2	Q8ZNG4 PYRAE	Q8zng4 pyrobaculum	363	84.5	7.4	250	2	Q5AP52 CANAL	Q5ap52 candida alb
291	87	7.7	721	2	Q97UG7 SULSO	Q97ug7 sulfobolus	364	84.5	7.4	274	2	Q54W22 DICDI	Q54w22 dictyosteli
292	87	7.7	722	2	Q59644 SULSO	Q59644 sulfobolus	365	84.5	7.4	320	2	Q4SCG1 TETNG	Q4scg1 tetraodon n
293	87	7.7	802	2	Q60LR3 CAEBR	Q60lr3 caenorhabdi	366	84.5	7.4	333	2	Q6QJ76 CAEBR	Q6qj76 caenorhabdi
294	87	7.7	881	2	Q8IMS9 DROME	Q8ims9 drosophila	367	84.5	7.4	346	2	Q7S973 NEUCR	Q7s973 neurospora
295	87	7.7	1055	2	Q55G65 DICDI	Q55g65 dictyosteli	368	84.5	7.4	752	2	Q9YC61 AEPPE	Q9yc61 aeropyrum p
296	87	7.7	1506	2	P79927_XENLA	P79927 xenopus lae	369	84.5	7.4	814	2	Q6C247 YARLI	Q6c247 yarrowia li
297	86.5	7.6	400	1	MUAL_XENLA	P10667 xenopus lae	370	84.5	7.4	834	2	Q877B7 ASPOR	Q877b7 aspergillus
298	86.5	7.6	483	2	Q5AT96 EMENI	Q5at96 aspergillus	371	84.5	7.4	1161	1	DANA_YEAST	Q54194 dictyosteli
299	86.5	7.6	585	2	Q5SE79 GMONO	Q5se79 avian pneum	372	84.5	7.4	1186	2	Q54194 DICDI	Q54194 dictyosteli
300	86.5	7.6	629	2	Q4QGJ0 LEIMA	Q4qgj0 leishmania	373	84.5	7.4	1218	2	Q54Y26 DICDI	Q54y26 dictyosteli
301	86.5	7.6	768	2	Q60279 HUMAN	Q60279 homo sapien	374	84.5	7.4	2163	2	Q61TS1 CAEBR	Q61ts1 caenorhabdi
302	86.5	7.6	838	2	Q7UNP4 RHORA	Q7unp4 rhodopirell	375	84.5	7.4	22152	2	Q8WX17 HUMAN	Q8wx17 homo sapien
303	86.5	7.6	928	2	Q4SLH0 TETNG	Q4slh0 tetraodon n	376	84	7.4	259	2	Q9N3B9 CAEBEL	Q9n3b9 caenorhabdi
304	86.5	7.6	941	2	Q8LTH0 ARATH	Q8lth0 arabidopsis	377	84	7.4	262	2	P74577 SYNY3	P74577 synchocyst
305	86.5	7.6	965	2	Q22286 CAEBEL	Q22286 caenorhabdi	378	84	7.4	273	2	Q61002 MOUSE	Q61002 mus musculu
306	86.5	7.6	980	2	Q84FUE CHLTR	Q84fue chlamydia t	379	84	7.4	335	2	Q9C7W2 ARATH	Q9c7w2 arabidopsis
307	86.5	7.6	980	2	Q84FUE CHLTR	Q84fue chlamydia t	380	84	7.4	421	2	Q6KCA6 CANDU	Q6kca6 candida dub
308	86.5	7.6	981	2	Q84FUE CHLTR	Q84fue chlamydia t	381	84	7.4	475	2	Q8FQJ1 COREP	Q8fqj1 corynebacte
309	86.5	7.6	4509	2	Q54T85 DICDI	Q54t85 dictyosteli	382	84	7.4	543	2	Q14879 HUMAN	Q14879 homo sapien
310	86	7.6	390	2	Q70LM3 PHLRA	Q70lm3 phlebia rad	383	84	7.4	641	2	Q6AJU8 DESPS	Q6aju8 desulfotale
311	86	7.6	390	2	Q967S5 PHLRA	Q967s5 phlebia rad	384	84	7.4	648	2	Q95QX0 CAEBEL	Q95qx0 caenorhabdi
312	86	7.6	431	2	Q51WK9 MAGGR	Q51wx9 magnaporthe	385	84	7.4	668	2	Q4QK4 LEIMA	Q4qk4 leishmania
313	86	7.6	477	2	Q86VC5 HUMAN	Q86vc5 homo sapien	386	84	7.4	713	2	Q5SRT5 CRYNE	Q5srt5 cryptococcu
314	86	7.6	591	2	Q4WHJ8 ASPFU	Q4whj8 aspergillus	387	84	7.4	927	2	Q21811 CAEBEL	Q21811 caenorhabdi
315	86	7.6	678	2	Q54U48 DICDI	Q54u48 dictyosteli	388	84	7.4	1331	1	MANB_CALSA	P22533 caldocellum
316	86	7.6	709	2	Q4PY77 USTWA	Q4py77 ustilago ma	389	84	7.4	1362	2	Q9V294 PYRAB	Q9v294 pyrococcus
317	86	7.6	1266	2	Q626F7 CAEBR	Q626f7 caenorhabdi	390	84	7.4	1370	2	Q6C3B8 YARLI	Q6c3b8 yarrowia li
318	86	7.6	2044	2	Q4H2P9 GIBZE	Q4h2p9 gibberella	391	84	7.4	1413	2	Q54F12 DICDI	Q54f12 dictyosteli
319	85.5	7.5	178	2	Q8FOU3 COREP	Q8fou3 corynebacte	392	84	7.4	1779	2	O52374_9FIRM	O52374 caldicellul
320	85.5	7.5	346	2	Q5R230_9ZVGO	Q5r230 phymocetes	393	84	7.4	1832	2	Q96503_CRYPV	Q96503 cryptospori
321	85.5	7.5	363	2	Q91YK8 MOUSE	Q91yk8 mus musculu	394	83.5	7.4	216	2	Q28501_MACMU	Q28501 macaca mo
322	85.5	7.5	510	2	Q6SCJ8 ASPFU	Q6scj8 aspergillus	395	83.5	7.4	279	2	Q14888 HUMAN	Q14888 homo sapien
323	85.5	7.5	734	2	Q7S939_NEUCR	Q7s939 neurospora	396	83.5	7.4	571	2	Q4YHW1_PLABE	Q4yhw1 plasmodium











981	77.5	6.8	370	2	Q9XW5_CAEEL	Q9XW5	caenorhabdi	1054	77	6.8	345	2	Q691Y6_ANOSA	Q691Y6	anolis sagr
982	77.5	6.8	425	2	Q702W3_HV1	Q702W3	human herpe	1055	77	6.8	345	2	Q691Z2_ANOSA	Q691Z2	anolis sagr
983	77.5	6.8	430	2	Q6K4M7_ORISA	Q6K4M7	oryza sativ	1056	77	6.8	350	2	Q9RT72_DEIRA	Q9RT72	deinococcus
984	77.5	6.8	447	2	Q8SBG8_BPSF5	Q8SBG8	bacterioph	1057	77	6.8	369	2	Q7YUQ4_9TRYP	Q7YUQ4	trypanosoma
985	77.5	6.8	476	2	Q55RT1_CRYNE	Q55RT1	cryptococc	1058	77	6.8	381	2	Q59WN5_CANAL	Q59WN5	candida alb
986	77.5	6.8	486	2	Q563C8_AEDAE	Q563C8	aedes aegyp	1059	77	6.8	453	1	MALE_PYRAB	Q9V297	pyrococcus
987	77.5	6.8	497	2	Q7XHL3_ORISA	Q7XHL3	oryza sativ	1060	77	6.8	472	2	Q55U45_CRYNE	Q55U45	cryptococc
988	77.5	6.8	511	2	Q8U2G2_HV1	Q8U2G2	human herpe	1061	77	6.8	476	2	Q4JQF8_9PEZ1	Q4JQF8	chaetomium
989	77.5	6.8	513	2	Q4U8S8_THEAN	Q4U8S8	theileria a	1062	77	6.8	516	2	Q5CMZ9_CRYHO	Q5CMZ9	cryptospori
990	77.5	6.8	514	1	ACVR2_XENLA	P27039	xenopus lae	1063	77	6.8	521	2	Q54DL6_DICDI	Q54DL6	dictyosteli
991	77.5	6.8	514	2	Q5D043_XENLA	Q5D043	xenopus lae	1064	77	6.8	540	2	Q4ZZE2_PSESY	Q4ZZE2	pseudomonas
992	77.5	6.8	522	2	Q54RY2_DICDI	Q54RY2	dictyosteli	1065	77	6.8	573	2	Q5CWJ4_CRYPV	Q5CWJ4	cryptospori
993	77.5	6.8	540	1	CH60_STRSA	Q8KJ16	streptococc	1066	77	6.8	598	2	Q20747_CAEEL	Q20747	caenorhabdi
994	77.5	6.8	542	2	Q54SA9_DICDI	Q54SA9	dictyosteli	1067	77	6.8	608	2	Q4IKI0_GIBZE	Q4IKI0	gibberella
995	77.5	6.8	547	2	Q8IVB1_HUMAN	Q8IVB1	homo sapien	1068	77	6.8	615	2	Q5AQM3_EMENI	Q5AQM3	aspergillus
996	77.5	6.8	550	2	Q70KA7_9ACTO	Q70KA7	gordonia we	1069	77	6.8	625	2	Q58SF7_DROSI	Q58SF7	drosofila
997	77.5	6.8	561	2	Q4KLH5_RAT	Q4KLH5	rattus norv	1070	77	6.8	626	2	Q61LN4_CAEER	Q61LN4	caenorhabdi
998	77.5	6.8	577	2	Q6FSJ1_CANGA	Q6FSJ1	candida gla	1071	77	6.8	632	2	Q5ELJ2_DROME	Q5ELJ2	drosophila
999	77.5	6.8	592	2	Q23036_CAEEL	Q23036	caenorhabdi	1072	77	6.8	708	2	Q7R9K7_PLAYO	Q7R9K7	plasmodium
1000	77.5	6.8	602	2	Q58CS0_BOVIN	Q58CS0	bos taurus	1073	77	6.8	713	1	POLH_HUMAN	Q9Y253	homo sapien
1001	77.5	6.8	623	2	O17562_CAEEL	Q17562	caenorhabdi	1074	77	6.8	714	2	Q59TK9_CANAL	Q59TK9	candida alb
1002	77.5	6.8	624	2	Q7SD58_NEUCR	Q7SD58	neurospora	1075	77	6.8	714	2	Q59TP1_CANAL	Q59TP1	candida alb
1003	77.5	6.8	636	2	Q59H38_HUMAN	Q59H38	homo sapien	1076	77	6.8	717	2	Q8UIH5_PYRPU	Q8UIH5	pyrococcus
1004	77.5	6.8	668	2	Q5B5D4_EMENI	Q5B5D4	aspergillus	1077	77	6.8	750	2	Q9HFZ4_CANAL	Q9HFZ4	candida alb
1005	77.5	6.8	688	1	SIAP2_CLOTH	Q6G853	clostridium	1078	77	6.8	771	1	TWEN8_HUMAN	Q9HCN3	homo sapien
1006	77.5	6.8	760	2	Q6PJF7_HUMAN	Q6PJF7	homo sapien	1079	77	6.8	771	2	Q4TT33_HUMAN	Q4TT33	homo sapien
1007	77.5	6.8	806	2	Q9VCQ7_DROME	Q9VCQ7	drosophila	1080	77	6.8	772	2	Q82YF8_STRAM	Q82YF8	streptomyce
1008	77.5	6.8	820	2	Q520Y8_MAGGR	Q520Y8	magnaporthe	1081	77	6.8	773	2	Q61DE4_DROME	Q61DE4	drosophila
1009	77.5	6.8	839	2	Q614L9_CAEER	Q614L9	caenorhabdi	1082	77	6.8	802	2	Q7YVP9_9TRYP	Q7YVP9	trypanosoma
1010	77.5	6.8	939	2	Q592X1_BRARE	Q592X1	brachydanio	1083	77	6.8	902	2	Q8Q7H5_9HIV1	Q8Q7H5	human immun
1011	77.5	6.8	941	2	Q592W6_BRARE	Q592W6	brachydanio	1084	77	6.8	941	2	Q7ZSR7_HUMAN	Q7ZSR7	homo sapien
1012	77.5	6.8	941	2	Q592W7_BRARE	Q592W7	brachydanio	1085	77	6.8	948	2	Q8NDA4_HUMAN	Q8NDA4	homo sapien
1013	77.5	6.8	951	1	SFRS8_HUMAN	Q12872	homo sapien	1086	77	6.8	956	2	Q4SFS4_TETNG	Q4SFS4	tetradodon n
1014	77.5	6.8	982	2	Q6CGV5_YARLI	Q6CGV5	yarrowia li	1087	77	6.8	979	2	Q6C863_YARLI	Q6C863	yarrowia li
1015	77.5	6.8	1085	2	Q4QHD4_LEIMA	Q4QHD4	leishmania	1088	77	6.8	980	2	Q5TPB2_ANOCA	Q5TPB2	anopheles g
1016	77.5	6.8	1118	2	Q6CX19_KIULA	Q6CX19	kluyveromyc	1089	77	6.8	1055	2	Q55B14_CRYNE	Q55B14	cryptococc
1017	77.5	6.8	1127	2	Q6C608_ARATH	Q6C608	arabidopsis	1090	77	6.8	1072	2	Q4G0A4_HUMAN	Q4G0A4	homo sapien
1018	77.5	6.8	1258	2	QARGJ4_TETNG	QARGJ4	tetradodon n	1091	77	6.8	1081	2	Q59EAL_HUMAN	Q59EAL	homo sapien
1019	77.5	6.8	1316	2	Q70R05_ANOGA	Q70R05	anopheles g	1092	77	6.8	1092	1	NCA12_XENLA	P36335	xenopus lae
1020	77.5	6.8	1383	2	Q874K9_CANAL	Q874K9	candida alb	1093	77	6.8	1168	2	Q8S7C7_ORYSA	Q8S7C7	oryza sativ
1021	77.5	6.8	1390	2	Q54GX9_DICDI	Q54GX9	dictyosteli	1094	77	6.8	1168	2	Q7XC17_ORYSA	Q7XC17	oryza sativ
1022	77.5	6.8	1765	2	Q54WL2_DICDI	Q54WL2	dictyosteli	1095	77	6.8	1184	2	Q4IHX0_GIBZE	Q4IHX0	gibberella
1023	77.5	6.8	1842	2	QAN830_THERA	QAN830	theileria p	1096	77	6.8	1205	2	Q61E70_RAT	Q61E70	rattus norv
1024	77.5	6.8	1845	2	Q66JH8_DICDI	Q66JH8	dictyosteli	1097	77	6.8	1223	2	Q6ZS17_HUMAN	Q6ZS17	homo sapien
1025	77.5	6.8	1873	2	Q6S003_DICDI	Q6S003	dictyosteli	1098	77	6.8	1285	2	Q4RXD7_TETNG	Q4RXD7	tetradodon n
1026	77.5	6.8	1878	2	Q6CP24_KIULA	Q6CP24	kluyveromyc	1099	77	6.8	1346	2	Q54SH1_DICDI	Q54SH1	dictyosteli
1027	77.5	6.8	2761	2	Q19522_CAEEL	Q19522	caenorhabdi	1100	77	6.8	1404	2	Q59SG9_CANAL	Q59SG9	candida alb
1028	77.5	6.8	3300	2	Q4N127_THERA	Q4N127	theileria p	1101	77	6.8	1462	2	Q550D3_DICDI	Q550D3	dictyosteli
1029	77.5	6.8	4630	2	Q7UWV5_RHOBA	Q7UWV5	rhodopirell	1102	77	6.8	1462	2	Q86AR5_DICDI	Q86AR5	dictyosteli
1030	77	6.8	178	2	Q5B5J0_EMENI	Q5B5J0	aspergillus	1103	77	6.8	1513	1	MUC2_RAT	Q62635	rattus norv
1031	77	6.8	187	2	Q4R111_CAEEL	Q4R111	caenorhabdi	1104	77	6.8	1521	2	Q8CHS9_MOUSE	Q8CHS9	mus musculus
1032	77	6.8	187	2	Q77AU9_LYCVW	Q77AU9	lymphocytic	1105	77	6.8	1649	2	Q60K37_CAEER	Q60K37	caenorhabdi
1033	77	6.8	187	2	Q77AV0_LYCVW	Q77AV0	lymphocytic	1106	77	6.8	1706	2	Q7TGF2_9VIRU	Q7TGF2	hepatitis e
1034	77	6.8	187	2	Q9YJ85_LYCVW	Q9YJ85	lymphocytic	1107	77	6.8	1937	2	Q5CY21_CRYPV	Q5CY21	cryptospori
1035	77	6.8	187	2	Q9YPM0_LYCVW	Q9YPM0	lymphocytic	1108	77	6.8	2112	2	Q80U93_MOUSE	Q80U93	mus musculus
1036	77	6.8	213	2	Q6M959_NEUCR	Q6M959	neurospora	1109	77	6.8	2176	2	Q54VP0_DICDI	Q54VP0	dictyosteli
1037	77	6.8	277	2	Q5A5U6_CANAL	Q5A5U6	candida alb	1110	77	6.8	2187	1	NACAM_MOUSE	P70670	mus musculus
1038	77	6.8	292	2	Q7QJA0_ANOGA	Q7QJA0	anopheles g	1111	77	6.8	2300	2	Q7SFP6_NEUCR	Q7SFP6	neurospora
1039	77	6.8	321	2	Q4IK96_GIBZE	Q4IK96	gibberella	1112	77	6.8	2316	1	PTPR2_RAT	Q62656	rattus norv
1040	77	6.8	340	2	Q57H80_SALCH	Q57H80	salmonella	1113	77	6.8	2566	2	Q8TSE7_METAC	Q8TSE7	methanosaer
1041	77	6.8	340	2	Q8ZK01_SALTY	Q8ZK01	salmonella	1114	77	6.8	3443	2	Q8JZM8_MOUSE	Q8JZM8	mus musculus
1042	77	6.8	345	2	Q690T8_ANOSA	Q690T8	anolis sagr	1115	77	6.8	4782	2	Q8KIG6_MOUSE	Q8KIG6	mus musculus
1043	77	6.8	345	2	Q690U2_ANOSA	Q690U2	anolis sagr	1116	77	6.8	6011	2	Q4U447_POLCB	Q4U447	polyangium
1044	77	6.8	345	2	Q690U5_ANOSA	Q690U5	anolis sagr	1117	77	6.8	11696	2	Q5CV09_CRYPV	Q5CV09	cryptospori
1045	77	6.8	345	2	Q690U6_ANOSA	Q690U6	anolis sagr	1118	76.5	6.7	123	2	Q15773_TRYCR	Q15773	trypanosoma
1046	77	6.8	345	2	Q690U8_ANOSA	Q690U8	anolis sagr	1119	76.5	6.7	232	2	Q69EW2_STRBO	Q69EW2	streptococc
1047	77	6.8	345	2	Q690V1_ANOSA	Q690V1	anolis sagr	1120	76.5	6.7	250	2	Q59UP6_CANAL	Q59UP6	candida alb
1048	77	6.8	345	2	Q690W8_ANOSA	Q690W8	anolis sagr	1121	76.5	6.7	250	2	Q9HFS1_CANAL	Q9HFS1	candida alb
1049	77	6.8	345	2	Q690X6_ANOSA	Q690X6	anolis sagr	1122	76.5	6.7	266	2	Q4HZD3_GIBZE	Q4HZD3	gibberella
1050	77	6.8	345	2	Q690X8_ANOSA	Q690X8	anolis sagr	1123	76.5	6.7	299	2	Q82SU2_STRAW	Q82SU2	streptomyce
1051	77	6.8	345	2	Q691U6_ANOSA	Q691U6	anolis sagr	1124	76.5	6.7	300	2	Q6CCZ0_YARLI	Q6CCZ0	yarrowia li
1052	77	6.8	345	2	Q691Y0_ANOSA	Q691Y0	anolis sagr	1125	76.5	6.7	304	2	Q6AW28_BACTU	Q6AW28	bacillus th
1053	77	6.8	345	2	Q691Y1_ANOSA	Q691Y1	anolis sagr	1126	76.5	6.7	308	2	Q9BRD2_HUMAN	Q9BRD2	homo sapien

1127	Q6UJMS_9SAUR	345	6.7	76.5	Q6UJMS diplodactyl	1200	76	6.7	309	2	Q7S0P9_NEUCR	Q7a0p9 neurospora
1128	Q52J80_9SAUR	346	6.7	76.5	Q52j80 heteronotia	1201	76	6.7	313	2	Q8BEJ1_9POXV	Q8bej1 skunkpox vi
1129	Q52J80_9SAUR	346	6.7	76.5	Q52j80 heteronotia	1202	76	6.7	340	2	Q82X28_SALT1	Q82x28 salmonella
1130	Q52J86_9SAUR	346	6.7	76.5	Q52j86 heteronotia	1203	76	6.7	345	2	Q690T5_ANOSA	Q690t5 anolis sagr
1131	Q52J84_9SAUR	346	6.7	76.5	Q52j84 heteronotia	1204	76	6.7	345	2	Q690T7_ANOSA	Q690t7 anolis sagr
1132	Q52J86_9SAUR	346	6.7	76.5	Q52j86 heteronotia	1205	76	6.7	345	2	Q690U0_ANOSA	Q690u0 anolis sagr
1133	Q9UF43_HUMAN	349	6.7	76.5	Q9uf43 homo sapien	1206	76	6.7	345	2	Q690U1_ANOSA	Q690u1 anolis sagr
1134	Q8NJ70_BIOOC	357	6.7	76.5	Q8nj70 bionectria	1207	76	6.7	345	2	Q690U3_ANOSA	Q690u3 anolis sagr
1135	Q6CCM7_YARLI	358	6.7	76.5	Q6ccm7 yarrowia li	1208	76	6.7	345	2	Q690W5_ANOSA	Q690w5 anolis sagr
1136	Q4HV07_GIBZE	360	6.7	76.5	Q4hv07 gibberella	1209	76	6.7	345	2	Q690W9_ANOSA	Q690w9 anolis sagr
1137	Q9NHU9_DROMI	385	6.7	76.5	Q9nhu9 drosophila	1209	76	6.7	345	2	Q691G5_ANOSA	Q691g5 anolis sagr
1138	Q9K6G1_BACHD	433	6.7	76.5	Q9k6g1 bacillus ha	1210	76	6.7	345	2	Q691G8_ANOSA	Q691g8 anolis sagr
1139	Q6XYT7_CANAL	452	6.7	76.5	Q6xyt7 candida alb	1211	76	6.7	345	2	Q691Q6_ANOSA	Q691q6 anolis sagr
1140	Q61PC9_CAEBR	456	6.7	76.5	Q61pc9 caenorhabdi	1212	76	6.7	345	2	Q691T7_ANOSA	Q691t7 anolis sagr
1141	Q86AK1_DICDI	457	6.7	76.5	Q86ak1 dictyosteli	1213	76	6.7	345	2	Q691U4_ANOSA	Q691u4 anolis sagr
1142	Q51D26_ENTHI	457	6.7	76.5	Q51d26 entamoeba h	1214	76	6.7	345	2	Q692A0_ANOSA	Q692a0 anolis sagr
1143	Q55D89_DICDI	459	6.7	76.5	Q55d89 dictyosteli	1215	76	6.7	345	2	Q692A2_ANOSA	Q692a2 anolis sagr
1144	Q753Y1_ASHGO	490	6.7	76.5	Q753y1 ashbya goss	1216	76	6.7	345	2	Q692A3_ANOSA	Q692a3 anolis sagr
1145	Q59ZU0_CANAL	491	6.7	76.5	Q59zu0 candida alb	1217	76	6.7	345	2	Q8WDI1_ANOSA	Q8wdi1 anolis sagr
1146	Q14395_HUMAN	505	6.7	76.5	Q14395 homo sapien	1218	76	6.7	345	2	Q4WG94_ASPFU	Q4wg94 aspergillus
1147	Q5AVH4_EWENI	514	6.7	76.5	Q5avh4 aspergillus	1219	76	6.7	360	2	VE2_HP7A5	P36794 human papil
1148	Q6CTM5_KLULA	520	6.7	76.5	Q6ctm5 kluyveromyc	1220	76	6.7	368	1	Q9FN39_ARATH	Q9fn39 arabidopsis
1149	Q51Z81_WAGER	533	6.7	76.5	Q51z81 magnaporthe	1221	76	6.7	370	2	Q5HS25_STABQ	Q5hs25 staphylococ
1150	Q59145_GAMMM	542	6.7	76.5	Q59145 aeromonas s	1222	76	6.7	372	2	Q8CQM2_STABP	Q8ccm2 staphylococ
1151	Q5CVT9_CRYPV	576	6.7	76.5	Q5cvt9 cryptospori	1223	76	6.7	372	2	Q8EC31_SHEON	Q8ec31 shewanella
1152	Q4JUC4_CORJK	601	6.7	76.5	Q4juc4 corynebacte	1224	76	6.7	374	2	ADHA_CFOAB	Q04944 clostridium
1153	Q4JUC4_CORJK	601	6.7	76.5	Q4juc4 corynebacte	1225	76	6.7	389	1	Q641C6_XENLA	Q641c6 xenopus lae
1154	Q59TT7_CANAL	634	6.7	76.5	Q59tt7 candida alb	1226	76	6.7	415	2	Q86DA4_CABEL	Q86da4 caenorhabdi
1155	Q4H446_HYLJA	645	6.7	76.5	Q4h446 hyla japoni	1227	76	6.7	428	2	Q7JMU4_CABEL	Q7jmu4 caenorhabdi
1156	LRRC4_HUMAN	653	6.7	76.5	LRRC4 homo sapien	1228	76	6.7	429	2	YMH7_CABEL	P34474 caenorhabdi
1157	SHK1_SCHPO	658	6.7	76.5	P50537 schizosacch	1229	76	6.7	431	1	Q72NA6_LEPIC	Q72na6 leptospira
1158	Q9VB94_DROME	676	6.7	76.5	Q9vb94 drosophila	1230	76	6.7	441	2	Q8F895_LEPIN	Q8f895 leptospira
1159	Q802U4_BRARN	695	6.7	76.5	Q802u4 brachydanio	1231	76	6.7	441	2	Q9ADQ9_STAAU	Q9adq9 staphylococ
1160	Q75YM4_STRPN	703	6.7	76.5	Q75ym4 streptococc	1232	76	6.7	452	2	Q524Z4_MAGGR	Q524z4 magnaporthe
1161	Q23447_CABEL	718	6.7	76.5	Q23447 caenorhabdi	1233	76	6.7	457	2	Q58SK3_DROSI	Q58sk3 drosophila
1162	Q93307_9ALPH	750	6.7	76.5	Q93307 equid herpe	1234	76	6.7	468	2	Q58SN0_DROME	Q58sn0 drosophila
1163	Q615W4_CAEBR	862	6.7	76.5	Q615w4 caenorhabdi	1235	76	6.7	495	2	Q01972_CABEL	Q01972 caenorhabdi
1164	Q8K0T1_MOUSE	862	6.7	76.5	Q8k0t1 mus musculu	1236	76	6.7	495	2	Q58SN4_DROME	Q58sn4 drosophila
1165	Q54J62_DICDI	912	6.7	76.5	Q54j62 dictyosteli	1237	76	6.7	508	2	Q6UX19_HUMAN	Q6ux19 homo sapien
1166	Q592W8_BRARE	939	6.7	76.5	Q592w8 brachydanio	1238	76	6.7	509	2	Q58SM8_DROME	Q58sm8 drosophila
1167	YL61_SCHPO	943	6.7	76.5	Q8tf59 schizosacch	1239	76	6.7	522	2	Q58SN0_DROME	Q58sn0 drosophila
1168	Q4KRH7_DICDI	948	6.7	76.5	Q4krh7 dictyosteli	1240	76	6.7	522	2	Q58SN3_DROME	Q58sn3 drosophila
1169	Q610Z8_CAEBR	954	6.7	76.5	Q610z8 dictyosteli	1241	76	6.7	522	2	Q01972_CABEL	Q01972 caenorhabdi
1170	Q9NH29_HELPN	1011	6.7	76.5	Q9nh29 helicoverpa	1242	76	6.7	532	2	Q7PAE0_RICSI	Q7pae0 rickettsia
1171	Q7M009_SCMVC	1023	6.7	76.5	Q7m009 simian cyto	1243	76	6.7	534	2	Q5Y9C0_LACPA	Q5y9c0 lactobacill
1172	Q8EZH2_LEPIN	1201	6.7	76.5	Q8ezh2 leptospira	1244	76	6.7	544	2	Q4PFW4_USTMA	Q4pfw4 ustilago ma
1173	Q68FE6_MOUSE	1223	6.7	76.5	Q68fe6 mus musculu	1245	76	6.7	545	2	Q9M1B1_ARATH	Q9m1b1 arabidopsis
1174	Q54JY4_DICDI	1230	6.7	76.5	Q54jy4 dictyosteli	1246	76	6.7	549	2	Q7PMB9_ANOGA	Q7pmb9 anopheles g
1175	Q72MU1_LEPIC	1259	6.7	76.5	Q72mu1 leptospira	1247	76	6.7	563	2	Q5B4U2_EWENI	Q5b4u2 aspergillus
1176	Q80T73_MOUSE	1262	6.7	76.5	Q80t73 mus musculu	1248	76	6.7	565	2	Q9SL10_ARATH	Q9sl10 arabidopsis
1177	Q8R0U9_BACGO	1284	6.7	76.5	Q8r0u9 bacillus gl	1249	76	6.7	569	2	Q61N12_CABER	Q61n12 caenorhabdi
1178	Q6FR84_CANGA	1326	6.7	76.5	Q6fr84 candida gla	1250	76	6.7	570	2	Q06604_YEAST	Q06604 saccharomyc
1179	Q54KH9_DICDI	1401	6.7	76.5	Q54kh9 dictyosteli	1251	76	6.7	582	2	Q58SG7_DROSI	Q58sg7 drosophila
1180	Q54H52_DICDI	1414	6.7	76.5	Q54h52 dictyosteli	1252	76	6.7	582	2	Q58SG8_DROSI	Q58sg8 drosophila
1181	Q53MF8_ORYSA	1420	6.7	76.5	Q53mf8 oryza sativ	1253	76	6.7	582	2	Q58SH3_DROSI	Q58sh3 drosophila
1182	Q4FWR7_LEIMA	1420	6.7	76.5	Q4fwr7 leishmania	1254	76	6.7	582	2	Q50PH5_ENTHI	Q50ph5 entamoeba h
1183	Q55C84_DICDI	1578	6.7	76.5	Q55c84 dictyosteli	1255	76	6.7	582	2	Q7R2J1_GIALA	Q7r2j1 giardia lam
1184	PMPB_CHLMU	1672	6.7	76.5	Q9pij2 chlamydia m	1256	76	6.7	582	2	Q5ELV4_DROSI	Q5elv4 drosophila
1185	Q80ZTB_MOUSE	1674	6.7	76.5	Q80z18 mus musculu	1257	76	6.7	582	2	Q5ELV5_DROSI	Q5elv5 drosophila
1186	Q69Q09_ORYSA	1696	6.7	76.5	Q69q09 oryza sativ	1258	76	6.7	582	2	Q5ELV8_DROSI	Q5elv8 drosophila
1187	Q54H52_DICDI	1704	6.7	76.5	Q54h52 dictyosteli	1259	76	6.7	582	2	Q5ELW0_DROSI	Q5elw0 drosophila
1188	Q5CWU1_CRYPV	2269	6.7	76.5	Q5cwu1 cryptospori	1260	76	6.7	607	2	Q4V8G0_RAT	Q4v8g0 rattus norv
1189	Q4WTG2_ASPFU	2306	6.7	76.5	Q4wtg2 aspergillus	1261	76	6.7	612	2	Q7NY06_CHRVO	Q7ny06 chromobacte
1190	Q7YVR5_CRYPV	2335	6.7	76.5	Q7yvr5 cryptospori	1262	76	6.7	622	2	Q6V6D8_DROSI	Q6v6d8 drosophila
1191	Q68CH7_STRCZ	3088	6.7	76.5	Q68ch7 streptomyce	1263	76	6.7	622	2	Q6V6E2_DROSI	Q6v6e2 drosophila
1192	Q6V7I2_EAV	3176	6.7	76.5	Q6v7i2 equine arte	1264	76	6.7	622	2	Q6V6E4_DROSI	Q6v6e4 drosophila
1193	Q6V7J1_EAV	3176	6.7	76.5	Q6v7j1 equine arte	1265	76	6.7	622	2	Q58SF6_DROSI	Q58sf6 drosophila
1194	Q4YTV6_PLABE	4015	6.7	76.5	Q4ytv6 plasmodium	1266	76	6.7	622	2	Q58SG2_DROSI	Q58sg2 drosophila
1195	Q7YTV9_MYTGA	4736	6.7	76.5	Q7ytv9 mytilus gal	1267	76	6.7	622	2	Q5ELQ5_DROSI	Q5elq5 drosophila
1196	Q4X239_ASPFU	162	6.7	76	Q4x239 aspergillus	1268	76	6.7	622	2	Q5ELQ9_DROSI	Q5elq9 drosophila
1197	Q14883_HUMAN	167	6.7	76	Q14883 homo sapien	1269	76	6.7	622	2		
1198	Q25335_LEIMA	243	6.7	76	Q25335 leishmania	1270	76	6.7	622	2		
1199	Q9VLN8_DROME	269	6.7	76	Q9vln8 drosophila	1271	76	6.7	622	2		
	Q924F9_GEOBU	301	6.7	76	Q924f9 geomys burs	1272	76	6.7	622	2		



1273	76	6.7	625	2	Q58SF3_DROSI	Q58sf3 drosophila	1346	75.5	6.6	329	2	Q9NWV8_HUMAN	Q9nwv8 homo sapien
1274	76	6.7	625	2	Q58SH8_DROSI	Q58sh8 drosophila	1347	75.5	6.6	329	2	Q5R7L2_PONPY	Q5r7l2 pongo pygma
1275	76	6.7	625	2	Q5ELN3_DROSI	Q5eln3 drosophila	1348	75.5	6.6	330	2	Q86AR7_DICDI	Q86ar7 dictyosteli
1276	76	6.7	625	2	Q5V6E1_DROSI	Q5v6e1 drosophila	1349	75.5	6.6	346	2	Q9TFU7_9SAUR	Q9tfu7 teratogscinc
1277	76	6.7	653	2	Q73TB8_MYCOPA	Q73tb8 mycobacteri	1350	75.5	6.6	346	2	Q52J83_9SAUR	Q52j83 heteronotia
1278	76	6.7	676	2	Q54PX8_DICDI	Q54px8 dictyosteli	1351	75.5	6.6	346	2	Q52J75_9SAUR	Q52j75 heteronotia
1279	76	6.7	679	2	Q69HN9_CIOIN	Q69hn9 ciona intes	1352	75.5	6.6	346	2	Q52J73_9SAUR	Q52j73 heteronotia
1280	76	6.7	686	2	Q61XJ6_CAEBR	Q61xj6 caenorhabdi	1353	75.5	6.6	355	2	Q554K2_DICDI	Q554k2 dictyosteli
1281	76	6.7	686	2	Q50194_MYCLE	Q50194 mycobacteri	1354	75.5	6.6	360	2	Q4SSY6_TETNG	Q4ssy6 tetraodon n
1282	76	6.7	725	2	Q6JAD6_WAIZE	Q6jad6 zea mays (m	1355	75.5	6.6	385	2	Q8T8L4_DROMI	Q8t8l4 drosophila
1283	76	6.7	729	2	Q51WE3_MAGGR	Q51we3 magnaporthe	1356	75.5	6.6	385	2	Q9N666_DROMI	Q9n666 drosophila
1284	76	6.7	768	2	Q8J2N4_GRIFR	Q8j2n4 grifolia fro	1357	75.5	6.6	385	2	Q9NHU6_DROMI	Q9nhu6 drosophila
1285	76	6.7	812	2	Q86AW3_DICDI	Q86aw3 dictyosteli	1358	75.5	6.6	385	2	Q9NHU7_DROMI	Q9nhu7 drosophila
1286	76	6.7	822	2	Q54ZS2_DICDI	Q54zs2 dictyosteli	1359	75.5	6.6	395	2	Q4HAL0_9DEIO	Q4hal0 deinococcus
1287	76	6.7	823	2	Q54Y28_DICDI	Q54y28 dictyosteli	1360	75.5	6.6	397	2	Q702W7_HHV1	Q702w7 human herpe
1288	76	6.7	858	2	Q5TYT7_BRARE	Q5tyt7 brachydanio	1361	75.5	6.6	397	2	Q702X1_HHV1	Q702x1 human herpe
1289	76	6.7	922	2	Q95U05_DROME	Q95u05 drosophila	1362	75.5	6.6	420	2	Q8N7W9_HUMAN	Q8n7w9 homo sapien
1290	76	6.7	927	2	Q52F88_MAGGR	Q52f88 magnaporthe	1363	75.5	6.6	430	1	P02F31_RAT	P425f1 rattus norv
1291	76	6.7	937	2	Q4Q7L1_LEIMA	Q4q7l1 leishmania	1364	75.5	6.6	430	1	Q4NLM7_9MICC	Q4nlm7 arthrobacte
1292	76	6.7	962	2	Q4K4X8_PSEFS	Q4k4x8 pseudomonas	1365	75.5	6.6	456	2	Q584V6_9TRYP	Q584v6 trypanosoma
1293	76	6.7	981	2	Q54SW0_DICDI	Q54sw0 dictyosteli	1366	75.5	6.6	459	2	Q54G90_DICDI	Q54g90 dictyosteli
1294	76	6.7	981	2	Q6GQI9_XENLA	Q6gqi9 xenopus lae	1367	75.5	6.6	464	2	Q90WQ6_ONCMY	Q90wq6 oncorhynch
1295	76	6.7	1016	1	ENGL1_SCHPO	Q9ut45 schizosacch	1368	75.5	6.6	468	1	VAS1_BOVIN	P406s2 bos taurus
1296	76	6.7	1067	2	Q6BUL7_DBEHA	Q6bul7 debaryomyce	1369	75.5	6.6	469	2	Q54P62_DICDI	Q54p62 dictyosteli
1297	76	6.7	1094	2	Q4P201_USTMA	Q4p201 ustilago ma	1370	75.5	6.6	469	2	Q82S40_NITEU	Q82s40 nitrosomona
1298	76	6.7	1154	2	Q54PP7_DICDI	Q54pp7 dictyosteli	1371	75.5	6.6	476	2	Q9CIS9_HUMIN	Q9cis9 humicola in
1299	76	6.7	1194	2	Q6C4Z0_YARLI	Q6c4z0 yarrowia li	1372	75.5	6.6	478	2	Q5K984_CRYNE	Q5k984 cryptococcu
1300	76	6.7	1216	2	Q527R4_MAGGR	Q527r4 magnaporthe	1373	75.5	6.6	478	2	Q61122_DICDI	Q61122 dictyosteli
1301	76	6.7	1228	2	Q44334_9RHIZ	Q44334 agrobacteri	1374	75.5	6.6	481	2	Q9VWK3_DROME	Q9vwk3 drosophila
1302	76	6.7	1263	2	Q8T0M2_DROME	Q8t0m2 drosophila	1375	75.5	6.6	492	2	Q94HR9_ARATH	Q94hr9 arabidopsis
1303	76	6.7	1267	2	Q54TJ5_DICDI	Q54tj5 dictyosteli	1376	75.5	6.6	496	1	CWLB_BAGSU	Q021l4 bacillus su
1304	76	6.7	1269	2	Q54CAL_DICDI	Q54cal dictyosteli	1377	75.5	6.6	496	2	Q54PX0_DICDI	Q54px0 dictyosteli
1305	76	6.7	1360	2	Q9TYK4_CAEBL	Q9tyk4 caenorhabdi	1378	75.5	6.6	500	2	Q54L47_DICDI	Q54l47 dictyosteli
1306	76	6.7	1423	2	Q6CRU1_KULLA	Q6cru1 kluveromycc	1379	75.5	6.6	505	2	Q61PF3_CAEBR	Q61pf3 caenorhabdi
1307	76	6.7	1426	2	Q9X3P6_9FIRM	Q9x3p6 caldicellul	1380	75.5	6.6	511	1	VGLC_HHV11	P102t8 human herpe
1308	76	6.7	1462	2	Q3V508_DROME	Q3v508 drosophila	1381	75.5	6.6	511	2	Q8UYA4_HHV1	Q8uy4 human herpe
1309	76	6.7	1489	2	Q23302_ARATH	Q23302 arabidopsis	1382	75.5	6.6	511	2	Q8UYE2_HHV1	Q8uy2 human herpe
1310	76	6.7	1505	2	Q55DJ9_DICDI	Q55dj9 dictyosteli	1383	75.5	6.6	511	2	Q8UYF2_HHV1	Q8uyf2 human herpe
1311	76	6.7	1586	2	Q59S88_CANAL	Q59sn8 candida alb	1384	75.5	6.6	511	2	Q8UZ65_HHV1	Q8uz65 human herpe
1312	76	6.7	1588	2	Q59SR0_CANAL	Q59sr0 candida alb	1385	75.5	6.6	511	2	Q8UZ68_HHV1	Q8uz68 human herpe
1313	76	6.7	1689	2	Q911R1_9VIRU	Q911r1 crimean-con	1386	75.5	6.6	511	2	Q8UZ69_HHV1	Q8uz69 human herpe
1314	76	6.7	1789	2	Q8T145_DICDI	Q8t145 dictyosteli	1387	75.5	6.6	511	2	Q8UZ70_HHV1	Q8uz70 human herpe
1315	76	6.7	1828	2	Q54VB5_DICDI	Q54vb5 dictyosteli	1388	75.5	6.6	511	2	Q8UZ71_HHV1	Q8uz71 human herpe
1316	76	6.7	2957	2	Q4REV8_TETNG	Q4rev8 tetraodon n	1389	75.5	6.6	511	2	Q9WIW3_HHV1	Q9wiw3 human herpe
1317	76	6.7	5376	1	ZAN_MOUSE	Q88799 mus musculu	1390	75.5	6.6	534	2	Q72BB2_DESVH	Q72bb2 desulfovibr
1318	75.5	6.6	127	2	O61035_TRYCR	O61035 trypanosoma	1391	75.5	6.6	541	2	Q51UA3_MAGGR	Q51ua3 magnaporthe
1319	75.5	6.6	154	2	Q4VT13_9CONI	Q4vt13 pinus chiap	1392	75.5	6.6	547	1	MUC13_RAT	P978r1 rattus norv
1320	75.5	6.6	161	2	Q322P4_MAGGR	Q322f4 magnaporthe	1393	75.5	6.6	559	1	NUPL_MOUSE	Q8k2k6 mus musculu
1321	75.5	6.6	169	2	Q870Y2_NEUCR	Q870y2 neurospora	1394	75.5	6.6	560	2	Q4N7W3_THERA	Q4n7w3 theileria p
1322	75.5	6.6	193	2	Q8XTI3_RALSO	Q8xti3 raistonia s	1395	75.5	6.6	560	2	Q9A6T7_CAUCR	Q9a6t7 caulobacter
1323	75.5	6.6	194	2	Q9Y9W0_AERPE	Q9y9w0 aeropyrum p	1396	75.5	6.6	610	2	Q52FM4_MAGGR	Q52fm4 magnaporthe
1324	75.5	6.6	198	2	Q4WAE1_ASPPU	Q4wae1 aspergillus	1397	75.5	6.6	613	2	Q51TE4_MAGGR	Q51te4 magnaporthe
1325	75.5	6.6	228	2	Q8H2B6_9PRIM	Q8hzb6 gorilla gor	1398	75.5	6.6	633	2	Q519D6_ENTHI	Q519d6 entamoeba h
1326	75.5	6.6	232	2	Q69EV5_STRBO	Q69ev5 streptococc	1399	75.5	6.6	639	2	Q8TPL3_METAC	Q8tpl3 methanosaar
1327	75.5	6.6	232	2	Q69EV7_STRBO	Q69ev7 streptococc	1400	75.5	6.6	650	2	Q8EYE4_LEPIN	Q8eye4 leptospira
1328	75.5	6.6	232	2	Q69EV8_STRBO	Q69ev8 streptococc	1401	75.5	6.6	665	2	Q97G25_CLOAB	Q97g25 clostridium
1329	75.5	6.6	232	2	Q69EX1_STRBO	Q69ex1 streptococc	1402	75.5	6.6	696	2	Q5F2D4_MOUSE	Q5f2d4 mus musculu
1330	75.5	6.6	260	2	Q27007_METTH	Q27007 methanobact	1403	75.5	6.6	736	2	Q8C0R7_MOUSE	Q8c0r7 mus musculu
1331	75.5	6.6	266	2	Q5A0C8_CANAL	Q5a0c8 candida alb	1404	75.5	6.6	737	1	KNS1_YEAST	P323s0 saccharomyc
1332	75.5	6.6	273	2	P87519_BHV4	P87519 bovine herp	1405	75.5	6.6	759	2	Q5HY92_HUMAN	Q5hy92 homo sapien
1333	75.5	6.6	273	2	Q39C20_BHV4	Q39c20 cryptococcu	1406	75.5	6.6	782	2	Q54WL9_DICDI	Q54wl9 dictyosteli
1334	75.5	6.6	275	2	Q55K40_CRYNE	Q55k40 cryptococcu	1407	75.5	6.6	783	2	Q63158_RAT	Q63158 rattus norv
1335	75.5	6.6	275	2	Q5K9F9_CRYNE	Q5k9f9 cryptococcu	1408	75.5	6.6	784	2	Q6C185_YARLI	Q6c185 yarrowia li
1336	75.5	6.6	275	2	Q8DLV5_SYNEL	Q8dlv5 synecococc	1409	75.5	6.6	795	2	Q7Q7F0_ANOGA	Q7q7f0 anopheles g
1337	75.5	6.6	282	2	Q8L8N4_ARATH	Q8l8n4 arabidopsis	1410	75.5	6.6	817	2	Q6PGX9_BRARE	Q6pgx9 brachydanio
1338	75.5	6.6	299	2	Q82ZP6_PYRAE	Q82zp6 pyrobaculum	1411	75.5	6.6	859	2	Q5VVE4_HUMAN	Q5vve4 homo sapien
1339	75.5	6.6	300	2	Q35XH5_CAEBL	Q35xh5 caenorhabdi	1412	75.5	6.6	864	1	AT7L11_HUMAN	Q5vye4 homo sapien
1340	75.5	6.6	301	2	Q41IK5_GIBZE	Q41ik5 gibberella	1413	75.5	6.6	864	2	Q5B9X1_EMENI	Q5b9x1 aspergillus
1341	75.5	6.6	306	2	Q5BFA2_EMENI	Q5bfa2 aspergillus	1414	75.5	6.6	864	2	Q5MYI2_SIVCZ	Q5myi2 chimpanzee
1342	75.5	6.6	306	2	Q88V34_LACPL	Q88v34 lactobacill	1415	75.5	6.6	877	2	Q9H3Q6_HUMAN	Q9h3q6 homo sapien
1343	75.5	6.6	313	2	Q57LA1_SALCH	Q57la1 salmonella	1416	75.5	6.6	877	2	Q8Q7I5_9HIV1	Q8q7i5 human immun
1344	75.5	6.6	321	2	Q9XUL7_CAEBL	Q9xul7 caenorhabdi	1417	75.5	6.6	878	2	Q9H3Q7_HUMAN	Q9h3q7 homo sapien
1345	75.5	6.6	329	2	Q6FIA0_HUMAN	Q6fia0 homo sapien	1418	75.5	6.6	932	1	RBMI2_MACMU	Q8sqz7 macaca mula



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Db 76 TALKASPETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSQFAAYCYNSSDTW 135
Qy 121 TNSCIPEIITTKDPIFNQTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 180
Db 136 TNSCIPEIITTKDPIFNQTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 195
Qy 181 RKKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFGG 220
Db 196 RKKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFGG 235

RESULT 2
Q8TC18_HUMAN
ID Q8TC18_HUMAN PRELIMINARY; PRT; 322 AA.
AC Q8TC18;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Extracellular link domain containing 1.
GN Name=XLKDI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alcegnul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan E., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M.M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026231; AAH26231.1; -, mRNA.
DR HSPB; P98066; 107B.
DR Ensembl; ENSG00000133800; Homo sapiens.
DR HGNC; HGNC:14687; XLKDI.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS0963; LINK_2; 1.
SQ SEQUENCE 322 AA; 35183 MW; 0B1EDBD76CE4610A CRC64;

Query Match 98.8%; Score 1122; DB 2; Length 322;
Best Local Similarity 99.5%; Pred. No. 1.2e-88;
Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTRLLVQGSRAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQVE 60
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Db 16 TTRLLVQGSRAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQVE 75
Qy 61 TALKASPETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSQFAAYCYNSSDTW 120
Db 76 TALKASPETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSQFAAYCYNSSDTW 135
Qy 121 TNSCIPEIITTKDPIFNQTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 180
Db 136 TNSCIPEIITTKDPIFNQTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 195
Qy 181 RKKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFGG 220
Db 196 RKKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFGG 235

RESULT 3
Q9Y5Y7_HUMAN
ID Q9Y5Y7_HUMAN PRELIMINARY; PRT; 322 AA.
AC Q9Y5Y7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9915698; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA Jackson D.G.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801 (1999).
DR EMBL; AF118108; AAD42764.1; -, mRNA.
DR HSPB; P98066; 107B.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR GO; GO:0009653; P:morphogenesis; TAS.
DR GO; GO:0009611; P:response to wounding; TAS.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS0963; LINK_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35238 MW; 0BBEA56729CEFF77 CRC64;

Query Match 98.3%; Score 1117; DB 2; Length 322;
Best Local Similarity 98.6%; Pred. No. 3.2e-88;
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTRLLVQGSRAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQVE 60
Db 16 TTRLLVQGSRAEELSIQVSCRMGITLVSKKANQQLNFTAEKACRLGLSLAGKQVD 75
Qy 61 TALKASPETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSQFAAYCYNSSDTW 120
Db 76 TALKASPETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSQFAAYCYNSSDTW 135
Qy 121 TNSCIPEIITTKDPIFNQTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 180
Db 136 TNSCIPEIITTKDPIFNQTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 195
Qy 181 RKKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAGFGG 220
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RESULT 4  
Q8BHC8 BOVIN PRELIMINARY; PRT; 322 AA.  
AC Q8UC88;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cell surface retention sequence binding protein-1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;  
RX Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,  
RY Huang J.S.,  
RT "Cloning, expression, characterization and role in autocrine cell  
RT growth of cell surface retention sequence binding protein-1.";  
RL J. Biol. Chem. 278:43855-43869(2003).  
DR EMBL; AY372937; AAQ85130.1; -; mRNA.  
DR GO; GO:0005540; P-hyaluronic acid binding; IEA.  
DR GO; GO:0007155; P-cell adhesion; IEA.  
DR InterPro; IPR000538; Link.  
DR Pfam; PF00193; Xlink; 1.  
DR PRINTS; P01265; LINKMODULE.  
DR DR PRODOM; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
DR PROSITE; PS01241; LINK 1; UNKNOWN\_1.  
DR PROSITE; PS00963; LINK 2; 1.  
SQ SEQUENCE 322 AA; 35561 MW; 4901DA18F92648AE CRC64;  
  
Query Match 64.3%; Score 730; DB 2; Length 322;  
Best Local Similarity 63.6%; Pred. No. 9.5e-55;  
Matches 140; Conservative 31; Mismatches 49; Indels 0; Gaps 0;  
  
QY 1 TTRLLVQGSURABELSIVSCRMIGITLVSKKANQQLNFTAEACRLGLSLAGKQDVE 60  
DB 16 TTRLLVQGSURSEIEISILGPRIMGVTLVTKTQPLNFTAEQACRLVGLTLASQDVE 75  
  
QY 61 TALKASFETCSYGMWGDGFVVISRNPKGKNGVGLVWKVPVSPQFAAYCNSSDTW 120  
DB 76 EARKFGFETCSYGMWKNQFVVIRIISNPKGSGGVGLVWRSLSRHSRHSCHNGSDIW 135  
  
QY 121 TNSCIPEIITKDPINFTOTATOTTEFIVSDSYSVASPYSTIPAPTTTPPAASIPR 180  
DB 136 INSCLEIITDDPLFNETATATVTKLWSDSTHSELSTGDPDVITVTTVAPLASTSTR 195  
  
QY 181 RKKLICVTEVFMTSTWSTSTETFEVENKAFKAEAGFGG 220  
DB 196 KRKLICITEAFMDTSVATERSIEDIQNRPAFKNVAGFGG 235  
  
RESULT 5  
Q8BHC0 MOUSE PRELIMINARY; PRT; 318 AA.  
AC Q8BHC0;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Extra cellular link domain-containing 1 (Mus musculus adult male lung  
DE cDNA, RIKEN full-length enriched library, clone:1200012G08  
DE product:extra cellular link domain-containing 1, full insert  
DE sequence).  
GN Names=Xlkdl;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I. J., Jarvis E. D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R. M., King B. L.,  
RA Konagaya A., Kurochkin I. V., Lee Y., Lenhard B., Lyons P. A.,  
RA Maglott D. R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W. J., Perte G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J. U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J. C., Reed D. J., Reid J., Ring B. Z., Ringwald M.,  
RA Sadelain A., Schneider C., Sempile C. A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M. S., Teasdale R. D., Tomita M.,  
RA Verardo L. G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Wilming L. G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Xuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E. S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573 (2002).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes";  
RL Genome Res. 10:1617-1630 (2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=2050913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer";  
RL Genome Res. 10:1757-1771 (2000).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC038653; AAH38653.1; -; mRNA.  
DR EMBL; BC038892; AAH38892.1; -; mRNA.  
DR EMBL; AK004726; BAC25094.1; -; mRNA.  
DR HSSP; P98066; 107B.  
DR Ensembl; ENSMUSG00000030787; Mus musculus.  
DR MGI; MGI:2136348; Xlkd1.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005886; C:plasma membrane; IDA.  
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.  
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.  
DR InterPro; IPR000538; Link.  
DR Pfam; PF00193; Xlink; 1.

DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
DR PROSITE; PS01241; LINK 1; UNKNOWN\_1.  
DR PROSITE; PS0963; LINK 2; 1.  
SQ SEQUENCE 318 AA; 34573 MW; 34AA31AEF5430B08 CRC64;  
Query Match 59.9%; Score 680; DB 2; Length 318;  
Best Local Similarity 61.4%; Pred. No. 2e-50;  
Matches 135; Conservative 28; Mismatches 53; Indels 4; Gaps 3;  
QY 1 TTRLLVQSLRAEELSIOVSCRMIGITLVSKANQOQLNFTAEACRLILGLSLAGKQDVE 60  
DB 16 TTRHPVQADLVQDLISL-TCRIMGVALVGRNKNQPNFTAEACRMLGLTLASRQVE 74  
QY 61 TALKASFTCSYGVWGDGVVVISRISPNPKGKNGVLIWKVPVSRQFAAYCYNSSDTW 120  
DB 75 SAQKSGFETCSYGVWGDGVVVISRISPNPKGKNGVLIWKVPVSRQFAAYCYNSSDTW 134  
QY 121 TNSCIPIITTKDPIFNQTQTATQTTEFIVSDSYVASPYSTIPAPTTPPAPASTSIPR 180  
DB 135 VNSCIPEIVTTFYPLVLTQ--TPATEFSVSSAYLASSPDSSTTPVSATT-RAPPLTSMAR 191  
QY 181 RKKLICVTEVFMETSTMSTETEPFVNKAAPKNEAAGFGG 220  
DB 192 KTKKICITEVTEPITWATEFAFVAGAAFKNEAAGFGG 231  
RESULT 6  
ID Q59NE4 MOUSE PRELIMINARY; PRT; 318 AA.  
AC Q59NE4.  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Hyaluronan receptor precursor.  
GN Name=Xlkd1; Synonyms=LYVE-1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c; TISSUE=Digestive tract;  
RX MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;  
RA Banerji S.;  
RT "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific  
RT receptor for hyaluronan";  
RL J. Cell Biol. 144:789-801 (1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c; TISSUE=Digestive tract;  
RX MEDLINE=21276443; PubMed=11278811; DOI=10.1074/jbc.M011004200;  
RA Prevo R., Banerji S., Ferguson D. J. P., Claasper S., Jackson D. G.;  
RT "Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic  
RT endothelium";  
RL J. Biol. Chem. 276:19420-19430 (2001).  
DR EMBL; AJ311501; CAC33082.1; -; mRNA.  
DR HSSP; P98066; 107B.  
DR MGI; MGI:2136348; Xlkd1.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005886; C:plasma membrane; IDA.  
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.  
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.  
DR InterPro; IPR000538; Link.  
DR Pfam; PF00193; Xlink; 1.  
DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
DR PROSITE; PS01241; LINK 1; UNKNOWN\_1.  
DR PROSITE; PS0963; LINK 2; 1.  
DR Receptor; Signal.

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FT SIGNAL 1 23 Potential.
FT CHAIN 24 318 LYVE-1.
SQ SEQUENCE 318 AA; 34641 MW; 1248974A16113330 CRC64;

Query Match 59.9%; Score 680; DB 2; Length 318;
Best Local Similarity 61.4%; Pred. No. 2e-50;
Matches 135; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

QY 1 TTRLLVQGSRAEELSIOVSCRMIGITLVSKKANQQLNFTAEKACRLGLSLAGKDOVE 60
DB 16 TTRHPVQGDVLVDLSIS--TCRIMGVALVGRNKPQNFTEANEAKCKLGLTLASRDQVE 74

QY 61 TALKASPETCSYGVGDFGVVIRISPNPKGKNGVGLVWKVPVSRQFAAYCNSSDTW 120
DB 75 SAQKSGPETCSYGVGDFGVVIRISPNPKGKNGVGLVWKVPVSRQFAAYCNSSDTW 134

QY 121 TNSCIPRIITKDPINFNTQTATQTTTEFIVSDSYVASPYSTTPAPTTTPPASTSIPR 180
DB 135 VNSCIPRIITKDPINFNTQTATQTTTEFIVSDSYVASPYSTTPAPTTTPPASTSIPR 191

QY 181 RKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAGFGG 220
DB 192 KTKKICITEVTEPTATTEAFVASGAAPKNEAGFGG 231

RESULT 7
QYYS22_PIG PRELIMINARY; PRT; 201 AA.
AC QYYS22_PIG
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)
DE Lymphatic endothelial hyaluronan receptor LYVE-1 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN NUCLEOTIDE SEQUENCE.
RA Michael K.W., Xu S.-H., Voisine P., Khan T.A., Feng J., Li J.,
RA Sellke F.W., Bianchi C.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY304537; AAP69946.1; -; mRNA.
DR GO; GO:0005540; F-hyaluronic acid binding; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PROSITE; PS50963; LINK_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 201
SQ SEQUENCE 201 AA; 22219 MW; BAAF34E7EACBBAE3 CRC64;

Query Match 46.3%; Score 526.5; DB 2; Length 201;
Best Local Similarity 64.6%; Pred. No. 2.1e-37;
Matches 102; Conservative 20; Mismatches 33; Indels 3; Gaps 2;

QY 66 SPFTCSYGVGDFGVVIRISPNPKGKNGVGLVWKVPVSRQFAAYCNSSDTWNSCI 125
DB 1 SPFTCSYGVGDFGVVIRISPNPKGKNGVGLVWKVPVSRQFAAYCNSSDTWNSCI 60

QY 126 PEIITTKDPINFNTQTATQTTTEFIVSDSYVAS--PYSTI-PAPTTTPPASTSIPR 182
DB 61 PEIITNDPNTNTAPTYTTEMTVNDRTSSSSGPPSSVMPVTVTSLPLATTSTPRKR 120

QY 183 KLICVTEVFMETSTMSTETEPFVENKAAPKNEAGFGG 220
DB 121 KLICITEAFMETSTIISTETELYENTAFKNEAGFGG 158
```

RESULT 8

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Q58E15 XENLA PRELIMINARY; PRT; 392 AA.
ID Q58E15
AC Q58E15
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN NUCLEOTIDE SEQUENCE.
RA TISSUE=Kidney;
RC TISSUE=Kidney;
RX MEDLINE-22341132; PubMed-12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Wagner L., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Gerhardt D.S.;
RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC092113; AAH92113.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 392
SQ SEQUENCE 392 AA; 43658 MW; AF47C05ACS50C6A1 CRC64;

Query Match 21.6%; Score 245; DB 2; Length 392;
Best Local Similarity 34.9%; Pred. No. 1.1e-12;
Matches 58; Conservative 18; Mismatches 70; Indels 20; Gaps 3;

QY 19 VSCRIMGITLVSKKANQQLNFTAEKACRLGLSLAGKDOVETALKASFETCSYGVGDFG 78
DB 33 ISCRPKGVHVEKNDYSLNQEDAVKLQGLMNTSIANYTQLEIALDFGFCRYGWIEDR 92

QY 79 FVVISRISPNPKGKNGVGLVWKVPVSRQFAAYCNSSDTWNSCIPR-----128
DB 93 -VLIPRIKENPICAANYTGIYTLGNNSLRDYVCYNASETEKSLCLVLLNLLNDFSHN 151

QY 129 -ITTKDPIINTQTATQTTTEFIVSDSYVASPYSTIPAPTTTPPAP 173
DB 152 TIDSVDPTLTQIQNSDKSGYOGDSV-----TDPAPAMITPDP 189
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RESULT 9
Q6GM56_XENLA
ID Q6GM56_XENLA PRELIMINARY; PRT; 441 AA.
AC Q6GM56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC443701 protein (Fragment).
GN Name=LOC443701;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC074228; AAH74228.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0005540; F:protein binding; IEA.
DR GO; GO:0007155; F:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS0963; LINK_2; 1.
FT NON TER
SQ SEQUENCE 441 AA; 49207 MW; DF9AA596D506D1A1 CRC64;
Query Match 21.2%; Score 241; DB 2; Length 441;
Best Local Similarity 34.3%; Pred. No. 2.7e-12;
Matches 57; Conservative 19; Mismatches 70; Indels 20; Gaps 3;

```







Db 75 KGFETCRYGI-EGHWIPRIHPNAICANNVTGYVILLASNTSHDYTCFNASAPLEBDC 133  
QY 125 IPEIITTKDPIENTOTATQTTEFVSDST-YSVASPYST 162  
Db 134 -----TSVTDLPNSFDGVPVITIVNRDTRYKKGERT 167

RESULT 14  
Q98SR5 ANAPL  
ID Q98SR5 ANAPL PRELIMINARY; PRT; 265 AA.  
AC Q98SR5  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE T cell antigen CD44 isoform b.  
OS Anas platyrhynchos (Domestic duck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archoauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
OX NCBI\_TaxID=8839;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=White Pekin;  
RA Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF332869; AAK18277.1; -; mRNA.  
DR HSP; P98066; 107B.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR001231; CD44 antigen.  
DR Pfam; PF00193; Xlink; 1.  
DR PRINTS; PR00658; CD44.  
DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
DR PROSITE; PS01241; LINK 1; UNKNOWN\_1.  
DR PROSITE; PS0963; LINK\_2; 1.  
SQ SEQUENCE 265 AA; 29215 MW; 77C176E0A89D081 CRC64;

Query Match 18.6%; Score 211; DB 2; Length 265;  
Best Local Similarity 28.4%; Pred. No. 5.8e-10;  
Matches 62; Conservative 31; Mismatches 93; Indels 32; Gaps 5;

QY 14 ELSIQVSCRMGITLVSKKANQQLNFTTEAKRLLGLSLAGKQVETALKASFETCSYG 73  
Db 21 ETQFNVSCTRYGVFHVKEKGRYSILRTEAADLCRALNSTLSTLEQLEKAHELGFETCRYG 80

QY 74 WVGDFVVISRISPNPKCGKNGVGLWLVKVPVSRQFAAYCNSDWTWNSCIP----- 126  
Db 81 FV-VGYIVIPRINPYHLCAANHGTGIYKLSANTTGRYDAYCYNATETRDKACEPIERIDTS 139

QY 127 -----EIIITKDP-----IFNTQTATQTTEFVSDSTYSVASPYSTIPAPT 175  
Db 140 FLNQGGEIVIDNEDGSRYNADGTRHSGDSTSGVDNENGVSGSSHDTTPVDTIRSSPS 199

QY 176 -----TSIPR-----RKLCIVTEVFMTSTMTSE 200  
Db 200 YGSGVTPVPHLSDHSSGGGKEFPVNTNSDDEISPTSTD 237

RESULT 15  
Q90ZL8 ANAPL  
ID Q90ZL8 ANAPL PRELIMINARY; PRT; 398 AA.  
AC Q90ZL8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE T cell antigen CD44 isoform a.  
OS Anas platyrhynchos (Domestic duck).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archoauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
OX NCBI\_TaxID=8839;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=White Pekin;  
RA Chan S.W.S., Middleton D.L., Warr G.W., Higgins D.A.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY029553; AAK40246.1; -; mRNA.  
DR HSP; P98066; 107B.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR001231; CD44 antigen.  
DR Pfam; PF00193; Xlink; 1.  
DR PRINTS; PR00658; CD44.  
DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
DR PROSITE; PS01241; LINK 1; UNKNOWN\_1.  
DR PROSITE; PS0963; LINK\_2; 1.  
SQ SEQUENCE 398 AA; 43673 MW; 25A944EE2F4AED6D CRC64;

Query Match 18.4%; Score 209.5; DB 2; Length 398;  
Best Local Similarity 30.1%; Pred. No. 1.3e-09;  
Matches 52; Conservative 27; Mismatches 75; Indels 19; Gaps 3;

QY 14 ELSIQVSCRMGITLVSKKANQQLNFTTEAKRLLGLSLAGKQVETALKASFETCSYG 73  
Db 21 ETQFNVSCTRYGVFHVKEKGRYSILRTEAADLCRALNSTLSTLEQLEKAHELGFETCRYG 80

QY 74 WVGDFVVISRISPNPKCGKNGVGLWLVKVPVSRQFAAYCNSDWTWNSCIP----- 126  
Db 81 FV-VGYIVIPRINPYHLCAANHGTGIYKLSANTTGRYDAYCYNATETRDKACEPIERIDTS 139

QY 127 -----EIIITKDP-----IFNTQTATQTTEFVSDSTYSVASPYSTIPAPT 168  
Db 140 FLNQGGEIVIDNEDGSRYNADGTRHSGDSTSGVDNENGVSGSSHDTTPVDTIS 192

Search completed: March 20, 2006, 14:13:19  
Job time : 70.4764 secs

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OM protein - protein search, using sw model  
 Run on: March 20, 2006, 14:17:31 ; Search time 44.1038 Seconds  
 (without alignments)  
 2191.725 Million cell updates/sec

Title: US-10-063-510-6\_COPY\_16\_235  
 Perfect score: 1136  
 Sequence: 1 TTRLIVQSLRAEELSIQVS.....TEPFVKNKAFKNEAAGFGG 220  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 2443163 seqs, 4393781 residues  
 Total number of hits satisfying chosen parameters: 2443163  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%

Database : A\_Geneseq\_21.\*  
 Listing first 1500 summaries

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAB34702	standard; protein; 250 AA.				
DE	Human secreted protein encoded by DNA clone vb28 1.					
PN	WO200055375-A1.					
PD	21-SEP-2000.					
PA	(ALPH-) ALPHAGENE INC.					
Query Match	100.0%;	Score 1136;	DB 3;	Length 250;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-103;				
RESULT 2						
ID	AAV13379	standard; protein; 322 AA.				
DE	Amino acid sequence of protein PRO263.					
PN	WO9914328-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1136;	DB 2;	Length 322;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-103;				
RESULT 3						
ID	AAV87287	standard; protein; 322 AA.				
DE	Human signal peptide containing protein HSP64					
PN	WO200000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match	100.0%;	Score 1136;	DB 3;	Length 322;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-103;				
RESULT 4						
ID	ADC78521	standard; protein; 322 AA.				
DE	Human PRO263 protein.					
PN	WO200015796-A2.					
PD	23-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1136;	DB 3;	Length 322;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-103;				
RESULT 5						
ID	AAB80247	standard; protein; 322 AA.				
DE	Human PRO263 protein.					
PN	WO200104311-A1.					
PD	18-JAN-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1136;	DB 4;	Length 322;		
Best Local Similarity	100.0%;	Pred. No. 3.3e-103;				
RESULT 6						
ID	AAB87528	standard; protein; 322 AA.				
DE	Human PRO263.					

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PN WO200116318-A2.  
 PD 08-MAR-2001.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 4; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 7  
 ID AAB88391 standard; protein; 322 AA.  
 DE Human membrane or secretory protein clone PSEC0135.  
 PN EP1067182-A2.  
 PD 10-JAN-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 100.0%; Score 1136; DB 4; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 8  
 ID ABG95853 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein PRO263.  
 PN US2002119130-A1.  
 PD 29-AUG-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 5; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 9  
 ID ABB84832 standard; protein; 322 AA.  
 DE Human PRO263 protein sequence SEQ ID NO:32.  
 PN WO200200690-A2.  
 PD 03-JAN-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 5; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 10  
 ID ABB95438 standard; protein; 322 AA.  
 DE Human angiogenesis related protein PRO263 SEQ ID NO: 32.  
 PN WO200208284-A2.  
 PD 31-JAN-2002.  
 PA (GETH) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 100.0%; Score 1136; DB 5; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 11  
 ID ABU71625 standard; protein; 322 AA.  
 DE Human PRO polypeptide #36.  
 PN US2002146709-A1.  
 PD 10-OCT-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 6; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 12  
 ID ABU71480 standard; protein; 322 AA.  
 DE Human PRO polypeptide #36.  
 PN US2002192659-A1.  
 PD 19-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 6; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 13  
 ID ABU71926 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein PRO263.  
 PN US2003003530-A1.  
 PD 02-JAN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 14  
ID ABO01809 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 15  
ID ABU90878 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 16  
ID ABO33937 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 17  
ID ABU71954 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 18  
ID ABUS4382 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 19  
ID ABO47397 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO263.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 20  
ID ABU71508 standard; protein; 322 AA.  
DE Human secreted polypeptide PRO263.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 21  
ID ABU72289 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 22  
ID ABU90962 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 23  
ID ABO27283 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO263.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 24  
ID ABU64534 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #38.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 25  
ID ABU67380 standard; protein; 322 AA.  
DE Human secreted protein PRO263.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 26  
ID ABU92478 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 27  
ID ABO14900 standard; protein; 322 AA.  
DE Human secreted / transmembrane polypeptide PRO263.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 28  
ID ABU81148 standard; protein; 322 AA.  
DE Human secreted polypeptide PRO263.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 29  
ID ABO53263 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 30  
ID ABU98265 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 31  
ID ABU89270 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;

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Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 32
ID ABU82477 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 33
ID ABUS9657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 34
ID ABUS96441 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 35
ID ABU72111 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 36
ID AB014839 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 37
ID ADB29406 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 38
ID ADB17063 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 39
ID AB044241 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 40
ID ADA18262 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 41
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 42
ID ADA19868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 43
ID ADB17251 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 44
ID ABO34851 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 45
ID ADA16237 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 46
ID ADA20040 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 47
ID ABO34169 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 48
ID ADA42382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 49
ID ABO17529 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1136; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 50
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ID ADA00337 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO 263.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 51  
ID ADA16661 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 52  
ID ADA13090 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 53  
ID ADA41958 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 54  
ID ADA17305 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 55  
ID ADA2808 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 56  
ID ABO17590 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 57  
ID ADB85579 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 58  
ID ADB77727 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 59  
ID ADB74863 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 60  
ID ADB68258 standard; protein; 322 AA.  
DE Human PRO263 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 61  
ID ADB68065 standard; protein; 322 AA.  
DE Human PRO263 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 62  
ID ADB90882 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 63  
ID ADC28509 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 64  
ID ADC39709 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 65  
ID ADC40223 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 66  
ID ADC19047 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 67  
ID ADC34347 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 68  
ID ADC29402 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.



PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 69  
ID ADC28933 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 70  
ID ADC40818 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 71  
ID ADC19475 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 72  
ID ADC06962 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 73  
ID ADC17141 standard; protein; 322 AA.  
DE Mammalian PRO polypeptide (SeqID 6).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 74  
ID ADC33923 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 75  
ID ADC12993 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 76  
ID ADC14839 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 77  
ID ADC52334 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003138882-A1.

PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 78  
ID ADC12445 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 79  
ID ADD10321 standard; protein; 322 AA.  
DE Human secreted/transmembrane PRO polypeptide #16.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 80  
ID ADD05000 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 81  
ID ADD11281 standard; protein; 322 AA.  
DE Human secreted/transmembrane PRO polypeptide #16.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 82  
ID ADD04006 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 83  
ID ADD03582 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 84  
ID ADD37074 standard; protein; 322 AA.  
DE Human secreted/transmembrane PRO polypeptide #16.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 85  
ID ADD36010 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 86  
ID ADE34834 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003077583-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 87  
ID ADG01011 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003078387-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 88  
ID ADG08564 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 89  
ID ADF95185 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 90  
ID ADH24038 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 91  
ID ADH34064 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 92  
ID ADH29897 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 93  
ID ADH23868 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 94  
ID ADG85272 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 95  
ID ADH24548 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 96  
ID ADH37404 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 97  
ID ADH01993 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 98  
ID ADH37574 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 99  
ID ADG85612 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 100  
ID ADH24208 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 101  
ID ADH38502 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 102  
ID ADG83623 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 103  
ID ADH29431 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 104  
ID ADH27547 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 105  
ID ADH29431 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 105  
ID ADH37744 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 106  
ID ADH37921 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 107  
ID ADH57341 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 108  
ID ADH59317 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 109  
ID ADH53483 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 110  
ID ADH53653 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 111  
ID ADH51989 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 112  
ID ADH49844 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 113  
ID ADI25354 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;

RESULT 114  
ID ADH90147 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 115  
ID ADI25524 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 116  
ID ADH97698 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 117  
ID ADI38096 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 118  
ID ADI03546 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 119  
ID ADI11903 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 120  
ID ADH89977 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 121  
ID ADH98378 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 122  
ID ADI11053 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 123  
ID ADI11053 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;

ID ADI11563 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 124  
ID ADH98208 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 125  
ID ADH98548 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 126  
ID ADH98038 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 127  
ID ADI05026 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 128  
ID ADI03376 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 129  
ID ADI04771 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 130  
ID ADH78225 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 131  
ID ADI19569 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 132  
ID ADH90317 standard; protein; 322 AA.

DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 133  
ID ADI03036 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 134  
ID ADH77885 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 135  
ID ADH97868 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 136  
ID ADI01253 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 137  
ID ADI01948 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 138  
ID ADI03206 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 139  
ID ADI11393 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 140  
ID ADI02295 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1136; DB 7; Length 322;  
Pred. No. 3.3e-103;  
RESULT 141  
ID ADI11733 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.

PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 142  
ID ADI05370 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 143  
ID ADH79442 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 144  
ID ADI19399 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 145  
ID ADI05200 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 146  
ID ADH79612 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191298-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 147  
ID ADI01438 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 148  
ID ADI01608 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 149  
ID ADI01778 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 150  
ID ADH79782 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191289-A1.

PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 151  
ID ADI04600 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 152  
ID ADI02736 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 153  
ID ADH78055 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 154  
ID ADI25694 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 155  
ID ADI25864 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 156  
ID ADK65376 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 157  
ID ADH98718 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 158  
ID ADH79959 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 159  
ID ADJ26364 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054349-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 160  
 ID ADL93690 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003040013-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 161  
 ID ADC52144 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003130483-A1.  
 PD 10-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 162  
 ID ADE79279 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003135025-A1.  
 PD 17-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 163  
 ID ADE79703 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003130489-A1.  
 PD 10-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 164  
 ID ADE73379 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003129592-A1.  
 PD 10-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 165  
 ID ADE41282 standard; protein; 322 AA.  
 DE Human secreted/transmembrane PRO polypeptide #16.  
 PN US2003100497-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 166  
 ID ADE71444 standard; protein; 322 AA.  
 DE Human PDEBC Incyte 3044710CD1.  
 PN US2003124543-A1.  
 PD 03-JUL-2003.  
 PA (STUA/) STUART S G.  
 PA (STRE/) STREETER D G.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 167  
 ID ADE73914 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003148370-A1.  
 PD 07-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 168  
 ID ADE99468 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US200311576-A1.  
 PD 13-NOV-2003.

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PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 169  
 ID ADE98587 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003211569-A1.  
 PD 13-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 170  
 ID ADE99014 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003211568-A1.  
 PD 13-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 171  
 ID ADG40484 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003225253-A1.  
 PD 04-DEC-2003.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 172  
 ID ADF73878 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003180312-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 173  
 ID ADF73454 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003166051-A1.  
 PD 04-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 174  
 ID ADH06576 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003180852-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 175  
 ID ADH06406 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003180853-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 176  
 ID ADG68827 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003180855-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;

RESULT 177  
ID ADH2717 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 178  
ID ADH25058 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 179  
ID ADH33690 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 180  
ID ADG92297 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 181  
ID ADH02333 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 182  
ID ADH07940 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 183  
ID ADG69337 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 184  
ID ADH39158 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 185  
ID ADG92724 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 186  
ID ADH33520 standard; protein; 322 AA.

ID ADG83898 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 187  
ID ADG85442 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 188  
ID ADH06236 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 189  
ID ADH30066 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 190  
ID ADH24378 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 191  
ID ADG69507 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 192  
ID ADH07770 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 193  
ID ADG85782 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 194  
ID ADH39328 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 195  
ID ADH33520 standard; protein; 322 AA.



DE Human PRO polypeptide #3.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 196  
ID ADH33860 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 197  
ID ADH01070 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 198  
ID ADG69677 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 199  
ID ADH02163 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 200  
ID ADG69167 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 201  
ID ADG85952 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 202  
ID ADH2488 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 203  
ID ADH39505 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 204  
ID ADH02503 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.

PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 205  
ID ADG68997 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 206  
ID ADH07600 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 207  
ID ADG86122 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 208  
ID ADH24718 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 209  
ID ADH25766 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 210  
ID ADH38332 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 211  
ID ADH20513 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 212  
ID ADH20513 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 213  
ID ADH57171 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1136; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
RESULT 214  
ID ADH43465 standard; protein; 322 AA.  
DE Human PRO polypeptide #16.  
PN US2003224984-A1.

PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 214  
 ID ADH07368 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2004006211-A1.  
 PD 08-JAN-2004.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 215  
 ID ADH52159 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003180921-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 216  
 ID ADH59913 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003215904-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 217  
 ID ADH49525 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003180857-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 218  
 ID ADH06941 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2004005665-A1.  
 PD 08-JAN-2004.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 219  
 ID ADH90487 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003181700-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 220  
 ID ADI11223 standard; protein; 322 AA.  
 DE Human PRO polypeptide #3.  
 PN US2003181683-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 221

ID ADI18693 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003152999-A1.  
 PD 14-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 222  
 ID ADH98888 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003190698-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 223  
 ID ADI65403 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003148419-A1.  
 PD 07-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 224  
 ID ADI02118 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003190699-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 225  
 ID ADH90657 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003181701-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 226  
 ID ADI37666 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003096340-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 227  
 ID ADH97462 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003190610-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 228  
 ID ADI65830 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003148371-A1.  
 PD 07-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1136; DB 8; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
 RESULT 229  
 ID ADH60573 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2004023331-A1.  
 PD 05-FEB-2004.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.

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PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 230
ID ADJ99630 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 231
ID ADL08823 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 232
ID ADJ98532 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 233
ID ADJ98702 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 234
ID ADH78861 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 235
ID ADJ99095 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 236
ID ADJ99265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 237
ID ADJ98883 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 238
ID ADH79031 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 239
ID ADK00891 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 240
ID ADK14412 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 241
ID ADM25164 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 242
ID ADM29914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 243
ID ADK82810 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 244
ID ADM80861 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 245
ID ADO06236 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 246
ID ADL1088 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1136; DB 8; Length 322;
  Best Local Similarity 100.0%; Pred. No. 3.3e-103;
RESULT 247
ID ADL17997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
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DE Human NOVX polypeptide #1.  
PN WO200290504-A2.  
PA (CURA-) CURAGEN CORP.  
Query Match 87.2%; Score 990.5; DB 6; Length 297;  
Best Local Similarity 88.6%; Pred. No. 6.7e-89;  
RESULT 260  
ID ADO08255 standard; protein; 297 AA.  
DE Human NOVX polypeptide #1.  
PN US2004018594-A1.  
PD 29-JAN-2004.  
PA (ALSO/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BOLD/) BOLD OG F L.  
PA (BURG/) BURGESS C E.  
PA (CASM/) CASMAN S J.  
PA (CHAP/) CHAPOVAL A.  
PA (EDIN/) EDINGER S R.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUNT/) GUNTHER E.  
PA (GUOX/) GUO X S.  
PA (KEKU/) KEKUDA R.  
PA (LEPL/) LEPLEY D M.  
PA (LILL/) LI L.  
PA (LIUX/) LIU X.  
PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLER C E.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATV/) PATURAJAN M.  
PA (PENA/) PENA C E A.  
PA (RIEG/) RIEGER D K.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (SPVT/) SPYTEK K A.  
PA (TAUP/) TAUPIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERR/) ZERRHUSEN B D.  
Query Match 87.2%; Score 990.5; DB 8; Length 297;  
Best Local Similarity 88.6%; Pred. No. 6.7e-89;  
RESULT 261  
ID ABB72376 standard; protein; 255 AA.  
DE Murine protein isolated from skin cells SEQ ID NO: 700.  
PN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 59.9%; Score 680; DB 5; Length 255;  
Best Local Similarity 61.4%; Pred. No. 2.3e-58;  
RESULT 262  
ID AAE05364 standard; protein; 318 AA.  
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.  
PN WO200148192-A1.  
PD 05-JUL-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 59.9%; Score 680; DB 4; Length 318;  
Best Local Similarity 61.4%; Pred. No. 3.1e-58;  
RESULT 263  
ID RAY12323 standard; protein; 116 AA.  
DE Human 5' EST secreted protein SEQ ID NO:354.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 45.3%; Score 515; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 1.5e-42;  
RESULT 264  
ID ADM24431 standard; protein; 364 AA.  
DE Rat CD44.  
PN WO200024869-A2.  
PD 04-MAY-2000.  
PA (UYVA) UNIV YALE.  
PA (VIGN/) VIGNERY A.

Query Match 18.8%; Score 213.5; DB 3; Length 364;  
Best Local Similarity 32.1%; Pred. No. 3.8e-12;  
RESULT 265  
ID ABB01033 standard; protein; 364 AA.  
DE Rat glycoprotein CD44 polypeptide.  
PN WO200238794-A2.  
PD 16-MAY-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 18.8%; Score 213.5; DB 5; Length 364;  
Best Local Similarity 32.1%; Pred. No. 3.8e-12;  
RESULT 266  
ID AAR14768 standard; protein; 503 AA.  
DE Metastasis-specific variant of CD44 glycoprotein.  
PN DE4014510-A.  
PD 14-NOV-1991.  
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.  
PA (UYKA-) UNIV KARLSRUHE.  
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.  
Query Match 18.8%; Score 213.5; DB 2; Length 503;  
Best Local Similarity 32.1%; Pred. No. 5.9e-12;  
RESULT 267  
ID ADE57911 standard; protein; 503 AA.  
DE Rat Protein P26051, SEQ ID NO 3777.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GERO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 18.8%; Score 213.5; DB 7; Length 503;  
Best Local Similarity 32.1%; Pred. No. 5.9e-12;  
RESULT 268  
ID ADZ51063 standard; protein; 778 AA.  
DE Amino acid sequence of murine CD44.  
PN WO2005034984-A1.  
PD 21-APR-2005.  
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
Query Match 18.4%; Score 209.5; DB 9; Length 778;  
Best Local Similarity 32.7%; Pred. No. 2.6e-11;  
RESULT 269  
ID ABU04619 standard; protein; 668 AA.  
DE Human expressed protein tag (EPT) #1285.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 18.4%; Score 208.5; DB 6; Length 668;  
Best Local Similarity 29.3%; Pred. No. 2.7e-11;  
RESULT 270  
ID ADQ39384 standard; protein; 668 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 18.4%; Score 208.5; DB 8; Length 668;  
Best Local Similarity 29.3%; Pred. No. 2.7e-11;  
RESULT 271  
ID AAR07355 standard; protein; 362 AA.  
DE E7 adhesion receptor.  
PN WO9011365-A.  
PD 04-OCT-1990.  
PA (HUTC-) HUTCHINSON F CANCER.  
Query Match 17.9%; Score 203.5; DB 2; Length 362;  
Best Local Similarity 27.3%; Pred. No. 3.7e-11;  
RESULT 272  
ID ABU04653 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1319.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.9%; Score 203; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
RESULT 273  
ID ABU04616 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1282.

PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 17.9%; Score 203; DB 6; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
 RESULT 274  
 ID ADP65295 standard; protein; 742 AA.  
 DE Human CD44 antigen (homolog function and Indian blood group system), CD44.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 17.9%; Score 203; DB 7; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
 RESULT 275  
 ID ADL61252 standard; protein; 742 AA.  
 DE Human protein tyrosine kinase biomarker CD44 antigen protein.  
 PN WO2004020583-A2.  
 PD 11-MAR-2004.  
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
 Query Match 17.9%; Score 203; DB 8; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
 RESULT 276  
 ID ADQ39391 standard; protein; 742 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 17.9%; Score 203; DB 8; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
 RESULT 277  
 ID ADR67253 standard; protein; 742 AA.  
 DE Human bladder cancer associated amino acid sequence.  
 PN WO2004076613-A2.  
 PD 10-SEP-2004.  
 PA (HERR/) HERR A.  
 PA (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (STAU/) STAU E.  
 PA (PILA/) PILARSKY C.  
 PA (SPEC/) SPECHT T.  
 Query Match 17.9%; Score 203; DB 8; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
 RESULT 278  
 ID ADU06304 standard; protein; 742 AA.  
 DE Novel bronchial cancer-associated human protein SeqID528.  
 PN DE10316701-A1.  
 PD 04-NOV-2004.  
 PA (HINZ/) HINZMANN B.  
 PA (HERM/) HERMANN K.  
 PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
 Query Match 17.9%; Score 203; DB 8; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
 RESULT 279  
 ID ADY15336 standard; protein; 742 AA.  
 DE PRO polypeptide SEQ ID NO 1142.  
 PN WO2005016962-A2.  
 PD 24-FEB-2005.  
 PA (GETH) GENENTECH INC.  
 Query Match 17.9%; Score 203; DB 9; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
 RESULT 280  
 ID ADV15338 standard; protein; 742 AA.  
 DE PRO polypeptide SEQ ID NO 1144.  
 PN WO2005016962-A2.  
 PD 24-FEB-2005.  
 PA (GETH) GENENTECH INC.  
 Query Match 17.9%; Score 203; DB 9; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-10;  
 RESULT 281  
 ID ABU04618 standard; protein; 675 AA.  
 DE Human expressed protein tag (EPT) #1284.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 17.8%; Score 202; DB 6; Length 675;  
 Best Local Similarity 26.0%; Pred. No. 1.2e-10;  
 RESULT 282  
 ID ABU04621 standard; protein; 691 AA.  
 DE Human expressed protein tag (EPT) #1287.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 17.8%; Score 202; DB 6; Length 691;  
 Best Local Similarity 26.0%; Pred. No. 1.2e-10;  
 RESULT 283  
 ID ADQ39390 standard; protein; 691 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 17.8%; Score 202; DB 8; Length 691;  
 Best Local Similarity 26.0%; Pred. No. 1.2e-10;  
 RESULT 284  
 ID ABU04620 standard; protein; 742 AA.  
 DE Human expressed protein tag (EPT) #1286.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 17.8%; Score 202; DB 6; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
 RESULT 285  
 ID ABU04645 standard; protein; 742 AA.  
 DE Human expressed protein tag (EPT) #1311.  
 PN WO200278524-A2.  
 PD 10-OCT-2002.  
 PA (ZYCO-) ZYCOS INC.  
 Query Match 17.8%; Score 202; DB 6; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
 RESULT 286  
 ID ADN95511 standard; protein; 742 AA.  
 DE Human BEC/LEC-related protein sequence SeqID434.  
 PN WO2003080840-A1.  
 PD 02-OCT-2003.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN) LICENTIA LTD.  
 Query Match 17.8%; Score 202; DB 7; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
 RESULT 287  
 ID ADI93506 standard; protein; 742 AA.  
 DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.  
 PN WO2004024750-A2.  
 PD 25-MAR-2004.  
 PA (DYAX-) DYAX CORP.  
 Query Match 17.8%; Score 202; DB 8; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
 RESULT 288  
 ID ADO55181 standard; protein; 742 AA.  
 DE Protein #83 with increased gene expression in renal cell carcinoma.  
 PN WO2004032842-A2.  
 PD 22-APR-2004.  
 PA (VAND-) VAN ANDEL INST.  
 Query Match 17.8%; Score 202; DB 8; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
 RESULT 289  
 ID ADQ39383 standard; protein; 742 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 17.8%; Score 202; DB 8; Length 742;  
 Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
 RESULT 290  
 ID ADQ39386 standard; protein; 742 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.  
Query Match 17.8%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
RESULT 291  
ID ADW72142 standard; protein; 742 AA.  
DE Human CD44 protein as biomarker for colorectal cancer.  
PN US2005014165-A1.  
PD 20-JAN-2005.  
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.  
Query Match 17.8%; Score 202; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
RESULT 292  
ID ADZ51062 standard; protein; 742 AA.  
DE Amino acid sequence of human CD44.  
PN WO2005034984-A1.  
PD 21-APR-2005.  
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
Query Match 17.8%; Score 202; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 1.4e-10;  
RESULT 293  
ID ABP72424 standard; protein; 608 AA.  
DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.  
PN WO2003014160-A2.  
PD 20-FEB-2003.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 17.6%; Score 200.5; DB 6; Length 608;  
Best Local Similarity 25.2%; Pred. No. 1.5e-10;  
RESULT 294  
ID ADD90596 standard; protein; 699 AA.  
DE Human CD44v glycoprotein SEQ ID NO:6.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match 17.6%; Score 200.5; DB 7; Length 699;  
Best Local Similarity 25.2%; Pred. No. 1.8e-10;  
RESULT 295  
ID ADW43570 standard; protein; 699 AA.  
DE CD44v3-v10.  
PN WO2005007700-A1.  
PD 27-JAN-2005.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 17.8%; Score 200.5; DB 9; Length 699;  
Best Local Similarity 25.2%; Pred. No. 1.8e-10;  
RESULT 296  
ID AAY97579 standard; protein; 700 AA.  
DE Human CD44 splice variant (RA-CD44) protein sequence.  
PN WO200075312-A1.  
PD 14-DEC-2000.  
PA (YISS) YISSUM RES & DEV CO.  
Query Match 17.6%; Score 200.5; DB 4; Length 700;  
Best Local Similarity 25.2%; Pred. No. 1.8e-10;  
RESULT 297  
ID ABU04640 standard; protein; 700 AA.  
DE Human expressed protein tag (EPT) #1306.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.6%; Score 200.5; DB 6; Length 700;  
Best Local Similarity 25.2%; Pred. No. 1.8e-10;  
RESULT 298  
ID ADD90594 standard; protein; 700 AA.  
DE Human CD44v glycoprotein SEQ ID NO:4.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 17.6%; Score 200.5; DB 7; Length 700;  
Best Local Similarity 25.2%; Pred. No. 1.8e-10;  
RESULT 299  
ID ADW43568 standard; protein; 700 AA.  
DE CD44vRA.  
PN WO2005007700-A1.

PD 27-JAN-2005.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 17.6%; Score 200.5; DB 9; Length 700;  
Best Local Similarity 25.2%; Pred. No. 1.8e-10;  
RESULT 300  
ID AAV12853 standard; protein; 58 AA.  
DE Human 5' EST secreted protein SEQ ID NO:443.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 17.6%; Score 200; DB 2; Length 58;  
Best Local Similarity 97.7%; Pred. No. 7.1e-12;  
RESULT 301  
ID AAR20817 standard; protein; 493 AA.  
DE Epithelial CD44 Antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 17.6%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 302  
ID AAR31445 standard; protein; 493 AA.  
DE Human epithelial CD44 antigen.  
PN US5506126-A.  
PD 09-APR-1996.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 17.6%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 303  
ID AAW80454 standard; protein; 493 AA.  
DE Human CD44 antigen (epithelial form).  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 17.6%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 304  
ID AAW89151 standard; protein; 493 AA.  
DE Human CD44 antigen (epithelial form).  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 17.6%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 305  
ID AAY36140 standard; protein; 493 AA.  
DE Human epithelial CD44.  
PN US6111053-A.  
PD 29-AUG-2000.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 17.6%; Score 199.5; DB 3; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 306  
ID AAU02449 standard; protein; 493 AA.  
DE Human epithelial antigen CD44 polypeptide.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 17.6%; Score 199.5; DB 4; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 307  
ID ABU04637 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1303.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.6%; Score 199.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 308  
ID ABU04627 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1293.  
PN WO200278524-A2.  
PD 10-OCT-2002.



PA (ZYCO-) ZYCOS INC.  
Query Match 17.6%; Score 199.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 309  
ID ABU04639 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1305.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.6%; Score 199.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 310  
ID ABU04631 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1297.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.6%; Score 199.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 311  
ID ABU04633 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1299.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.6%; Score 199.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 312  
ID ABU04635 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1301.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.6%; Score 199.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 313  
ID ABU04613 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1279.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.6%; Score 199.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 314  
ID ADO49375 standard; protein; 493 AA.  
DE Human CD44 #2.  
PN US2004072283-A1.  
PD 15-APR-2004.  
PA (SEED/) SEED B.  
PA (ALIE/) ALLEN J.  
PA (ARUF/) ARUFFO A.  
PA (CAME/) CAMERINI D.  
PA (LAUF/) LAUFFER L.  
PA (OQUE/) OQUENDO C.  
PA (SINN/) SIMMONS D.  
PA (STAM/) STAMENKOVIC I.  
PA (STEN/) STENGELIN S.  
PA (AMIO/) AMIOT M.  
Query Match 17.6%; Score 199.5; DB 8; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 315  
ID AEB87764 standard; protein; 493 AA.  
DE Human CD44, breast tumor marker.  
PN WO2005071419-A2.  
PD 04-AUG-2005.  
PA (IPSO-) IPSOGEN.  
PA (INRM-) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (PAOL-) INST PAOLI CALMETTES.  
Query Match 17.6%; Score 199.5; DB 9; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.4e-10;  
RESULT 316  
ID AB079109 standard; protein; 365 AA.  
DE CD44 protein.

PN US2002177551-A1.  
PD 28-NOV-2002.  
PA (TERM/) TERMAN D S.  
Query Match 17.5%; Score 198.5; DB 6; Length 365;  
Best Local Similarity 31.8%; Pred. No. 1.2e-10;  
RESULT 317  
ID ADF43353 standard; protein; 365 AA.  
DE CD44 receptor polypeptide seq id 73.  
PN US2003157113-A1.  
PD 21-AUG-2003.  
PA (TERM/) TERMAN D S.  
Query Match 17.5%; Score 198.5; DB 7; Length 365;  
Best Local Similarity 31.8%; Pred. No. 1.2e-10;  
RESULT 318  
ID AEA03024 standard; protein; 365 AA.  
DE CD14 receptor amino acid sequence SEQ ID NO:50.  
PN US2005112141-A1.  
PD 26-MAY-2005.  
PA (TERM/) TERMAN D S.  
Query Match 17.5%; Score 198.5; DB 9; Length 365;  
Best Local Similarity 31.8%; Pred. No. 1.2e-10;  
RESULT 319  
ID AAU99123 standard; protein; 493 AA.  
DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.  
PN WO200244342-A2.  
PD 06-JUN-2002.  
PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 17.5%; Score 198.5; DB 5; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.7e-10;  
RESULT 320  
ID ABU04623 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1289.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.5%; Score 198.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.7e-10;  
RESULT 321  
ID ABU04612 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1278.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.5%; Score 198.5; DB 6; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.7e-10;  
RESULT 322  
ID ADU93507 standard; protein; 493 AA.  
DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.  
PN WO2004024750-A2.  
PD 25-MAR-2004.  
PA (DYAX-) DYAX CORP.  
Query Match 17.5%; Score 198.5; DB 8; Length 493;  
Best Local Similarity 23.6%; Pred. No. 1.7e-10;  
RESULT 323  
ID ABU04617 standard; protein; 425 AA.  
DE Human expressed protein tag (EPT) #1283.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.4%; Score 198; DB 6; Length 425;  
Best Local Similarity 24.4%; Pred. No. 1.6e-10;  
RESULT 324  
ID AAR20816 standard; protein; 361 AA.  
DE Haematopoietic CD44 Antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GSHO-) GEN HOSPITAL CORP.  
Query Match 17.3%; Score 197; DB 2; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 325  
ID AAR91444 standard; protein; 361 AA.  
DE Human haematopoietic CD44 antigen.  
PN US5506126-A.

PD 09-APR-1996.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 17.3%; Score 197; DB 2; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 326  
ID AAW80453 standard; protein; 361 AA.  
DE Human CD44 antigen (membrane form).  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 17.3%; Score 197; DB 2; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 327  
ID AAW86200 standard; protein; 361 AA.  
DE Human CD44 antigen (membrane form).  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 17.3%; Score 197; DB 2; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 328  
ID AAY9851 standard; protein; 361 AA.  
DE Human CD44 cell surface adhesion receptor.  
PN WO200035935-A1.  
PD 22-JUN-2000.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 17.3%; Score 197; DB 3; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 329  
ID AAY96139 standard; protein; 361 AA.  
DE Human haematopoietic CD44.5.  
PN US6111093-A.  
PD 29-AUG-2000.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 17.3%; Score 197; DB 3; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 330  
ID AAU02448 standard; protein; 361 AA.  
DE Human haematopoietic antigen CD44 polypeptide.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 17.3%; Score 197; DB 4; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 331  
ID ABU04632 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1298.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 332  
ID ABU04643 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1309.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 333  
ID ABU04610 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1276.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 334  
ID ABU04638 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1304.  
PN WO200278524-A2.  
PD 10-OCT-2002.

PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 335  
ID ABU04634 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1300.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 336  
ID ABU04626 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1292.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 337  
ID ABU04630 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1296.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 338  
ID ABU04609 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1275.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 339  
ID ABU04644 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1310.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 340  
ID ABU04636 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1302.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 341  
ID ADO49373 standard; protein; 361 AA.  
DE Human CD44 #1.  
PN US2004072283-A1.  
PD 15-APR-2004.  
PA (SEED/) SEED B.  
PA (ALIE/) ALLEN J.  
PA (ARUF/) ARUFFO A.  
PA (CAME/) CAMERINI D.  
PA (LAUF/) LAUFFER L.  
PA (OQUE/) OQUENDO C.  
PA (SIMM/) SIMMONS D.  
PA (STAM/) STAMENKOVIC I.  
PA (STEN/) STENGLIN S.  
PA (AMIO/) AMIOT M.  
Query Match 17.3%; Score 197; DB 8; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 342  
ID ADV70207 standard; protein; 361 AA.  
DE Tumor-associated antigenic target polypeptide TAT449.  
PN WO2004112829-A2.  
PD 29-DEC-2004.

PA (GETH ) GENENTECH INC.  
Query Match 17.3%; Score 197; DB 9; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 343  
ID ADY19504 standard; protein; 361 AA.  
DE PRO polypeptide SEQ ID NO 5310.  
FN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 17.3%; Score 197; DB 9; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 344  
ID ABA63870 standard; protein; 361 AA.  
DE Protein of human anti-CD44 antibody.  
FN JP2005154389-A.  
PD 16-JUN-2005.  
PA (UYTY ) UNIV TOKYO.  
PA (FUYI ) FUJII PHARM IND CO LTD.  
Query Match 17.3%; Score 197; DB 9; Length 361;  
Best Local Similarity 30.9%; Pred. No. 1.6e-10;  
RESULT 345  
ID AAY97650 standard; protein; 431 AA.  
DE CD44HextraFASm/cyto protein sequence.  
FN WO200100854-A2.  
PD 04-JAN-2001.  
PA (ANGI-) ANGIOGENE PHARM LTD.  
Query Match 17.3%; Score 197; DB 4; Length 431;  
Best Local Similarity 30.9%; Pred. No. 2e-10;  
RESULT 346  
ID ABU04641 standard; protein; 431 AA.  
DE Human expressed protein tag (EPT) #1307.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 431;  
Best Local Similarity 30.9%; Pred. No. 2e-10;  
RESULT 347  
ID AAY97651 standard; protein; 436 AA.  
DE CD44Hextra/tmFAScyto protein sequence.  
FN WO200100854-A2.  
PD 04-JAN-2001.  
PA (ANGI-) ANGIOGENE PHARM LTD.  
Query Match 17.3%; Score 197; DB 4; Length 436;  
Best Local Similarity 30.9%; Pred. No. 2.1e-10;  
RESULT 348  
ID ABU04642 standard; protein; 436 AA.  
DE Human expressed protein tag (EPT) #1308.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 436;  
Best Local Similarity 30.9%; Pred. No. 2.1e-10;  
RESULT 349  
ID ABU04604 standard; protein; 719 AA.  
DE Human expressed protein tag (EPT) #1270.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 719;  
Best Local Similarity 26.3%; Pred. No. 4e-10;  
RESULT 350  
ID ABU04650 standard; protein; 719 AA.  
DE Human expressed protein tag (EPT) #1316.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 197; DB 6; Length 719;  
Best Local Similarity 26.3%; Pred. No. 4e-10;  
RESULT 351  
ID ABM83594 standard; protein; 535 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.  
FN WO2004023973-A2.  
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.  
Query Match 17.3%; Score 196.5; DB 8; Length 535;  
Best Local Similarity 25.4%; Pred. No. 3.1e-10;  
RESULT 352  
ID ADQ39381 standard; protein; 535 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.  
FN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 17.3%; Score 196.5; DB 8; Length 535;  
Best Local Similarity 25.4%; Pred. No. 3.1e-10;  
RESULT 353  
ID ABU56470 standard; protein; 699 AA.  
DE Lung cancer-associated polypeptide #63.  
FN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 17.3%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 4.4e-10;  
RESULT 354  
ID ABU04647 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1313.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 4.4e-10;  
RESULT 355  
ID ABU04614 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1280.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 4.4e-10;  
RESULT 356  
ID ABU04608 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1274.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.3%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 4.4e-10;  
RESULT 357  
ID ADV73230 standard; protein; 699 AA.  
DE Human colon tumor cell upregulated protein SEQ ID NO 71.  
FN WO2004110345-A2.  
PD 23-DEC-2004.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 17.3%; Score 196.5; DB 9; Length 699;  
Best Local Similarity 25.4%; Pred. No. 4.4e-10;  
RESULT 358  
ID ADY16689 standard; protein; 699 AA.  
DE PRO polypeptide SEQ ID NO 2495.  
FN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 17.3%; Score 196.5; DB 9; Length 699;  
Best Local Similarity 25.4%; Pred. No. 4.4e-10;  
RESULT 359  
ID ADI60182 standard; protein; 261 AA.  
DE Secreted polypeptide #66.  
FN WO2003025142-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 17.3%; Score 196; DB 7; Length 261;  
Best Local Similarity 30.9%; Pred. No. 1.3e-10;  
RESULT 360  
ID ABU04611 standard; protein; 293 AA.  
DE Human expressed protein tag (EPT) #1277.  
FN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.

Query Match  
Best Local Similarity 17.3%; Score 196; DB 6; Length 293;  
RESULT 361  
ID ABU04624 standard; protein; 294 AA.  
DE Human expressed protein tag (EPT) #1290.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 6; Length 294;  
RESULT 362  
ID ABU04646 standard; protein; 294 AA.  
DE Human expressed protein tag (EPT) #1312.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 6; Length 294;  
RESULT 363  
ID ADH18898 standard; protein; 330 AA.  
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 8; Length 330;  
RESULT 364  
ID ABU04622 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1288.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 6; Length 361;  
RESULT 365  
ID AAE30338 standard; protein; 361 AA.  
DE Human CD44 antigen.  
PN WO200276510-A1.  
PD 03-OCT-2002.  
PA (AGYT-) AGY THERAPEUTICS INC.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 6; Length 361;  
RESULT 366  
ID ADD90592 standard; protein; 361 AA.  
DE Human CD48cd glycoprotein SEQ ID NO:2.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (VEDA ) YEDA RES & DEV CO LTD.  
PA (VISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 7; Length 361;  
RESULT 367  
ID ADL93508 standard; protein; 361 AA.  
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.  
PN WO2004024750-A2.  
PD 25-MAR-2004.  
PA (DYAX-) DYAX CORP.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 8; Length 361;  
RESULT 368  
ID ADQ39385 standard; protein; 361 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 8; Length 361;  
RESULT 369  
ID ADW43572 standard; protein; 361 AA.  
DE CD44.  
PN WO2005007700-A1.  
PD 27-JAN-2005.  
PA (VISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

Query Match  
Best Local Similarity 17.3%; Score 196; DB 9; Length 361;  
RESULT 370  
ID ADY16699 standard; protein; 361 AA.  
DE PRO polypeptide SEQ ID NO 2505.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 9; Length 361;  
RESULT 371  
ID ABU04615 standard; protein; 395 AA.  
DE Human expressed protein tag (EPT) #1281.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 6; Length 395;  
RESULT 372  
ID ADQ39389 standard; protein; 395 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 8; Length 395;  
RESULT 373  
ID ADQ39382 standard; protein; 425 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 8; Length 425;  
RESULT 374  
ID ADQ39388 standard; protein; 493 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 17.3%; Score 196; DB 8; Length 493;  
RESULT 375  
ID ABG17071 standard; protein; 742 AA.  
DE Novel human diagnostic protein #17062.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 17.1%; Score 194.5; DB 4; Length 742;  
RESULT 376  
ID AAM48306 standard; protein; 194 AA.  
DE Protein R2 SEQ ID 29.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match  
Best Local Similarity 17.1%; Score 194; DB 5; Length 194;  
RESULT 377  
ID AAM48307 standard; protein; 200 AA.  
DE Protein R3 SEQ ID 30.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match  
Best Local Similarity 17.1%; Score 194; DB 5; Length 200;  
RESULT 378  
ID AAM48308 standard; protein; 273 AA.  
DE Protein R4 SEQ ID 31.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match  
Best Local Similarity 17.1%; Score 194; DB 5; Length 273;

Best Local Similarity 30.8%; Pred. No. 2.2e-10;  
RESULT 379  
ID ABU04607 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1273.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 17.1%; Score 194; DB 6; Length 361;  
Best Local Similarity 30.9%; Pred. No. 3.2e-10;  
RESULT 380  
ID ADS75483 standard; protein; 361 AA.  
DE Human cell surface glycoprotein CD44 amino acid sequence.  
PN JP2004275060-A.  
PD 07-OCT-2004.  
PA (SANY ) SANKYO CO LTD.  
Query Match 17.1%; Score 194; DB 8; Length 361;  
Best Local Similarity 30.9%; Pred. No. 3.2e-10;  
RESULT 381  
ID ABU04602 standard; protein; 676 AA.  
DE Human expressed protein tag (EPT) #1268.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 16.9%; Score 191.5; DB 6; Length 676;  
Best Local Similarity 25.8%; Pred. No. 1.3e-09;  
RESULT 382  
ID ABU04652 standard; protein; 676 AA.  
DE Human expressed protein tag (EPT) #1318.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 16.9%; Score 191.5; DB 6; Length 676;  
Best Local Similarity 25.8%; Pred. No. 1.3e-09;  
RESULT 383  
ID ABU04648 standard; protein; 271 AA.  
DE Human expressed protein tag (EPT) #1314.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 16.8%; Score 191; DB 6; Length 271;  
Best Local Similarity 31.5%; Pred. No. 4.3e-10;  
RESULT 384  
ID ABU04606 standard; protein; 271 AA.  
DE Human expressed protein tag (EPT) #1272.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 16.8%; Score 191; DB 6; Length 271;  
Best Local Similarity 31.5%; Pred. No. 4.3e-10;  
RESULT 385  
ID ABU04649 standard; protein; 338 AA.  
DE Human expressed protein tag (EPT) #1315.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 16.8%; Score 191; DB 6; Length 338;  
Best Local Similarity 31.5%; Pred. No. 5.8e-10;  
RESULT 386  
ID ABU04605 standard; protein; 338 AA.  
DE Human expressed protein tag (EPT) #1271.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 16.8%; Score 191; DB 6; Length 338;  
Best Local Similarity 31.5%; Pred. No. 5.8e-10;  
RESULT 387  
ID ABU04651 standard; protein; 470 AA.  
DE Human expressed protein tag (EPT) #1317.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 16.8%; Score 191; DB 6; Length 470;  
Best Local Similarity 31.5%; Pred. No. 9e-10;

RESULT 388  
ID ABU04603 standard; protein; 470 AA.  
DE Human expressed protein tag (EPT) #1269.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 16.8%; Score 191; DB 6; Length 470;  
Best Local Similarity 31.5%; Pred. No. 9e-10;  
RESULT 389  
ID AM48305 standard; protein; 170 AA.  
DE Protein RI SEQ ID 28.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 16.5%; Score 188; DB 5; Length 170;  
Best Local Similarity 35.7%; Pred. No. 4.6e-10;  
RESULT 390  
ID ABP73148 standard; protein; 112 AA.  
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 16.5%; Score 187; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 3.3e-10;  
RESULT 391  
ID ABP73150 standard; protein; 113 AA.  
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 16.4%; Score 186.5; DB 6; Length 113;  
Best Local Similarity 36.3%; Pred. No. 3.7e-10;  
RESULT 392  
ID ABP73151 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 16.3%; Score 185; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 5.2e-10;  
RESULT 393  
ID AAY12170 standard; protein; 69 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 483.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 16.2%; Score 184; DB 2; Length 69;  
Best Local Similarity 95.1%; Pred. No. 3.4e-10;  
RESULT 394  
ID ABP73152 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 16.1%; Score 183; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 8.1e-10;  
RESULT 395  
ID ABP73149 standard; protein; 112 AA.  
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 16.0%; Score 182; DB 6; Length 112;

Best Local Similarity 34.2%; Pred. No. 1e-09;  
RESULT 396  
ID ABP73153 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 15.9%; Score 181; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 1.3e-09;  
RESULT 397  
ID ABG17067 standard; protein; 920 AA.  
DE Novel human diagnostic protein #17058.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.4%; Score 175.5; DB 4; Length 920;  
Best Local Similarity 25.9%; Pred. No. 7.4e-08;  
RESULT 398  
ID AD160410 standard; protein; 920 AA.  
DE Secreted polypeptide encoded by gene splice variant #46.  
PN WO2003025142-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.4%; Score 175.5; DB 7; Length 920;  
Best Local Similarity 25.9%; Pred. No. 7.4e-08;  
RESULT 399  
ID AAM28056 standard; protein; 34 AA.  
DE Peptide #2093 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 15.0%; Score 170; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
RESULT 400  
ID ABG37308 standard; peptide; 34 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 15.0%; Score 170; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
RESULT 401  
ID ADB64426 standard; protein; 510 AA.  
DE Human protein encoded by clone FEBRA20038970.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 13.2%; Score 150; DB 7; Length 510;  
Best Local Similarity 23.6%; Pred. No. 1.1e-05;  
RESULT 402  
ID ABP73154 standard; protein; 80 AA.  
DE Deletion mutant of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 13.1%; Score 148.5; DB 6; Length 80;  
Best Local Similarity 37.0%; Pred. No. 1.3e-06;  
RESULT 403  
ID ADP07712 standard; protein; 162 AA.  
DE Human secreted protein, seq id 195.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.8%; Score 145; DB 8; Length 162;  
Best Local Similarity 33.0%; Pred. No. 7.5e-06;  
RESULT 404  
ID ADM80807 standard; protein; 237 AA.  
DE Human CAECM-36 protein SEQ ID NO:36.

PN WO2004015396-A2.  
PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.8%; Score 145; DB 8; Length 237;  
Best Local Similarity 33.0%; Pred. No. 1.2e-05;  
RESULT 405  
ID AAR26044 standard; protein; 277 AA.  
DE Tumour necrosis factor-induced glycoprotein TSG-6.  
PN WO9212175-A1.  
PD 23-JUL-1992.  
PA (UNIV) UNIV NEW YORK STATE.  
Query Match 12.8%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 406  
ID AAM1654 standard; protein; 277 AA.  
DE Tumour necrosis factor-stimulated gene-6 protein.  
PN WO9704075-A1.  
PD 06-FEB-1997.  
PA (UNIV) UNIV NEW YORK STATE.  
Query Match 12.8%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 407  
ID AAW84087 standard; protein; 277 AA.  
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.  
PN US5846763-A.  
PD 08-DEC-1998.  
PA (UNIV) UNIV NEW YORK STATE.  
Query Match 12.8%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 408  
ID AAE02361 standard; protein; 277 AA.  
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.  
PN US6210905-B1.  
PD 03-APR-2001.  
PA (UNIV) UNIV NEW YORK STATE.  
Query Match 12.8%; Score 145; DB 4; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 409  
ID ABG70870 standard; protein; 277 AA.  
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.  
PN US2002090708-A1.  
PD 11-JUL-2002.  
PA (UNIV) UNIV NEW YORK STATE.  
Query Match 12.8%; Score 145; DB 5; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 410  
ID ABR58556 standard; protein; 277 AA.  
DE Human cancer related protein SEQ ID NO:213.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 12.8%; Score 145; DB 6; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 411  
ID ABUS6653 standard; protein; 277 AA.  
DE Lung cancer-associated polypeptide #246.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 12.8%; Score 145; DB 6; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 412  
ID ADE25781 standard; protein; 277 AA.  
DE Human protein differentially expressed in foam cells #58.  
PN US2003194721-A1.  
PD 16-OCT-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 12.8%; Score 145; DB 7; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 413  
ID ADN39919 standard; protein; 277 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.  
PN WO2003042661-A2.

PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 12.8%; Score 145; DB 7; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 414  
ID ADN18974 standard; protein; 277 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 12.8%; Score 145; DB 7; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 415  
ID ADQ21506 standard; protein; 277 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 12.8%; Score 145; DB 8; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 416  
ID ADR51534 standard; protein; 277 AA.  
DE Human lipopolysaccharide-sensitive polypeptide #14.  
PN WO2004069870-A2.  
PD 19-AUG-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 12.8%; Score 145; DB 8; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 417  
ID ADW38508 standard; protein; 277 AA.  
DE Immunomodulatory gene TNFa induced protein 6.  
PN WO2005000999-A2.  
PD 06-JAN-2005.  
PA (GENZ) GENZYME CORP.  
Query Match 12.8%; Score 145; DB 9; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 418  
ID AEA23596 standard; protein; 277 AA.  
DE Human PRO polypeptide SEQ ID NO 138.  
PN WO2005051988-A2.  
PD 09-JUN-2005.  
PA (GETH) GENENTECH INC.  
Query Match 12.8%; Score 145; DB 9; Length 277;  
Best Local Similarity 33.0%; Pred. No. 1.5e-05;  
RESULT 419  
ID ADK67822 standard; protein; 2626 AA.  
DE Human BRCC300 polypeptide.  
PN WO2004012755-A1.  
PD 12-FEB-2004.  
PA (WIST-) WISTAR INST.  
Query Match 12.8%; Score 145; DB 8; Length 2626;  
Best Local Similarity 33.0%; Pred. No. 0.00031;  
RESULT 420  
ID ADS85081 standard; protein; 275 AA.  
DE Mouse atopic dermatitis-related protein sequence SeqID83.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UVJU-) UNIV JUNTENDO.  
Query Match 12.7%; Score 144; DB 8; Length 275;  
Best Local Similarity 33.0%; Pred. No. 1.9e-05;  
RESULT 421  
ID ABM84174 standard; protein; 2285 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 11.7%; Score 132.5; DB 8; Length 2285;  
Best Local Similarity 27.4%; Pred. No. 0.0044;  
RESULT 422  
ID ABM84173 standard; protein; 2384 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.  
PN WO2004023973-A2.

PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 11.7%; Score 132.5; DB 8; Length 2384;  
Best Local Similarity 27.4%; Pred. No. 0.0046;  
RESULT 423  
ID ABP72603 standard; protein; 883 AA.  
DE Rat mutant brain-enriched hyaluronan binding protein.  
PN WO2003007880-A2.  
PD 30-JAN-2003.  
PA (UYVA) UNIV YALE.  
PA (HOCK/) HOCKFIELD S.  
PA (MATT/) MATTHEWS R T.  
Query Match 11.6%; Score 131.5; DB 6; Length 883;  
Best Local Similarity 24.3%; Pred. No. 0.0015;  
RESULT 424  
ID ADK67779 standard; protein; 883 AA.  
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYVA) UNIV YALE.  
Query Match 11.6%; Score 131.5; DB 8; Length 883;  
Best Local Similarity 24.3%; Pred. No. 0.0015;  
RESULT 425  
ID AEB34752 standard; protein; 883 AA.  
DE Mammalian mutant BEHAB protein.  
PN WO2005069852-A2.  
PD 04-AUG-2005.  
PA (UYVA) UNIV YALE.  
Query Match 11.6%; Score 131.5; DB 9; Length 883;  
Best Local Similarity 24.3%; Pred. No. 0.0015;  
RESULT 426  
ID AAB61242 standard; protein; 883 AA.  
DE Murine brevidin protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.5%; Score 130.5; DB 4; Length 883;  
Best Local Similarity 24.4%; Pred. No. 0.0019;  
RESULT 427  
ID ABO32678 standard; protein; 883 AA.  
DE Secretd polypeptide-related protein #119.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 11.5%; Score 130.5; DB 6; Length 883;  
Best Local Similarity 24.4%; Pred. No. 0.0019;  
RESULT 428  
ID ADB90787 standard; protein; 883 AA.  
DE Mouse brevicin protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.5%; Score 130.5; DB 7; Length 883;  
Best Local Similarity 24.4%; Pred. No. 0.0019;  
RESULT 429  
ID ADF71522 standard; protein; 883 AA.  
DE Murine brevidin protein.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.5%; Score 130.5; DB 7; Length 883;  
Best Local Similarity 24.4%; Pred. No. 0.0019;  
RESULT 430



ID ADQ10338 standard; protein; 883 AA.  
DE Human polypeptide #172.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.5%; Score 130.5; DB 8; Length 883;  
Best Local Similarity 24.4%; Pred. No. 0.0019;  
RESULT 431  
ID ADX15811 standard; protein; 2316 AA.  
DE Human aggreccan.  
PN WO2005012512-A1.  
PD 10-FEB-2005.  
PA (NAXA/) NAXAMURA N.  
Query Match 11.5%; Score 130.5; DB 9; Length 2316;  
Best Local Similarity 27.4%; Pred. No. 0.007;  
RESULT 432  
ID AAM47675 standard; protein; 1431 AA.  
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.  
PN WO200181544-A2.  
PD 01-NOV-2001.  
PA (WEIG/) WEIGEL P A.  
PA (ZHOU/) ZHOU B.  
PA (WEIG/) WEIGEL J A.  
Query Match 11.4%; Score 129; DB 5; Length 1431;  
Best Local Similarity 32.3%; Pred. No. 0.0052;  
RESULT 433  
ID ABG72498 standard; protein; 1431 AA.  
DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).  
PN WO200286093-A2.  
PD 31-OCT-2002.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Query Match 11.4%; Score 129; DB 6; Length 1431;  
Best Local Similarity 32.3%; Pred. No. 0.0052;  
RESULT 434  
ID AAB08023 standard; protein; 95 AA.  
DE The domain of hyaluronic acid which interacts with CD44.  
PN WO200047163-A2.  
PD 17-AUG-2000.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match 11.3%; Score 128.5; DB 3; Length 95;  
Best Local Similarity 28.7%; Pred. No. 0.00016;  
RESULT 435  
ID ABU04625 standard; protein; 95 AA.  
DE Human expressed protein tag (EPT) #1291.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 11.3%; Score 128.5; DB 6; Length 95;  
Best Local Similarity 28.7%; Pred. No. 0.00016;  
RESULT 436  
ID AAB61236 standard; protein; 649 AA.  
DE Mature human TANGO 332 protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 127.5; DB 4; Length 649;  
Best Local Similarity 24.7%; Pred. No. 0.0025;  
RESULT 437  
ID ABO32673 standard; protein; 649 AA.  
DE Secreted polypeptide-related protein #74.  
PN US200302279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
Query Match 11.2%; Score 127.5; DB 7; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 438  
ID ADB90778 standard; protein; 649 AA.  
DE Human TANGO 332 mature protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 649;  
Best Local Similarity 24.7%; Pred. No. 0.0025;  
RESULT 439  
ID ADF71513 standard; protein; 649 AA.  
DE Human TANGO 332 mature protein.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 649;  
Best Local Similarity 24.7%; Pred. No. 0.0025;  
RESULT 440  
ID ADQ10331 standard; protein; 649 AA.  
DE Human polypeptide #167.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 649;  
Best Local Similarity 24.7%; Pred. No. 0.0025;  
RESULT 441  
ID AAB61234 standard; protein; 671 AA.  
DE Human TANGO 332 protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 127.5; DB 4; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 442  
ID ABO32671 standard; protein; 671 AA.  
DE Secreted polypeptide-related protein #73.  
PN US200302279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 11.2%; Score 127.5; DB 6; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 443  
ID ADB90776 standard; protein; 671 AA.  
DE Human TANGO 332 protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 444  
ID ADF71511 standard; protein; 671 AA.  
DE Human TANGO 332.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 445  
ID ADQ10329 standard; protein; 671 AA.  
DE Human polypeptide #165.  
PN US2004121396-A1.

PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 446  
ID ADV70173 standard; protein; 671 AA.  
DE Tumor-associated antigenic target polypeptide TAT152.  
PN WO2004112829-A2.  
PD 29-DEC-2004.  
PA (GETH) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 9; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 447  
ID AEA00138 standard; protein; 671 AA.  
DE Human TAT152 protein SEQ ID NO:90.  
PN US2005106644-A1.  
PD 19-MAY-2005.  
PA (GETH) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 9; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 448  
ID AEA00658 standard; protein; 671 AA.  
DE Human TAT152 protein sequence SeqID90.  
PN US2005107595-A1.  
PD 19-MAY-2005.  
PA (GETH) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 9; Length 671;  
Best Local Similarity 24.7%; Pred. No. 0.0026;  
RESULT 449  
ID ABW83434 standard; protein; 761 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 11.2%; Score 127.5; DB 8; Length 761;  
Best Local Similarity 24.7%; Pred. No. 0.0031;  
RESULT 450  
ID ADH1892 standard; protein; 806 AA.  
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 11.2%; Score 127.5; DB 8; Length 806;  
Best Local Similarity 24.7%; Pred. No. 0.0034;  
RESULT 451  
ID ABW83431 standard; protein; 825 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 11.2%; Score 127.5; DB 8; Length 825;  
Best Local Similarity 24.7%; Pred. No. 0.0035;  
RESULT 452  
ID ABW83430 standard; protein; 863 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 11.2%; Score 127.5; DB 8; Length 863;  
Best Local Similarity 24.7%; Pred. No. 0.0037;  
RESULT 453  
ID ABP72604 standard; protein; 893 AA.  
DE Rat brain-enriched hyaluronan binding protein.  
PN WO2003007880-A2.  
PD 30-JAN-2003.  
PA (UYVA) UNIV YALE.  
PA (HOCK/) HOCKFIELD S.  
PA (MATT/) MATTHEWS R T.  
Query Match 11.2%; Score 127.5; DB 6; Length 883;  
Best Local Similarity 23.0%; Pred. No. 0.0038;  
RESULT 454  
ID ADR62581 standard; protein; 893 AA.  
DE Rat Protein P55068, SEQ ID NO 8512.

PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GSHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 11.2%; Score 127.5; DB 7; Length 883;  
Best Local Similarity 23.0%; Pred. No. 0.0038;  
RESULT 455  
ID ADK67782 standard; protein; 883 AA.  
DE Rat glycosylation-variant BEHAB isoform.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYVA) UNIV YALE.  
Query Match 11.2%; Score 127.5; DB 8; Length 883;  
Best Local Similarity 23.0%; Pred. No. 0.0038;  
RESULT 456  
ID AEB34755 standard; protein; 883 AA.  
DE Rat poly-sialylated brain-enriched hyaluronan binding protein.  
PN WO2005069852-A2.  
PD 04-AUG-2005.  
PA (UYVA) UNIV YALE.  
Query Match 11.2%; Score 127.5; DB 9; Length 883;  
Best Local Similarity 23.0%; Pred. No. 0.0038;  
RESULT 457  
ID AAY97583 standard; protein; 911 AA.  
DE Human secreted protein PRO6018.  
PN WO200075317-A2.  
PD 14-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 4; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 458  
ID ABG34055 standard; protein; 911 AA.  
DE Human Pro peptide #26.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 5; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 459  
ID ADI28032 standard; protein; 911 AA.  
DE EGMCAD protein 6755002CD1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.2%; Score 127.5; DB 5; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 460  
ID AAE30340 standard; protein; 911 AA.  
DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.  
PN WO200276510-A1.  
PD 03-OCT-2002.  
PA (AGYT-) AGY THERAPEUTICS INC.  
Query Match 11.2%; Score 127.5; DB 6; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 461  
ID ADA01320 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003068779-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 6; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 462  
ID ADA43749 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 6; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 463  
ID ADA43517 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.

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PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 464
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 465
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 466
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 467
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 468
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 469
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 470
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 471
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 472
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 473
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 474
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 475
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (seqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 476
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 477
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 478
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 479
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 480
ID ADD88153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.2%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 481
ID ADD95448 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
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PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 482  
ID ADE06378 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003073195-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 483  
ID ADE38153 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 484  
ID ADD88269 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 485  
ID ADD90850 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 486  
ID ADF99405 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 487  
ID ADS06498 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 488  
ID ADG05449 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 489  
ID ADG82450 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 490  
ID ADN38942 standard; protein; 911 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.  
PN WO2003042661-A2.  
PD 22-MAY-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 11.2%; Score 127.5; DB 7; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 491  
ID ADE51703 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 492  
ID ADE51819 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 493  
ID ADE37677 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 494  
ID ADE37561 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 495  
ID ADD95332 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 496  
ID ADE38032 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 497  
ID ADE76121 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 498  
ID ADE39444 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 499  
ID ADE04248 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 500
ID ADE39845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 501
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 502
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 503
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 504
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124683-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 505
ID ADE37916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 506
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 507
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US200309363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 508
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 509
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 510
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 511
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 512
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 513
ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 514
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 515
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 516
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
RESULT 517
ID ADD88932 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.2%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.004;
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RESULT 518  
ID ADE19826 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide #26.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 519  
ID ADE77404 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 520  
ID ADE5280 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 521  
ID ADE39328 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 522  
ID ADE38513 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 523  
ID ADG11066 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 524  
ID ADG10950 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 525  
ID ADH31478 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 526  
ID ADH38726 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 527  
ID ADH40040 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 528  
ID ADH23664 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 529  
ID ADH26994 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 530  
ID ADH38262 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 531  
ID ADH26878 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 532  
ID ADH38146 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 533  
ID ADH38842 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 534  
ID ADH23780 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 535  
ID ADH40156 standard; protein; 911 AA.  
DE Human PRO6018 protein.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 536  
ID ADH40040 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;

DE Human PRO6018 protein.  
PN US2003119133-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 537  
ID ADH31362 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 538  
ID ADH29240 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 539  
ID ADH49455 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 540  
ID ADH51919 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 541  
ID ADH49774 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 542  
ID ADH52375 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 543  
ID ADH52491 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 544  
ID ADH58488 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 545  
ID ADH51803 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.

PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 546  
ID ADH58364 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 547  
ID ADI13561 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 548  
ID ADK00817 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 549  
ID ADL08558 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 550  
ID ADK67784 standard; protein; 911 AA.  
DE Human glycosylation-variant BEHAB isoform.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYVA ) UNIV YALE.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 551  
ID ARM80156 standard; protein; 911 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 8; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 552  
ID AEA00137 standard; protein; 911 AA.  
DE Human TAT145 protein SEQ ID NO:89.  
PN US2005106644-A1.  
PD 19-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 9; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 553  
ID AEA00657 standard; protein; 911 AA.  
DE Human TAT145 protein sequence SeqID89.  
PN US2005107595-A1.  
PD 19-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 11.2%; Score 127.5; DB 9; Length 911;  
Best Local Similarity 24.7%; Pred. No. 0.004;  
RESULT 554  
ID AEB34757 standard; protein; 911 AA.  
DE Human poly-sialylated brain-enriched hyaluronan binding protein.  
PN WO2005069852-A2.

PD 04-AUG-2005.  
 PA (UYVA ) UNIV.YALE.  
 Query Match 11.2%; Score 127.5; DB 9; Length 911;  
 Best Local Similarity 24.7%; Pred. No. 0.004;  
 RESULT 555  
 ID ABR58557 standard; protein; 277 AA.  
 DE Human cancer related protein SEQ ID NO:214.  
 PN WO2003025138-A2.  
 PD 27-MAR-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 11.2%; Score 127; DB 6; Length 277;  
 Best Local Similarity 30.7%; Pred. No. 0.00091;  
 RESULT 556  
 ID ABU56654 standard; protein; 277 AA.  
 DE Lung cancer-associated polypeptide #247.  
 PN WO200286443-A2.  
 PD 31-OCT-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 11.2%; Score 127; DB 6; Length 277;  
 Best Local Similarity 30.7%; Pred. No. 0.00091;  
 RESULT 557  
 ID ADN38976 standard; protein; 277 AA.  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.  
 PN WO2003042861-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 11.2%; Score 127; DB 7; Length 277;  
 Best Local Similarity 30.7%; Pred. No. 0.00091;  
 RESULT 558  
 ID ADO24439 standard; protein; 277 AA.  
 DE Human PRO87335 protein SEQ ID NO:78.  
 PN WO2004043397-A2.  
 PD 27-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 11.2%; Score 127; DB 8; Length 277;  
 Best Local Similarity 30.7%; Pred. No. 0.00091;  
 RESULT 559  
 ID ADRI4117 standard; protein; 277 AA.  
 DE Human NF-kappaB pathway-associated protein SeqID118.  
 PN WO2004065577-A2.  
 PD 05-AUG-2004.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 Query Match 11.2%; Score 127; DB 8; Length 277;  
 Best Local Similarity 30.7%; Pred. No. 0.00091;  
 RESULT 560  
 ID ADO24485 standard; protein; 277 AA.  
 DE Human PRO87343 protein SEQ ID NO:124.  
 PN WO2004043397-A2.  
 PD 27-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 11.1%; Score 126; DB 8; Length 277;  
 Best Local Similarity 34.1%; Pred. No. 0.0011;  
 RESULT 561  
 ID ADB65640 standard; protein; 482 AA.  
 DE Human protein encoded by clone THYMU20143230.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 10.9%; Score 124; DB 7; Length 482;  
 Best Local Similarity 34.5%; Pred. No. 0.0038;  
 RESULT 562  
 ID ABR82200 standard; protein; 2570 AA.  
 DE Human CLEVER-1 protein SEQ ID NO:1.  
 PN WO2003057130-A2.  
 PD 17-JUL-2003.  
 PA (JALK/) JALKANEN S.  
 PA (IRJA/) IRJALA H.  
 PA (SALM/) SALMI M.  
 Query Match 10.9%; Score 124; DB 6; Length 2570;  
 Best Local Similarity 34.5%; Pred. No. 0.035;  
 RESULT 563  
 ID AAY93911 standard; protein; 457 AA.

DE A human hyaluronan-binding protein, designated WF-HABP.  
 PN WO20039166-A1.  
 PD 06-JUL-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AWNA-) AMERICAN NAT RED CROSS.  
 Query Match 10.8%; Score 123; DB 3; Length 457;  
 Best Local Similarity 33.3%; Pred. No. 0.0044;  
 RESULT 564  
 ID ABR90349 standard; protein; 1082 AA.  
 DE Human polypeptide SEQ ID NO 2725.  
 PN WO200190304-A2.  
 PD 29-NOV-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 10.8%; Score 123; DB 5; Length 1082;  
 Best Local Similarity 33.3%; Pred. No. 0.014;  
 RESULT 565  
 ID AAY93910 standard; protein; 2157 AA.  
 DE A human hyaluronan-binding protein, designated WF-HABP.  
 PN WO20039166-A1.  
 PD 06-JUL-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AWNA-) AMERICAN NAT RED CROSS.  
 Query Match 10.8%; Score 123; DB 3; Length 2157;  
 Best Local Similarity 33.3%; Pred. No. 0.035;  
 RESULT 566  
 ID ABR80463 standard; protein; 2570 AA.  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.8%; Score 123; DB 8; Length 2570;  
 Best Local Similarity 33.3%; Pred. No. 0.044;  
 RESULT 567  
 ID ADM80804 standard; protein; 259 AA.  
 DE Human CADECM-33 protein SEQ ID NO:33.  
 PN WO2004015396-A2.  
 PD 19-FEB-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 10.7%; Score 121.5; DB 8; Length 259;  
 Best Local Similarity 34.9%; Pred. No. 0.0029;  
 RESULT 568  
 ID AAY13381 standard; protein; 360 AA.  
 DE Amino acid sequence of protein PRO271.  
 PN WO9914328-A2.  
 PD 25-MAR-1999.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.7%; Score 121.5; DB 2; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.0045;  
 RESULT 569  
 ID ADC78533 standard; protein; 360 AA.  
 DE Human PRO271 protein.  
 PN WO200015796-A2.  
 PD 23-MAR-2000.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.7%; Score 121.5; DB 3; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.0045;  
 RESULT 570  
 ID AAB80249 standard; protein; 360 AA.  
 DE Human PRO271 protein.  
 PN WO200104311-A1.  
 PD 18-JAN-2001.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.7%; Score 121.5; DB 4; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.0045;  
 RESULT 571  
 ID AAU29037 standard; protein; 360 AA.  
 DE Human PRO polypeptide sequence #14.  
 PN WO200168848-A2.  
 PD 20-SEP-2001.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.7%; Score 121.5; DB 4; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.0045;  
 RESULT 572



DE Human PRO polypeptide #38.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 583  
ID ARK68089 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 584  
ID ABU96142 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 585  
ID ABU92573 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 586  
ID ABO08650 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 587  
ID ABO02702 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 588  
ID ARK74856 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 589  
ID ARK94618 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 590  
ID ABU85591 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 591  
ID ABU98751 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 592  
ID ABU97966 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.

PN US2003017544-A1.  
 PD 23-JAN-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 593 34.9%; Pred. No. 0.0045;  
 ID ABU91672 standard; protein; 360 AA.  
 DE Novel human secreted and transmembrane protein PRO271.  
 PN US2003027277-A1.  
 PD 06-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 594 34.9%; Pred. No. 0.0045;  
 ID ABU71928 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein PRO271.  
 PN US2003035330-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 595 34.9%; Pred. No. 0.0045;  
 ID ABU89365 standard; protein; 360 AA.  
 DE Human PRO polypeptide #14.  
 PN US2003036141-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 596 34.9%; Pred. No. 0.0045;  
 ID ABU86206 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003036146-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 597 34.9%; Pred. No. 0.0045;  
 ID ABU67419 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003036162-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 598 34.9%; Pred. No. 0.0045;  
 ID ABU80447 standard; protein; 360 AA.  
 DE Human PRO protein #14.  
 PN US2003036137-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 599 34.9%; Pred. No. 0.0045;  
 ID AB001811 standard; protein; 360 AA.  
 DE Novel human secreted and transmembrane protein PRO271.  
 PN US2002197671-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 600 34.9%; Pred. No. 0.0045;  
 ID ABR99365 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003040063-A1.  
 PD 27-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 601 34.9%; Pred. No. 0.0045;  
 ID ABR98755 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003040064-A1.  
 PD 27-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 602 34.9%; Pred. No. 0.0045;

ID AB016278 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003027267-A1.  
 PD 06-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 603 34.9%; Pred. No. 0.0045;  
 ID ABR92178 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003036160-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 604 34.9%; Pred. No. 0.0045;  
 ID AB018819 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003044925-A1.  
 PD 06-MAR-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 605 34.9%; Pred. No. 0.0045;  
 ID ABR78240 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003054474-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 606 34.9%; Pred. No. 0.0045;  
 ID ABU84976 standard; protein; 360 AA.  
 DE Novel human secreted and transmembrane protein PRO271.  
 PN US2003032114-A1.  
 PD 13-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 607 34.9%; Pred. No. 0.0045;  
 ID ABO00115 standard; protein; 360 AA.  
 DE Novel human secreted and transmembrane protein PRO271.  
 PN US2003032101-A1.  
 PD 13-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 608 34.9%; Pred. No. 0.0045;  
 ID AB011447 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003036124-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 609 34.9%; Pred. No. 0.0045;  
 ID ABO02092 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003040054-A1.  
 PD 27-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 610 34.9%; Pred. No. 0.0045;  
 ID ABU54384 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein PRO271.  
 PN US2002132240-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 611 34.9%; Pred. No. 0.0045;  
 ID ABU88666 standard; protein; 360 AA.  
 DE Novel human secreted and transmembrane protein PRO271.  
 PN US2003036133-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
 RESULT 612 34.9%; Pred. No. 0.0045;  
 ID ABU83361 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 613  
ID ABO06162 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 614  
ID ABR59198 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 615  
ID ABO09260 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 616  
ID ABO19124 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 617  
ID ABO11142 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 618  
ID ABR66760 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 619  
ID ABO15973 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 620  
ID ABO13679 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 621  
ID ABO47399 standard; protein; 360 AA.  
DE Human secreted/transmembrane polypeptide PRO271.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 622  
ID ABO65582 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, SEQ ID 28.

PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 623  
ID ABO07430 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 624  
ID ABO03617 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 625  
ID ABR67065 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 626  
ID ABO15668 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 627  
ID ABU55949 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, PRO271.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 628  
ID ABU65277 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 629  
ID ABU95222 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 630  
ID ABU71125 standard; protein; 360 AA.  
DE Human PRO271 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 631  
ID ABO07735 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 632  
ID ABR69976 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032138-A1.  
PD 13-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 633  
ID ABR69309 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 634  
ID ABO01450 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003008953-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 635  
ID ABU81252 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 636  
ID ABR60049 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 637  
ID ABR67784 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 638  
ID ABR65172 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 639  
ID ABR68394 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 640  
ID ABR71806 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 641  
ID ABU85286 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 642  
ID ABU88976 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 643  
ID ABU83056 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 644  
ID ABU94912 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
FN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 645  
ID ABU90460 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
FN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 646  
ID ABU83971 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 647  
ID ABU93622 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
FN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 648  
ID ABR64867 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 649  
ID ABR68699 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 650  
ID ABO06515 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 651  
ID ABR99060 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 652  
ID ABU56944 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;

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RESULT 653
ID ABU64536 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 654
ID ABU85896 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US200302300-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 655
ID ABU67382 standard; protein; 360 AA.
DE Human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 656
ID ABU82183 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 657
ID ABU87194 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 658
ID ABU83666 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 659
ID ABO08040 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 660
ID ABO14902 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003036050-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 661
ID ABU81751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 662
ID ABU65915 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 663
ID ABR59744 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 664
ID ABU93932 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 665
ID ABU99785 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 666
ID ABR66455 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 667
ID ABR90873 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 668
ID ABU94300 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 669
ID ABU79182 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 670
ID ABU86511 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 671
ID ABU86816 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 672
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 10.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 673
ID ABO04532 standard; protein; 360 AA.
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DE Human PRO polypeptide #14.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 674  
ID ABR70281 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 675  
ID ABU98446 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 676  
ID ABR65845 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 677  
ID ABR64562 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 678  
ID ABU79487 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 679  
ID ABU92878 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 680  
ID ABU95837 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 681  
ID ABU91057 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 682  
ID ABU90150 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 683  
ID ABO09565 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044931-A1.

PD 06-MAR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 684  
ID ABO10837 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 685  
ID ABR70891 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 686  
ID ABU87499 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 687  
ID ABU91367 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 688  
ID ABU84581 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 689  
ID ABR69671 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 690  
ID ABU80048 standard; protein; 360 AA.  
DE Human PRO protein #14.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 691  
ID ABU96959 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 692  
ID ABU93317 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;  
RESULT 693  
ID ABO09870 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Pred. No. 0.0045;

Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 694  
ID ABO08955 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US20030306152-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 695  
ID ABU10523 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein #14.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 696  
ID ABU95532 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 697  
ID ABU96741 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 698  
ID ABR70586 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 699  
ID ABO04937 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 700  
ID ABO08345 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US200304922-A1.  
PD 06-MAR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 701  
ID ABO14841 standard; protein; 360 AA.  
DE Human secreted / transmembrane polypeptide PRO271.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 702  
ID ABO05552 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 703  
ID ABR73941 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US20030316135-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 704  
ID ABR95533 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 705  
ID ABR80830 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 706  
ID ABR81135 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 707  
ID ABM00831 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 708  
ID ABR88433 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 709  
ID ABM77254 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 710  
ID ABO28738 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 711  
ID ABO31483 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 712  
ID ABM07900 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 713  
ID ABO40380 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 714  
ID ABO35805 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 715  
ID ABO43944 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 716  
ID ADA77780 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 717  
ID ABM24739 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 718  
ID ADB29418 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 719  
ID ABO03007 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 720  
ID ABR90263 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 721  
ID ABM17177 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 722  
ID ABR94923 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 723  
ID ABR95228 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 724  
ID ABO21466 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 725  
ID ABR97730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 726  
ID ABR87518 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 727  
ID ABM77559 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 728  
ID AEM27789 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 729  
ID AEM06070 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 730  
ID ABO3576 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 731  
ID ABR95027 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.



Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 732  
ID ABM26264 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 733  
ID AB048046 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 734  
ID ABR92798 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 735  
ID ABO24549 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 736  
ID ABM11560 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 737  
ID ABM02661 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 738  
ID ABM15957 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 739  
ID AB027518 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 740  
ID ABM29009 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 741  
ID ABM06985 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 742  
ID ABM21079 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 743  
ID ABM09425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 744  
ID ABO41295 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 745  
ID ABO36110 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 746  
ID ABO43639 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 747  
ID ABM76339 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 748  
ID ABM76035 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 749  
ID ABM25654 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 750  
ID ABM25959 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 751  
ID ABO03312 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US20030316127-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 752  
ID ABO02397 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 753  
ID ABR90568 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 754  
ID ABR73636 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 755  
ID ABO16888 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 756  
ID ABR94313 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 757  
ID ABR75820 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 758  
ID ADA18274 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 759  
ID ABO32793 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein PRO271.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 760

ID ABR71196 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 761  
ID ABR93093 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 762  
ID ABR93398 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 763  
ID ABR87823 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 764  
ID ABO27823 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 765  
ID ABO29958 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 766  
ID ABO33167 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 767  
ID ABO4855 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 768  
ID ABM08815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 769  
ID ABO36415 standard; protein; 360 AA.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 779  
ID ABM10950 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 780  
ID ABM28094 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 781  
ID AB032093 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 782  
ID ABM15220 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 783  
ID ABM06375 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 784  
ID ABM04186 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 785  
ID ABM22299 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 786  
ID ABM07595 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 787  
ID AB040695 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068684-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 788  
ID ABM35332 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 789  
ID ABM33095 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 790  
ID ABO52621 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 791  
ID ABO50181 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 792  
ID ABU99175 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 793  
ID ABO04227 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 794  
ID ABO05857 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 795  
ID ABO34853 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 796  
ID ABM18397 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 797  
ID ADA16249 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 798  
ID ABR97425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 799  
ID ABR80525 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 800  
ID ABM01136 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 801  
ID ABR88738 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 802  
ID ABM13390 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 803  
ID ABM20774 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 804  
ID ABO41905 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 805  
ID ABO42515 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 806  
ID ABM10035 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003067478-A1.

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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 807
ID ABO38550 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 808
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 809
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 810
ID ABM74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 811
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 812
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 813
ID ABM02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 814
ID ABR86298 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 815
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 816
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
ID ABM16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 817
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 818
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 819
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 820
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 821
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 822
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 823
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 824
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.7%; Score 121.5; DB 6; Length 360;
  Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 825
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
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PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 826  
ID ABM75730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 827  
ID ABM34010 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 828  
ID ABM34315 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US200310061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 829  
ID ABO20246 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 830  
ID ABO21161 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 831  
ID ABO22076 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 832  
ID ABR96510 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 833  
ID ABR8568 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 834  
ID ABR9670 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 835  
ID ABO0221 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 836  
ID ABO0526 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 837  
ID ABO29653 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 838  
ID ABM23519 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 839  
ID ABM29314 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 840  
ID ABO38245 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 841  
ID ABO45545 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 842  
ID ABM20469 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 843  
ID ADA42394 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 844  
ID ADA81299 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 845  
ID ABO16583 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 846  
ID ABO18209 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 847  
ID ABO22636 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 848  
ID ABO22941 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 849  
ID ABR92483 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 850  
ID ABR81440 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 851  
ID ABO17531 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 852  
ID ABO17864 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 853  
ID ABR99653 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 854  
ID ABO26569 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 855  
ID ABO13695 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 856  
ID ABO28433 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 857  
ID ABO30263 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 858  
ID ABO07290 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 859  
ID ABO03881 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 860  
ID ABO37025 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 861  
ID ABO41600 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 862  
ID ABO35195 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 863  
ID ABO35195 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;

ID ABM25044 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 864  
DE ABO47436 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 865  
DE ABO47741 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 866  
DE ABO48351 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 867  
DE ABO51401 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 868  
DE ABO51706 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 869  
DE ABO50486 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 870  
DE ABR79610 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 871  
DE ABM16872 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 872  
DE ABO17904 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044918-A1.

PD 06-MAR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 873  
DE ABO20856 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 874  
DE ABR96815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 875  
ID ABM12170 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 876  
ID ABM16262 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 877  
ID ABM24129 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 878  
ID ABM14610 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 879  
ID ABM04491 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 880  
ID ABM06680 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 881  
ID ABM09120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
RESULT 882



ID ABO39160 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068775-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 883  
ID ABO75425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 884  
ID ABM25349 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 885  
ID ABM19859 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 886  
ID ABO46765 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 887  
ID ABO47070 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 888  
ID ADA83097 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 889  
ID ABR71501 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 890  
ID ABR72111 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 891  
ID ABR98450 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036129-A1.  
PD 20-FEB-2003.

Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 892  
ID ABO06820 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 893  
ID ABR84773 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 894  
ID ABR73331 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 895  
ID ABR76425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 896  
ID ABR73026 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 897  
ID ABM18092 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 898  
ID ABO20551 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 899  
ID ABO25294 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 900  
ID ABO25599 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 901  
ID ABR94008 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059879-A1.

PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 902  
ID ABR79915 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 903  
ID ABM11255 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 904  
ID ABO32862 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 905  
ID ABO30568 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 906  
ID ABO30873 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 907  
ID ABM27179 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 908  
ID ABM29924 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 909  
ID ABM05460 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 910  
ID ABM15525 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 911  
ID ABM08510 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 912  
ID ABO42210 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 913  
ID ABO37940 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 914  
ID ABO45850 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 915  
ID ABM66653 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 916  
ID ADB20140 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003082767-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 917  
ID ABM19554 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 918  
ID ABO49266 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 919  
ID ABO49571 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 920  
ID ABM15525 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

RESULT 920  
ID ADA78392 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 921  
ID ABR88128 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 922  
ID ABM26874 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 923  
ID ABM03271 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 924  
ID AB039770 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 925  
ID AB049876 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 926  
ID AB050791 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 927  
ID AB005247 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003031626-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 928  
ID ABR74551 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 929  
ID ABR77030 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 930  
ID ADA16673 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 931  
ID ABM17787 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 932  
ID ABR5838 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 933  
ID ADA13102 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 934  
ID AB021771 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 935  
ID AB019941 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 936  
ID AB024244 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 937  
ID ABR85993 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 938  
ID ABM10645 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;

RESULT 939  
ID ABM76644 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 940  
ID ABR89348 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 941  
ID ABM12475 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 942  
ID ABM05765 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 943  
ID ABO34890 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 944  
ID ABM02966 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 945  
ID ABM18944 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 946  
ID ABM19249 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 947  
ID ABO46460 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 948  
ID ABO48961 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 949  
ID ADA41970 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 950  
ID ABR69004 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 951  
ID ABR89043 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 952  
ID ABR72416 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 953  
ID ABR74246 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 954  
ID ABO18514 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 955  
ID ADA17317 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 956  
ID ABR80220 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 957  
ID ABM01441 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;

Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 958  
ID ABM02051 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 959  
ID ABR87213 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 960  
ID ABM12780 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 961  
ID ABM30534 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 962  
ID ABM24434 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 963  
ID ABO29348 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 964  
ID ABO31178 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 965  
ID ABM14305 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 966  
ID ABM09730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 967  
ID ABO38955 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 968  
ID ABM34620 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 969  
ID ABO51096 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 970  
ID AD442820 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 971  
ID ABO03922 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 972  
ID ABO10392 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 973  
ID ABR77635 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 974  
ID ABR78845 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 975  
ID ABO23939 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 976  
ID ABR93703 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 977  
ID ABO01746 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 978  
ID ABO01746 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 979  
ID ABR89958 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 980  
ID ABO27484 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 981  
ID ABO13085 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 982  
ID ABO31788 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 983  
ID ABO14000 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 984  
ID ABO08205 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 985  
ID ABO40075 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 986  
ID ABO17482 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.

ID ABO17482 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068683-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 987  
ID ABO33705 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 988  
ID ABO20164 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 989  
ID ABO48656 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 990  
ID ABR72721 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 991  
ID ABO15363 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 992  
ID ABR85078 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 993  
ID ABO15058 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 994  
ID ABO17193 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 995  
ID ABO17482 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 996  
ID ABM85383 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 997  
ID ABM17592 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 998  
ID ABM76949 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 999  
ID ABM28128 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1000  
ID ABM22909 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1001  
ID ABM30229 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1002  
ID ABM21689 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1003  
ID ABM21384 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1004  
ID ABM14915 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1005  
ID ABO40990 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1006  
ID ABO36720 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1007  
ID ABO37330 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1008  
ID ABM75120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1009  
ID ABM33400 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1010  
ID ABO46155 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1011  
ID ADA82463 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1012  
ID ABM31754 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1013  
ID ABM31144 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1014  
ID ADB77739 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1015  
ID ADB74875 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1016  
ID ADB85771 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1017  
ID ADB32059 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1018  
ID ADB32364 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1019  
ID ADB31449 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1020  
ID ADB30839 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1021  
ID ADC28521 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1022  
ID ADC39721 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1023  
ID ADC40235 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082541-A1.

PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1024  
ID ADC19059 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1025  
ID ADC34359 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1026  
ID ADC29414 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1027  
ID ADC28945 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1028  
ID ADC40830 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1029  
ID ADC19487 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1030  
ID ADC33935 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1031  
ID ADC13005 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.7%; Score 121.5; DB 7; Length 360;  
RESULT 1032  
ID ADC12457 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082541-A1.



PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1033  
ID ADD05501 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1034  
ID ADD05012 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1035  
ID ADD04018 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1036  
ID ADD03594 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1037  
ID ADE34846 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1038  
ID ADG02496 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1039  
ID ADG01203 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1040  
ID ADF95378 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1041  
ID ADG12193 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207392-A1.  
PD 06-NOV-2003.

Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1042  
ID ADH0853 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1043  
ID ADH59329 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1044  
ID ADI38108 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1045  
ID ADJ26376 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1046  
ID ADL32634 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1047  
ID ADM30168 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1048  
ID ADE79291 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1049  
ID ADE79715 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1050  
ID ADE73391 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;

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Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1051
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1052
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1053
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1054
ID ADE99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1055
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1056
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1057
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1058
ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1059
ID ADF95990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1060
ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1061
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1062
ID ADG00421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1063
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1064
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1065
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1066
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1067
ID ADH32927 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0045;
RESULT 1068
ID ADH20525 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.

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Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1069
ID ADH07380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1070
ID ADH59925 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1071
ID ADH6953 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1072
ID ADI18695 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1073
ID ADI65415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1074
ID ADI37678 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1075
ID ADH97474 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1076
ID ADI65842 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1077
ID ADH60585 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1078
ID ADJ99642 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1079
ID ADL08835 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1080
ID ADJ54666 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1081
ID ADM25176 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1082
ID ADM29926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1083
ID ADJ64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.7%; Score 121.5; DB 8; Length 360;
RESULT 1084
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
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PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 10.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1092  
ID ADS74648 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein #42.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 10.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1093  
ID AUT03685 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003152922-A1.  
PD 14-AUG-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1094  
ID AEA37923 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH/) GENENTECH INC.  
Query Match 10.7%; Score 121.5; DB 9; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.0045;  
RESULT 1095  
ID AEA20028 standard; protein; 422 AA.  
DE Novel human polypeptide SEQ ID NO 722.  
PN WO2005049806-A2.  
PD 02-JUN-2005.  
PA (NUVE-) NUVELO INC.  
Query Match 10.7%; Score 121.5; DB 9; Length 422;  
Best Local Similarity 34.9%; Pred. No. 0.0056;  
RESULT 1096  
ID AAW59882 standard; protein; 528 AA.  
DE Amino acid sequence of the cDNA clone BEF (HSXCK41).  
PN WO9831800-A2.  
PD 23-JUL-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (AUCC-) AUCKLAND UNISERVICES LTD.  
Query Match 10.7%; Score 121; DB 2; Length 528;  
Best Local Similarity 24.1%; Pred. No. 0.0084;  
RESULT 1097

ID AAB61241 standard; protein; 528 AA.  
DE Human BRF protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 121; DB 4; Length 528;  
Best Local Similarity 24.1%; Pred. No. 0.0084;  
RESULT 1098  
ID ABO32677 standard; protein; 528 AA.  
DE Secreted polypeptide-related protein #75.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 10.7%; Score 121; DB 6; Length 528;  
Best Local Similarity 24.1%; Pred. No. 0.0084;  
RESULT 1099  
ID ABB90786 standard; protein; 528 AA.  
DE Human BRF protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 121; DB 7; Length 528;  
Best Local Similarity 24.1%; Pred. No. 0.0084;  
RESULT 1100  
ID ADF71521 standard; protein; 528 AA.  
DE Human BRF protein.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 121; DB 7; Length 528;  
Best Local Similarity 24.1%; Pred. No. 0.0084;  
RESULT 1101  
ID ADQ10337 standard; protein; 528 AA.  
DE Human polypeptide #171.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.7%; Score 121; DB 8; Length 528;  
Best Local Similarity 24.1%; Pred. No. 0.0084;  
RESULT 1102  
ID AAR85442 standard; protein; 912 AA.  
DE Bovine brevicin core protein.  
PN WO9526201-A1.  
PD 05-OCT-1995.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Query Match 10.6%; Score 120.5; DB 2; Length 912;  
Best Local Similarity 24.6%; Pred. No. 0.02;  
RESULT 1103  
ID ADB47827 standard; protein; 457 AA.  
DE Novel human secreted protein #3.  
PN US2003054443-A1.  
PD 20-MAR-2003.  
PA (RUBE/) RUBEN S M.  
PA (SOPP/) SOPPET D R.  
PA (EBNE/) EBNER R.  
PA (OLSE/) OLSEN H S.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (BREW/) BREWER L A.

PA (JANA/) JANAT F.  
PA (BIRS/) BIRSE C E.  
Query Match 10.5%; Score 119; DB 7; Length 457;  
Best Local Similarity 33.3%; Pred. No. 0.011;  
RESULT 1104  
ID ADJ55382 standard; protein; 457 AA.  
DE Novel human secreted protein #3.  
PN US2004023283-A1.  
PD 05-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.5%; Score 119; DB 8; Length 457;  
Best Local Similarity 33.3%; Pred. No. 0.011;  
RESULT 1105  
ID ADQ39513 standard; protein; 1642 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 10.4%; Score 118.5; DB 8; Length 1642;  
Best Local Similarity 25.5%; Pred. No. 0.067;  
RESULT 1106  
ID ADQ39515 standard; protein; 1642 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 10.4%; Score 118.5; DB 8; Length 1642;  
Best Local Similarity 25.5%; Pred. No. 0.067;  
RESULT 1107  
ID ADN04531 standard; protein; 2000 AA.  
DE Antipsoriatic protein sequence #458.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 10.4%; Score 118.5; DB 8; Length 2000;  
Best Local Similarity 25.5%; Pred. No. 0.088;  
RESULT 1108  
ID ADP23738 standard; protein; 2000 AA.  
DE PRO polypeptide SEQ ID NO:916.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 10.4%; Score 118.5; DB 8; Length 2000;  
Best Local Similarity 25.5%; Pred. No. 0.088;  
RESULT 1109  
ID ADD48597 standard; protein; 3396 AA.  
DE Human Protein P13611, SEQ ID NO 14303.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 10.4%; Score 118.5; DB 7; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1110  
ID ADN95526 standard; protein; 3396 AA.  
DE Human BEC/LEC-related protein sequence SeqID449.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN-) LICENTIA LTD.  
Query Match 10.4%; Score 118.5; DB 7; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1111  
ID ADJ75521 standard; protein; 3396 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:773.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 10.4%; Score 118.5; DB 8; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1112  
ID ADQ39509 standard; protein; 3396 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.

PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 10.4%; Score 118.5; DB 8; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1113  
ID ADQ95510 standard; protein; 3396 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 10.4%; Score 118.5; DB 8; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1114  
ID ADR99164 standard; protein; 3396 AA.  
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Query Match 10.4%; Score 118.5; DB 8; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1115  
ID ADZ09841 standard; protein; 3396 AA.  
DE Human breast cancer marker CSPG2 protein.  
PN EPI522594-A2.  
PD 13-APR-2005.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 10.4%; Score 118.5; DB 9; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1116  
ID ADZ70548 standard; protein; 3396 AA.  
DE Human protein from lung cancer marker gene CSPG2.  
PN WO2005032495-A2.  
PD 14-APR-2005.  
PA (FARB) BAYER PHARM CORP.  
Query Match 10.4%; Score 118.5; DB 9; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1117  
ID AEA04473 standard; protein; 3396 AA.  
DE Human protein from gene overexpressed in cancer, CSPG2.  
PN WO2005044990-A2.  
PD 19-MAY-2005.  
PA (FARB) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 10.4%; Score 118.5; DB 9; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1118  
ID AEB17604 standard; protein; 3396 AA.  
DE Human CSPG2 protein SeqID18.  
PN JP2005110602-A.  
PD 28-APR-2005.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
PA (SONO) SUMITOMO CHEM CO LTD.  
Query Match 10.4%; Score 118.5; DB 9; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.18;  
RESULT 1119  
ID ADZ09886 standard; protein; 6792 AA.  
DE Human breast cancer marker CSPG2 protein.  
PN EPI522594-A2.  
PD 13-APR-2005.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 10.4%; Score 118.5; DB 9; Length 6792;  
Best Local Similarity 25.5%; Pred. No. 0.45;  
RESULT 1120  
ID AAR46627 standard; protein; 1257 AA.  
DE Neurocan core protein.  
PN WO9403601-A2.  
PD 17-FEB-1994.  
PA (UTNY) UNIV NEW YORK STATE.  
Query Match 10.3%; Score 116.5; DB 2; Length 1257;  
Best Local Similarity 23.9%; Pred. No. 0.074;  
RESULT 1121  
ID ADU76266 standard; protein; 2397 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1518.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 10.2%; Score 116; DB 8; Length 2397;  
Best Local Similarity 28.4%; Pred. No. 0.2;  
RESULT 1122  
ID AAR85443 standard; protein; 908 AA.  
DE Rat brevicain core protein.  
PN WO9526201-A1.  
PD 05-OCT-1995.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Query Match 10.1%; Score 115; DB 2; Length 908;  
Best Local Similarity 22.2%; Pred. No. 0.068;  
RESULT 1123  
ID ADA48595 standard; protein; 656 AA.  
DE Rat Protein AF072892, SEQ ID NO 14301.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.0%; Score 114; DB 7; Length 656;  
Best Local Similarity 28.4%; Pred. No. 0.055;  
RESULT 1124  
ID ADP71273 standard; protein; 191 AA.  
DE Human LP2 protein B-B' domain SeqID8.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG) SEIKAGAKU KOGYO CO LTD.  
Query Match 9.9%; Score 112.5; DB 8; Length 191;  
Best Local Similarity 26.6%; Pred. No. 0.015;  
RESULT 1125  
ID ABB10268 standard; protein; 287 AA.  
DE Human CDNA SEQ ID NO: 576.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 112.5; DB 4; Length 287;  
Best Local Similarity 25.7%; Pred. No. 0.026;  
RESULT 1126  
ID ABP6855 standard; protein; 287 AA.  
DE Human polypeptide SEQ ID NO 576.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 112.5; DB 5; Length 287;  
Best Local Similarity 25.7%; Pred. No. 0.026;  
RESULT 1127  
ID ADM87304 standard; protein; 340 AA.  
DE Human protein SEQ ID NO:397.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 9.9%; Score 112.5; DB 8; Length 340;  
Best Local Similarity 26.6%; Pred. No. 0.032;  
RESULT 1128  
ID ABU11635 standard; protein; 343 AA.  
DE Human MDDT polypeptide SEQ ID 582.  
PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.9%; Score 112.5; DB 6; Length 343;  
Best Local Similarity 26.6%; Pred. No. 0.033;  
RESULT 1129  
ID ABJ10588 standard; protein; 897 AA.  
DE Human novel protein NOV1c SEQ ID NO: 211.  
PN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 112; DB 5; Length 897;  
Best Local Similarity 29.0%; Pred. No. 0.13;

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RESULT 1130
ID ADH71312 standard; protein; 897 AA.
DE Human protein of the invention NOV9a SEQ ID NO:208.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 112; DB 8; Length 897;
Best Local Similarity 29.0%; Pred. No. 0.13;
RESULT 1131
ID ADO09968 standard; protein; 897 AA.
DE Human NOV1C cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATI/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KERU/) KERODA R.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (LIUK/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJU/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match
Best Local Similarity 9.9%; Score 112; DB 8; Length 897;
Best Local Similarity 29.0%; Pred. No. 0.13;
RESULT 1132
ID AAM47684 standard; protein; 1394 AA.
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 9.9%; Score 112; DB 5; Length 1394;
Best Local Similarity 29.0%; Pred. No. 0.24;
RESULT 1133
ID ABG72499 standard; protein; 1416 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #1.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 9.9%; Score 112; DB 6; Length 1416;
Best Local Similarity 29.0%; Pred. No. 0.24;
RESULT 1134
ID ADH71356 standard; protein; 1502 AA.
DE Human protein of the invention NOV9w SEQ ID NO:252.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 112; DB 8; Length 1502;
Best Local Similarity 29.0%; Pred. No. 0.26;
RESULT 1135
ID ADH71358 standard; protein; 1510 AA.
DE Human protein of the invention NOV9x SEQ ID NO:254.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 112; DB 8; Length 1510;
Best Local Similarity 29.0%; Pred. No. 0.26;
RESULT 1136
ID ABG72514 standard; protein; 1653 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 9.9%; Score 112; DB 6; Length 1653;
Best Local Similarity 29.0%; Pred. No. 0.3;
RESULT 1137
ID ADM90835 standard; protein; 1895 AA.
DE Human pharmaceutically useful protein SeqID 228.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match
Best Local Similarity 9.9%; Score 112; DB 8; Length 1895;
Best Local Similarity 29.0%; Pred. No. 0.36;
RESULT 1138
ID ADH71360 standard; protein; 2551 AA.
DE Human protein of the invention NOV9y SEQ ID NO:256.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 112; DB 8; Length 2551;
Best Local Similarity 29.0%; Pred. No. 0.53;
RESULT 1139
ID ADP71271 standard; protein; 200 AA.
DE Human aggregan protein B-B' domain SeqID6.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match
Best Local Similarity 9.8%; Score 111; DB 8; Length 200;
Best Local Similarity 37.4%; Pred. No. 0.022;
RESULT 1140
ID AAM52242 standard; protein; 655 AA.
DE Human versican isoform V3 SEQ ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (MERR/) MERRILEES M.
Query Match
Best Local Similarity 9.8%; Score 111; DB 5; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.11;
RESULT 1141
ID ADO39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 9.8%; Score 111; DB 8; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.11;
RESULT 1142
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match
Best Local Similarity 9.8%; Score 111; DB 2; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.62;
RESULT 1143
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLINIUM PHARM INC.
Query Match
Best Local Similarity 9.8%; Score 111; DB 6; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.62;
RESULT 1144
ID ADO39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.

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PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 9.8%; Score 111; DB 8; Length 2409;  
 Best Local Similarity 29.4%; Pred. No. 0.62;  
 RESULT 1145  
 ID ADQ39512 standard; protein; 2409 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 9.8%; Score 111; DB 8; Length 2409;  
 Best Local Similarity 29.4%; Pred. No. 0.62;  
 RESULT 1146  
 ID ADV70260 standard; protein; 2409 AA.  
 DE Tumor-associated antigenic target polypeptide TAT498.  
 PN WO2004112829-A2.  
 PD 29-DEC-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 9.8%; Score 111; DB 9; Length 2409;  
 Best Local Similarity 29.4%; Pred. No. 0.62;  
 RESULT 1147  
 ID ADQ31200 standard; protein; 1257 AA.  
 DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.  
 PN WO2004041197-A2.  
 PD 21-MAY-2004.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 Query Match 9.7%; Score 110.5; DB 8; Length 1257;  
 Best Local Similarity 23.4%; Pred. No. 0.29;  
 RESULT 1148  
 ID ABJ10586 standard; protein; 2675 AA.  
 DE Human novel protein NOVIA SEQ ID NO: 2.  
 PN WO200259315-A2.  
 PD 01-AUG-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 9.7%; Score 110; DB 5; Length 2675;  
 Best Local Similarity 28.0%; Pred. No. 0.89;  
 RESULT 1149  
 ID ADO09971 standard; protein; 2675 AA.  
 DE Human NOVIA variant.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.  
 PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERR/) ZERRHUSEN B D.  
 PA (LJUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJJ/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (MILL/) MILLET I.  
 PA (ROTH/) ROTHENBERG M E.  
 Query Match 9.7%; Score 110; DB 8; Length 2675;  
 Best Local Similarity 28.0%; Pred. No. 0.89;  
 RESULT 1150  
 ID ADO09971 standard; protein; 1321 AA.  
 DE Tumor-associated antigenic target protein TAT185 SEQ ID NO:82.  
 PN WO2003024392-A2.  
 PD 27-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 9.6%; Score 109; DB 6; Length 1321;  
 Best Local Similarity 21.4%; Pred. No. 0.44;  
 RESULT 1153  
 ID ADJ69615 standard; protein; 1321 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SeqID1421.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match 9.6%; Score 109; DB 7; Length 1321;  
 Best Local Similarity 21.4%; Pred. No. 0.44;  
 RESULT 1154  
 ID ADN38944 standard; protein; 1321 AA.  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 9.6%; Score 109; DB 7; Length 1321;  
 Best Local Similarity 21.4%; Pred. No. 0.44;  
 RESULT 1155  
 ID ADO31196 standard; protein; 1321 AA.  
 DE Human neurocan protein for glucosaminoglycan reduction in glial scars.  
 PN WO2004041197-A2.  
 PD 21-MAY-2004.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 Query Match 9.6%; Score 109; DB 8; Length 1321;  
 Best Local Similarity 21.4%; Pred. No. 0.44;  
 RESULT 1156  
 ID ABU56909 standard; protein; 322 AA.  
 DE 151P3D4 v-2 protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.

PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.  
 PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERR/) ZERRHUSEN B D.  
 PA (LJUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJJ/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (MILL/) MILLET I.  
 PA (ROTH/) ROTHENBERG M E.  
 Query Match 9.7%; Score 110; DB 8; Length 2675;  
 Best Local Similarity 28.0%; Pred. No. 0.89;  
 RESULT 1151  
 ID AAY93913 standard; protein; 353 AA.  
 DE A human hyaluronan-binding protein, designated BM-HABP.  
 PN WO200039166-A1.  
 PD 06-JUL-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AMVA-) AMERICAN NAT RED CROSS.  
 Query Match 9.6%; Score 109; DB 3; Length 353;  
 Best Local Similarity 24.3%; Pred. No. 0.075;  
 RESULT 1152  
 ID ABP97200 standard; protein; 1321 AA.  
 DE Tumor-associated antigenic target protein TAT185 SEQ ID NO:82.  
 PN WO2003024392-A2.  
 PD 27-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 9.6%; Score 109; DB 6; Length 1321;  
 Best Local Similarity 21.4%; Pred. No. 0.44;  
 RESULT 1153  
 ID ADJ69615 standard; protein; 1321 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SeqID1421.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match 9.6%; Score 109; DB 7; Length 1321;  
 Best Local Similarity 21.4%; Pred. No. 0.44;  
 RESULT 1154  
 ID ADN38944 standard; protein; 1321 AA.  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 9.6%; Score 109; DB 7; Length 1321;  
 Best Local Similarity 21.4%; Pred. No. 0.44;  
 RESULT 1155  
 ID ADO31196 standard; protein; 1321 AA.  
 DE Human neurocan protein for glucosaminoglycan reduction in glial scars.  
 PN WO2004041197-A2.  
 PD 21-MAY-2004.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 Query Match 9.6%; Score 109; DB 8; Length 1321;  
 Best Local Similarity 21.4%; Pred. No. 0.44;  
 RESULT 1156  
 ID ABU56909 standard; protein; 322 AA.  
 DE 151P3D4 v-2 protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.



PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 322;  
Best Local Similarity 28.6%; Pred. No. 0.083;  
RESULT 1157  
ID ABJ56908 standard; protein; 322 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 322;  
Best Local Similarity 28.6%; Pred. No. 0.083;  
RESULT 1158  
ID ABJ56918 standard; protein; 353 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 353;  
Best Local Similarity 28.6%; Pred. No. 0.094;  
RESULT 1159  
ID AAY57081 standard; protein; 354 AA.  
DE Human proteoglycan link protein precursor amino acid sequence.  
PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 9.5%; Score 108; DB 3; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1160  
ID AAY57084 standard; protein; 354 AA.  
DE Human proteoglycan link protein precursor #2.  
PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 9.5%; Score 108; DB 3; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1161  
ID ABJ56902 standard; protein; 354 AA.  
DE 151P3D4 v-1 354aa protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1162  
ID ABJ56906 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1163  
ID ABJ56914 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1164  
ID ABJ56898 standard; protein; 354 AA.  
DE 151P3D4 v-8 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1165  
ID ABJ56895 standard; protein; 354 AA.  
DE 151P3D4 v-5 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.

Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1166  
ID ABJ56897 standard; protein; 354 AA.  
DE 151P3D4 v-7 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1167  
ID ABJ56901 standard; protein; 354 AA.  
DE 151P3D4 v-11 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1168  
ID ABJ56894 standard; protein; 354 AA.  
DE 151P3D4 v-4 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1169  
ID ABJ56905 standard; protein; 354 AA.  
DE Human cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1170  
ID ABJ56899 standard; protein; 354 AA.  
DE 151P3D4 v-9 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1171  
ID ABJ56912 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1172  
ID ABJ56893 standard; protein; 354 AA.  
DE 151P3D4 v-3 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1173  
ID ABJ56891 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1174  
ID ABJ56896 standard; protein; 354 AA.  
DE 151P3D4 v-6 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1175  
ID ABJ56895 standard; protein; 354 AA.  
DE 151P3D4 v-5 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.

Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1175  
ID ABJ56900 standard; protein; 354 AA.  
DE 151P3D4 v-10 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1176  
ID ABJ56889 standard; protein; 354 AA.  
DE Transcript variant 121P1F1 v-1.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1177  
ID ABJ56904 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1178  
ID ADP07795 standard; protein; 354 AA.  
DE Human secreted protein, seq id 278.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 9.5%; Score 108; DB 8; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.095;  
RESULT 1179  
ID AAR77034 standard; protein; 355 AA.  
DE Rat brain-enriched hyaluronan binding protein.  
PN WO9527785-A1.  
PD 19-OCT-1995.  
PA (UYVA) UNIV YALE.  
Query Match 9.5%; Score 108; DB 2; Length 355;  
Best Local Similarity 28.9%; Pred. No. 0.095;  
RESULT 1180  
ID ADH71348 standard; protein; 552 AA.  
DE Human protein of the invention NOV9s SEQ ID NO:244.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.5%; Score 108; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.17;  
RESULT 1181  
ID ABJ56890 standard; protein; 721 AA.  
DE Transcript variant 151P3D4 v-2.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 721;  
Best Local Similarity 28.6%; Pred. No. 0.24;  
RESULT 1182  
ID ABJ56892 standard; protein; 721 AA.  
DE 151P3D4 v-2 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 721;  
Best Local Similarity 28.6%; Pred. No. 0.24;  
RESULT 1183  
ID ABJ56903 standard; protein; 721 AA.  
DE 151P3D4 v-1 721aa protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.5%; Score 108; DB 6; Length 721;  
Best Local Similarity 28.6%; Pred. No. 0.24;

RESULT 1184  
ID ABG72500 standard; protein; 93 AA.  
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.  
PN WO200286093-A2.  
PD 31-OCT-2002.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Query Match 9.4%; Score 107; DB 6; Length 93;  
Best Local Similarity 29.2%; Pred. No. 0.02;  
RESULT 1185  
ID AAB83358 standard; protein; 315 AA.  
DE NOV2 protein sequence.  
PN WO200136638-A2.  
PD 25-MAY-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 4; Length 315;  
Best Local Similarity 29.2%; Pred. No. 0.1;  
RESULT 1186  
ID ADH71316 standard; protein; 315 AA.  
DE Human protein of the invention NOV9c SEQ ID NO:212.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 315;  
Best Local Similarity 29.2%; Pred. No. 0.1;  
RESULT 1187  
ID AAY57083 standard; protein; 339 AA.  
DE Rat proteoglycan link protein precursor.  
PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 9.4%; Score 107; DB 3; Length 339;  
Best Local Similarity 28.6%; Pred. No. 0.11;  
RESULT 1188  
ID ABJ56915 standard; protein; 354 AA.  
DE Rat cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.4%; Score 107; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.12;  
RESULT 1189  
ID AAY57082 standard; protein; 355 AA.  
DE Chicken proteoglycan link protein precursor.  
PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 9.4%; Score 107; DB 3; Length 355;  
Best Local Similarity 34.9%; Pred. No. 0.12;  
RESULT 1190  
ID ABJ56907 standard; protein; 355 AA.  
DE Mouse cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.4%; Score 107; DB 6; Length 355;  
Best Local Similarity 28.6%; Pred. No. 0.12;  
RESULT 1191  
ID ADH71336 standard; protein; 533 AA.  
DE Human protein of the invention NOV9m SEQ ID NO:232.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 533;  
Best Local Similarity 29.2%; Pred. No. 0.2;  
RESULT 1192  
ID ADH71334 standard; protein; 533 AA.  
DE Human protein of the invention NOV9l SEQ ID NO:230.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 533;  
Best Local Similarity 29.2%; Pred. No. 0.2;

RESULT 1193  
ID ADH71340 standard; protein; 552 AA.  
DE Human protein of the invention NOV90 SEQ ID NO:236.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.21;  
RESULT 1194  
ID ADH71346 standard; protein; 552 AA.  
DE Human protein of the invention NOV9r SEQ ID NO:242.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.21;  
RESULT 1195  
ID ADH71354 standard; protein; 552 AA.  
DE Human protein of the invention NOV9v SEQ ID NO:250.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.21;  
RESULT 1196  
ID ADH71344 standard; protein; 552 AA.  
DE Human protein of the invention NOV9q SEQ ID NO:240.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.21;  
RESULT 1197  
ID ADH71342 standard; protein; 552 AA.  
DE Human protein of the invention NOV9p SEQ ID NO:238.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.21;  
RESULT 1198  
ID ADH71350 standard; protein; 552 AA.  
DE Human protein of the invention NOV9t SEQ ID NO:246.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.21;  
RESULT 1199  
ID ADH71314 standard; protein; 556 AA.  
DE Human protein of the invention NOV9b SEQ ID NO:210.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 556;  
Best Local Similarity 29.2%; Pred. No. 0.22;  
RESULT 1200  
ID ABM83433 standard; protein; 774 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 9.4%; Score 107; DB 8; Length 774;  
Best Local Similarity 21.5%; Pred. No. 0.34;  
RESULT 1201  
ID ABM83432 standard; protein; 822 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 9.4%; Score 107; DB 8; Length 822;  
Best Local Similarity 21.5%; Pred. No. 0.36;  
RESULT 1202

ID ADO31202 standard; protein; 1268 AA.  
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.  
PN WO2004041197-A2.  
PD 21-MAY-2004.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
Query Match 9.4%; Score 107; DB 8; Length 1268;  
Best Local Similarity 26.2%; Pred. No. 0.65;  
RESULT 1203  
ID ADH71332 standard; protein; 2417 AA.  
DE Human protein of the invention NOV9k SEQ ID NO:228.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 8; Length 2417;  
Best Local Similarity 29.2%; Pred. No. 1.5;  
RESULT 1204  
ID ABJ10587 standard; protein; 2420 AA.  
DE Human novel protein NOV1b SEQ ID NO: 4.  
PN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 107; DB 5; Length 2420;  
Best Local Similarity 29.2%; Pred. No. 1.5;  
RESULT 1205  
ID ADO09838 standard; protein; 2420 AA.  
DE Human NOV1b.  
PN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHIMKETS R A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (MADY/) MADIYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (MILL/) MILLER C E.  
PA (BOLD/) BOLDOG F L.  
PA (LILL/) LI L.  
PA (TAUF/) TAUPIER R J.  
PA (KEKU/) KEKUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERH/) ZERHUSEN B D.  
PA (LIUX/) LIU X.  
PA (COLM/) COLMAN S D.  
PA (TCHE/) TCHERNEV V T.  
PA (SIJ/) SI J.  
PA (EDIN/) EDINGER S R.  
PA (STON/) STONE D J.  
PA (SCIO/) SCIORE P.  
PA (MILL/) MILLET I.  
PA (ROTH/) ROTHENBERG M E.  
Query Match 9.4%; Score 107; DB 8; Length 2420;  
Best Local Similarity 29.2%; Pred. No. 1.5;  
RESULT 1206  
ID ADH71338 standard; protein; 552 AA.  
DE Human protein of the invention NOV9n SEQ ID NO:234.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.3%; Score 106; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.27;  
RESULT 1207  
ID AAB12304 standard; protein; 341 AA.  
DE Human secreted protein encoded by gene 4 clone HFXHC41.  
PN WO200029422-A1.  
PD 25-MAY-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.3%; Score 105.5; DB 3; Length 341;  
Best Local Similarity 28.9%; Pred. No. 0.16;  
RESULT 1208  
ID AAY57080 standard; protein; 354 AA.  
DE Human link protein precursor amino acid sequence.

PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (RRGC ) UNIV CALIFORNIA.  
Query Match 9.2%; Score 105; DB 3; Length 354;  
Best Local Similarity 33.7%; Pred. No. 0.19;  
RESULT 1209  
ID ABJ56913 standard; protein; 354 AA.  
DE Bovine cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 9.2%; Score 105; DB 6; Length 354;  
Best Local Similarity 33.7%; Pred. No. 0.19;  
RESULT 1210  
ID ABU07339 standard; protein; 139 AA.  
DE Human expressed protein tag (EPT) #2040.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.2%; Score 104; DB 6; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.067;  
RESULT 1211  
ID ABU07336 standard; protein; 139 AA.  
DE Human expressed protein tag (EPT) #2037.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.2%; Score 104; DB 6; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.067;  
RESULT 1212  
ID ADQ39387 standard; protein; 139 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.2%; Score 104; DB 8; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.067;  
RESULT 1213  
ID ADY16502 standard; protein; 139 AA.  
DE PRO polypeptide SEQ ID NO 2308.  
PN WO2005018962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 9.2%; Score 104; DB 9; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.067;  
RESULT 1214  
ID ABE29759 standard; protein; 139 AA.  
DE Human CD44 isoform RC.  
PN WO2005067667-A2.  
PD 28-JUL-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 9.2%; Score 104; DB 9; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.067;  
RESULT 1215  
ID ADP71269 standard; protein; 195 AA.  
DE Human LP1 protein B-B' domain SeqID4.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG ) SEIKAGAKU KOGYO CO LTD.  
Query Match 9.2%; Score 104; DB 8; Length 195;  
Best Local Similarity 33.7%; Pred. No. 0.11;  
RESULT 1216  
ID ADP71267 standard; protein; 200 AA.  
DE Human versican protein B-B' domain SeqID2.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG ) SEIKAGAKU KOGYO CO LTD.  
Query Match 9.2%; Score 104; DB 8; Length 200;  
Best Local Similarity 32.5%; Pred. No. 0.11;  
RESULT 1217  
ID ADH71352 standard; protein; 552 AA.  
DE Human protein of the invention NOV9u SEQ ID NO:248.  
PN WO2003102155-A2..

PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.2%; Score 104; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.42;  
RESULT 1218  
ID ADN23553 standard; protein; 380 AA.  
DE Bacterial polypeptide #6206.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 8.8%; Score 101.5; DB 8; Length 380;  
Best Local Similarity 25.5%; Pred. No. 0.45;  
RESULT 1219  
ID AAU76528 standard; protein; 402 AA.  
DE Human LP polypeptide #1.  
PN WO200216578-A2.  
PD 28-FEB-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 8.8%; Score 100.5; DB 5; Length 402;  
Best Local Similarity 30.9%; Pred. No. 0.62;  
RESULT 1220  
ID AAU09883 standard; protein; 402 AA.  
DE Novel human secreted protein #23.  
PN WO200179454-A1.  
PD 25-OCT-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 8.8%; Score 100.5; DB 5; Length 402;  
Best Local Similarity 30.9%; Pred. No. 0.62;  
RESULT 1221  
ID ADF59259 standard; protein; 402 AA.  
DE Human polypeptide sequence SEQ ID NO:1667.  
PN WO2003080795-A2.  
PD 02-OCT-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 8.8%; Score 100.5; DB 7; Length 402;  
Best Local Similarity 30.9%; Pred. No. 0.62;  
RESULT 1222  
ID ADF74155 standard; protein; 412 AA.  
DE Human novel brain/hippocampus protein #43.  
PN JP2003009886-A.  
PD 14-JAN-2003.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
PA (PROT-) PROTEIN EXPRESS KK.  
Query Match 8.8%; Score 100.5; DB 7; Length 412;  
Best Local Similarity 30.9%; Pred. No. 0.64;  
RESULT 1223  
ID AAR77035 standard; protein; 378 AA.  
DE Cat brain-enriched hyaluronan binding protein.  
PN WO9527785-A1.  
PD 19-OCT-1995.  
PA (UYVA ) UNIV YALE.  
Query Match 8.8%; Score 100; DB 2; Length 378;  
Best Local Similarity 24.1%; Pred. No. 0.63;  
RESULT 1224  
ID ABP57346 standard; protein; 402 AA.  
DE Human secreted protein SECP-17 SEQ ID NO:17.  
PN WO2003004615-A2.  
PD 16-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
PA (LUYY/) LU Y.  
Query Match 8.8%; Score 99.5; DB 6; Length 402;  
Best Local Similarity 30.9%; Pred. No. 0.77;  
RESULT 1225  
ID ABJ56917 standard; protein; 201 AA.  
DE Human cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.

Query Match 8.7%; Score 99; DB 6; Length 201;  
Best Local Similarity 28.0%; Pred. No. 0.34;  
RESULT 1226  
ID ABJ56916 standard; protein; 201 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 8.7%; Score 99; DB 6; Length 201;  
Best Local Similarity 28.0%; Pred. No. 0.34;  
RESULT 1227  
ID ABJ56919 standard; protein; 600 AA.  
DE 151P3D4 v-2 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 8.7%; Score 99; DB 6; Length 600;  
Best Local Similarity 28.0%; Pred. No. 1.5;  
RESULT 1228  
ID ABB70377 standard; protein; 1428 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 8.7%; Score 99; DB 4; Length 1428;  
Best Local Similarity 28.4%; Pred. No. 4.7;  
RESULT 1229  
ID ABB60403 standard; protein; 2112 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 8.6%; Score 98; DB 4; Length 2112;  
Best Local Similarity 25.9%; Pred. No. 9.9;  
RESULT 1230  
ID AAY95559 standard; protein; 2870 AA.  
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).  
PN WO200040711-A2.  
PD 13-JUL-2000.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 8.5%; Score 96; DB 3; Length 2870;  
Best Local Similarity 22.4%; Pred. No. 24;  
RESULT 1231  
ID ADN07634 standard; protein; 2870 AA.  
DE Caenorhabditis elegans LOV -1 deletion mutant protein.  
PN US6723557-B1.  
PD 20-APR-2004.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 8.5%; Score 96; DB 8; Length 2870;  
Best Local Similarity 22.4%; Pred. No. 24;  
RESULT 1232  
ID ADW79951 standard; protein; 2870 AA.  
DE Nematode location of vulva (lov-1) mutant protein.  
PN US6849717-B1.  
PD 01-FEB-2005.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 8.5%; Score 96; DB 9; Length 2870;  
Best Local Similarity 22.4%; Pred. No. 24;  
RESULT 1233  
ID AAY95556 standard; protein; 3178 AA.  
DE Caenorhabditis elegans LOV-1 (location of vulva) protein.  
PN WO200040711-A2.  
PD 13-JUL-2000.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 8.5%; Score 96; DB 3; Length 3178;  
Best Local Similarity 22.4%; Pred. No. 27;  
RESULT 1234  
ID ADN07623 standard; protein; 3178 AA.  
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.  
PN US6723557-B1.  
PD 20-APR-2004.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 8.5%; Score 96; DB 8; Length 3178;  
Best Local Similarity 22.4%; Pred. No. 27;  
RESULT 1235  
ID ADW79940 standard; protein; 3178 AA.  
DE Nematode location of vulva (lov-1) protein.  
PN US6849717-B1.  
PD 01-FEB-2005.  
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 8.5%; Score 96; DB 9; Length 3178;  
Best Local Similarity 22.4%; Pred. No. 27;  
RESULT 1236  
ID ADO41972 standard; protein; 231 AA.  
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.  
PN WO2004048529-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 8.4%; Score 95.5; DB 8; Length 231;  
Best Local Similarity 30.2%; Pred. No. 0.91;  
RESULT 1237  
ID ABB65987 standard; protein; 183 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 8.3%; Score 94.5; DB 4; Length 183;  
Best Local Similarity 34.5%; Pred. No. 0.84;  
RESULT 1238  
ID ABB69806 standard; protein; 1795 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 8.3%; Score 94.5; DB 4; Length 1795;  
Best Local Similarity 33.0%; Pred. No. 18;  
RESULT 1239  
ID AAU18060 standard; protein; 258 AA.  
DE Human immunoglobulin polypeptide SEQ ID NO 205.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.2%; Score 93.5; DB 4; Length 258;  
Best Local Similarity 24.6%; Pred. No. 1.7;  
RESULT 1240  
ID ABB10532 standard; protein; 258 AA.  
DE Human cDNA SEQ ID NO: 840.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.2%; Score 93.5; DB 4; Length 258;  
Best Local Similarity 24.6%; Pred. No. 1.7;  
RESULT 1241  
ID ABP67119 standard; protein; 258 AA.  
DE Human polypeptide SEQ ID NO 840.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 8.2%; Score 93.5; DB 5; Length 258;  
Best Local Similarity 24.6%; Pred. No. 1.7;  
RESULT 1242  
ID ADB31684 standard; protein; 258 AA.  
DE Human novel protein SEQ ID NO 205.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.2%; Score 93.5; DB 7; Length 258;  
Best Local Similarity 24.6%; Pred. No. 1.7;  
RESULT 1243  
ID AAU17999 standard; protein; 261 AA.  
DE Human immunoglobulin polypeptide SEQ ID NO 144.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match  
Best Local Similarity 8.2%; Score 93.5; DB 4; Length 261;  
RESULT 1244  
ID ABB10361 standard; protein; 261 AA.  
DE Human cDNA SEQ ID NO: 669.  
FN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 8.2%; Score 93.5; DB 4; Length 261;  
RESULT 1245  
ID ABF6948 standard; protein; 261 AA.  
DE Human polypeptide SEQ ID NO 669.  
FN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 8.2%; Score 93.5; DB 5; Length 261;  
RESULT 1246  
ID ADB31623 standard; protein; 261 AA.  
DE Human novel protein SEQ ID NO 144.  
FN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 8.2%; Score 93.5; DB 7; Length 261;  
RESULT 1247  
ID ABP73157 standard; protein; 40 AA.  
DE Deletion mutant of a CD44-hyaluronic acid binding domain.  
FN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match  
Best Local Similarity 8.1%; Score 92.5; DB 6; Length 40;  
RESULT 1248  
ID ADP04445 standard; protein; 1381 AA.  
DE Sea squirt protein with tissue specific expression in development Seq40.  
FN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 8.1%; Score 92.5; DB 8; Length 1381;  
RESULT 1249  
ID AAU18036 standard; protein; 166 AA.  
DE Human immunoglobulin polypeptide SEQ ID NO 181.  
FN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 8.1%; Score 91.5; DB 4; Length 166;  
RESULT 1250  
ID ABB10469 standard; protein; 166 AA.  
DE Human cDNA SEQ ID NO: 777.  
FN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 8.1%; Score 91.5; DB 4; Length 166;  
RESULT 1251  
ID ABP67056 standard; protein; 166 AA.  
DE Human polypeptide SEQ ID NO 777.  
FN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 8.1%; Score 91.5; DB 5; Length 166;  
RESULT 1252  
ID AAY52550 standard; protein; 416 AA.  
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).  
FN WO958658-A2.

ID ADB31660 standard; protein; 166 AA.  
DE Human novel protein SEQ ID NO 181.  
FN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 8.1%; Score 91.5; DB 7; Length 166;  
RESULT 1253  
ID ABB69720 standard; protein; 1126 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 8.1%; Score 91.5; DB 4; Length 1126;  
RESULT 1254  
ID ABU36285 standard; protein; 402 AA.  
DE Protein encoded by Prokaryotic essential gene #21812.  
FN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITPA PHARM INC.  
Query Match  
Best Local Similarity 8.0%; Score 90.5; DB 6; Length 402;  
RESULT 1255  
ID ADG73740 standard; protein; 505 AA.  
DE Aspergillus niger Brsa-109.  
FN US2003215950-A1.  
PD 20-NOV-2003.  
PA (LASU/) LASURE L L.  
PA (DAIZ/) DAI Z.  
Query Match  
Best Local Similarity 8.0%; Score 90.5; DB 8; Length 505;  
RESULT 1256  
ID ABB69419 standard; protein; 1976 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35049.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 8.0%; Score 90.5; DB 4; Length 1976;  
RESULT 1257  
ID ADN20575 standard; protein; 1103 AA.  
DE Bacterial polypeptide #3228.  
FN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 7.9%; Score 90; DB 8; Length 1103;  
RESULT 1258  
ID ABB65879 standard; protein; 307 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 7.8%; Score 89; DB 4; Length 307;  
RESULT 1259  
ID AAR69554 standard; protein; 416 AA.  
DE Human lysosomal membrane sialoglycoprotein lamp-1.  
FN WO9429342-A1.  
PD 22-DEC-1994.  
PA (IJOL-) LA JOLLA CANCER RES FOUND.  
PA (UNMI ) UNIV MICHIGAN.  
Query Match  
Best Local Similarity 7.8%; Score 89; DB 2; Length 416;  
RESULT 1260  
ID AAY52550 standard; protein; 416 AA.  
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).  
FN WO958658-A2.

PD 18-NOV-1999.  
PA (EPIM-) EPIMUNE INC. 7.8%; Score 89; DB 3; Length 416;  
Query Match 23.6%; Pred. No. 8.8;  
Best Local Similarity 23.6%; Pred. No. 8.8;  
RESULT 1261  
ID ADP65283 standard; protein; 416 AA.  
DE Human lysosomal-associated membrane protein 1.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 7.8%; Score 89; DB 7; Length 416;  
Best Local Similarity 23.6%; Pred. No. 8.8;  
RESULT 1262  
ID ADN03755 standard; protein; 416 AA.  
DE Antiposoriatic protein sequence #74.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC. 7.8%; Score 89; DB 8; Length 416;  
Query Match 23.6%; Pred. No. 8.8;  
Best Local Similarity 23.6%; Pred. No. 8.8;  
RESULT 1263  
ID ADP49321 standard; protein; 416 AA.  
DE Human lysosomal associated membrane protein LAMP #1.  
PN WO2004048537-A2.  
PD 10-JUN-2004.  
PA (EXEL-) EXELIXIS INC. 7.8%; Score 89; DB 8; Length 416;  
Query Match 23.6%; Pred. No. 8.8;  
Best Local Similarity 23.6%; Pred. No. 8.8;  
RESULT 1264  
ID ADP23231 standard; protein; 416 AA.  
DE PRO polypeptide SEQ ID NO:325.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC. 7.8%; Score 89; DB 8; Length 416;  
Query Match 23.6%; Pred. No. 8.8;  
Best Local Similarity 23.6%; Pred. No. 8.8;  
RESULT 1265  
ID ADU60107 standard; protein; 416 AA.  
DE Housekeeping gene protein, SEQ ID 68.  
PN US2004229233-A1.  
PD 18-NOV-2004.  
PA (NICA) NGK INSULATORS LTD.  
Query Match 7.8%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 8.8;  
RESULT 1266  
ID ADW85920 standard; protein; 416 AA.  
DE Human lysosomal-associated membrane protein-1.  
PN WO2005012912-A2.  
PD 10-FEB-2005.  
PA (CHIR) CHIRON CORP. 7.8%; Score 89; DB 9; Length 416;  
Query Match 23.6%; Pred. No. 8.8;  
Best Local Similarity 23.6%; Pred. No. 8.8;  
RESULT 1267  
ID ABO68455 standard; protein; 451 AA.  
DE Pseudomonas aeruginosa polypeptide #630.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP. 7.8%; Score 88.5; DB 7; Length 451;  
Query Match 20.7%; Pred. No. 11;  
Best Local Similarity 20.7%; Pred. No. 11;  
RESULT 1268  
ID AAY52525 standard; protein; 536 AA.  
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP. 7.7%; Score 87.5; DB 3; Length 536;  
Query Match 23.9%; Pred. No. 17;  
Best Local Similarity 23.9%; Pred. No. 17;  
RESULT 1269  
ID AAU96329 standard; protein; 536 AA.  
DE Der HMW-map polypeptide #16.  
PN WO200222807-A2.  
PD 21-MAR-2002.

PA (HESK-) HESKA CORP. 7.7%; Score 87.5; DB 5; Length 536;  
Query Match 23.9%; Pred. No. 17;  
Best Local Similarity 23.9%; Pred. No. 17;  
RESULT 1270  
ID AAY52523 standard; protein; 555 AA.  
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP. 7.7%; Score 87.5; DB 3; Length 555;  
Query Match 23.9%; Pred. No. 18;  
Best Local Similarity 23.9%; Pred. No. 18;  
RESULT 1271  
ID AAU96327 standard; protein; 555 AA.  
DE Der HMW-map polypeptide #14.  
PN WO200222807-A2.  
PD 21-MAR-2002.  
PA (HESK-) HESKA CORP. 7.7%; Score 87.5; DB 5; Length 555;  
Query Match 23.9%; Pred. No. 18;  
Best Local Similarity 23.9%; Pred. No. 18;  
RESULT 1272  
ID AAU96328 standard; protein; 555 AA.  
DE Der HMW-map polypeptide #15.  
PN WO200222807-A2.  
PD 21-MAR-2002.  
PA (HESK-) HESKA CORP. 7.7%; Score 87.5; DB 5; Length 555;  
Query Match 23.9%; Pred. No. 18;  
Best Local Similarity 23.9%; Pred. No. 18;  
RESULT 1273  
ID AAU54844 standard; protein; 1085 AA.  
DE Bovine parathyroid calcium receptor 1 protein 5Kb fragment.  
PN US5763569-A.  
PD 09-JUN-1998.  
PA (NPSP-) NPS PHARM INC. 7.7%; Score 87.5; DB 2; Length 1085;  
Query Match 22.7%; Pred. No. 44;  
Best Local Similarity 22.7%; Pred. No. 44;  
RESULT 1274  
ID AAY41778 standard; protein; 1085 AA.  
DE Bovine parathyroid calcium receptor 1 protein sequence.  
PN US5962314-A.  
PD 05-OCT-1999.  
PA (NPSP-) NPS PHARM INC. 7.7%; Score 87.5; DB 2; Length 1085;  
Query Match 22.7%; Pred. No. 44;  
Best Local Similarity 22.7%; Pred. No. 44;  
RESULT 1275  
ID AAW89563 standard; protein; 1085 AA.  
DE Bovine parathyroid calcium receptor BopCar 1.  
PN US5858684-A.  
PD 12-JAN-1999.  
PA (NPSP-) NPS PHARM INC. 7.7%; Score 87.5; DB 2; Length 1085;  
Query Match 22.7%; Pred. No. 44;  
Best Local Similarity 22.7%; Pred. No. 44;  
RESULT 1276  
ID AAY51825 standard; protein; 1085 AA.  
DE Bovine calcium receptor BopCar1 protein.  
PN US6031003-A.  
PD 29-FEB-2000.  
PA (NPSP-) NPS PHARM INC. 7.7%; Score 87.5; DB 3; Length 1085;  
Query Match 22.7%; Pred. No. 44;  
Best Local Similarity 22.7%; Pred. No. 44;  
RESULT 1277  
ID AAB47820 standard; protein; 1085 AA.  
DE BopCar1.  
PN US6313146-B1.  
PD 06-NOV-2001.  
PA (NPSP-) NPS PHARM INC. 7.7%; Score 87.5; DB 5; Length 1085;  
Query Match 22.7%; Pred. No. 44;  
Best Local Similarity 22.7%; Pred. No. 44;  
RESULT 1278  
ID ADJ93194 standard; protein; 1085 AA.

DE Bovine extracellular Ca-sensing receptor.  
 PN WO200296946-A1.  
 PD 05-DEC-2002.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 Query Match  
 Best Local Similarity 22.7%; Score 87.5; DB 7; Length 1085;  
 RESULT 1279  
 ID ADI40961 standard; protein; 1085 AA.  
 DE Bovine GPCR CASR.  
 PN US2004018976-A1.  
 PD 29-JAN-2004.  
 PA (FEDE/) FEDER J N.  
 PA (MINT/) MINTIER G.  
 PA (RAMA/) RAMANATHAN C S.  
 Query Match  
 Best Local Similarity 22.7%; Score 87.5; DB 8; Length 1085;  
 RESULT 1280  
 ID ADI41015 standard; protein; 1085 AA.  
 DE Bovine GPCR CASR #2.  
 PN US2004018976-A1.  
 PD 29-JAN-2004.  
 PA (FEDE/) FEDER J N.  
 PA (MINT/) MINTIER G.  
 PA (RAMA/) RAMANATHAN C S.  
 Query Match  
 Best Local Similarity 22.7%; Score 87.5; DB 8; Length 1085;  
 RESULT 1281  
 ID ADI44957 standard; protein; 235 AA.  
 DE Rat Protein CMA8213, SEQ ID NO 10428.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 Query Match  
 Best Local Similarity 27.8%; Score 87; DB 7; Length 235;  
 RESULT 1282  
 ID AAY29082 standard; protein; 288 AA.  
 DE T. gondii immunogenic protein.  
 PN WO9332633-A1.  
 PD 01-JUL-1999.  
 PA (HESK-) HESKA CORP.  
 Query Match  
 Best Local Similarity 29.7%; Score 87; DB 2; Length 288;  
 RESULT 1283  
 ID AAY29081 standard; protein; 288 AA.  
 DE T. gondii immunogenic protein.  
 PN WO9332633-A1.  
 PD 01-JUL-1999.  
 PA (HESK-) HESKA CORP.  
 Query Match  
 Best Local Similarity 29.7%; Score 87; DB 2; Length 288;  
 RESULT 1284  
 ID AAU25553 standard; protein; 288 AA.  
 DE T. gondii immunogenic protein PTG1397.  
 PN US2001014447-A1.  
 PD 16-AUG-2001.  
 PA (MILH/) MILHAUSEN M J.  
 Query Match  
 Best Local Similarity 29.7%; Score 87; DB 4; Length 288;  
 RESULT 1285  
 ID AAU25552 standard; protein; 288 AA.  
 DE T. gondii immunogenic protein PTG288.  
 PN US2001014447-A1.  
 PD 16-AUG-2001.  
 PA (MILH/) MILHAUSEN M J.  
 Query Match  
 Best Local Similarity 29.7%; Score 87; DB 4; Length 288;  
 RESULT 1286  
 ID ADG17391 standard; protein; 288 AA.  
 DE T. gondii protein #79.  
 PN US2003194393-A1.  
 PD 16-OCT-2003.  
 PA (MILH/) MILHAUSEN M J.

Query Match  
 Best Local Similarity 7.7%; Score 87; DB 7; Length 288;  
 RESULT 1287  
 ID ADG17394 standard; protein; 288 AA.  
 DE T. gondii protein #82.  
 PN US2003194393-A1.  
 PD 16-OCT-2003.  
 PA (MILH/) MILHAUSEN M J.  
 Query Match  
 Best Local Similarity 7.7%; Score 87; DB 7; Length 288;  
 RESULT 1288  
 ID AAR01940 standard; protein; 417 AA.  
 DE Tumour necrosis factor.  
 PN JP01285191-A.  
 PD 16-NOV-1989.  
 PA (GREC ) GREEN CROSS CORP.  
 Query Match  
 Best Local Similarity 7.7%; Score 87; DB 2; Length 417;  
 RESULT 1289  
 ID AAP91941 standard; peptide; 400 AA.  
 DE Sequence of preprospasmolysin.  
 PN DE3808456-A.  
 PD 28-SEP-1989.  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 Query Match  
 Best Local Similarity 7.6%; Score 86.5; DB 1; Length 400;  
 RESULT 1290  
 ID AAR69555 standard; protein; 410 AA.  
 DE Human lysosomal membrane sialoglycoprotein lamp-2.  
 PN WO9429342-A1.  
 PD 22-DEC-1994.  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 PA (UNMI ) UNIV MICHIGAN.  
 Query Match  
 Best Local Similarity 20.7%; Score 86.5; DB 2; Length 410;  
 RESULT 1291  
 ID AAY37234 standard; protein; 708 AA.  
 DE Chlamydia trachomatis cellular envelope protein.  
 PN WO9928475-A2.  
 PD 10-JUN-1999.  
 PA (GEST ) GENSET.  
 Query Match  
 Best Local Similarity 7.6%; Score 86.5; DB 2; Length 708;  
 RESULT 1292  
 ID ASM82857 standard; protein; 476 AA.  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3106.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 7.6%; Score 86; DB 8; Length 476;  
 RESULT 1293  
 ID ABM83144 standard; protein; 476 AA.  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3393.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 32.1%; Score 86; DB 8; Length 476;  
 RESULT 1294  
 ID ABP69313 standard; protein; 343 AA.  
 DE Human polypeptide SEQ ID NO 1360.  
 PN WO2002705339-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 30.2%; Score 85.5; DB 5; Length 343;  
 RESULT 1295  
 ID AAB09826 standard; protein; 346 AA.  
 DE Endoglycanase protein sequence 6.  
 PN WO200024879-A1.  
 PD 04-MAY-2000.  
 PA (MEIJ ) MEIJI SEIKA KAISHA LTD.



Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 3; Length 346;  
RESULT 1296  
ID AAO1507 standard; protein; 346 AA.  
DE Phycomyces nitens endoglucanase-related protein.  
PN WO200242474-A1.  
PD 30-MAY-2002.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 5; Length 346;  
RESULT 1297  
ID ABB08065 standard; protein; 346 AA.  
DE P. nitens CP99002 PCEI protein.  
PN WO200238754-A1.  
PD 16-MAY-2002.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 5; Length 346;  
RESULT 1298  
ID ADA37114 standard; protein; 346 AA.  
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.  
PN WO2003052105-A1.  
PD 26-JUN-2003.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 6; Length 346;  
RESULT 1299  
ID AAR57350 standard; protein; 354 AA.  
DE Human cartilage link protein.  
PN WO9415627-A1.  
PD 21-JUL-1994.  
PA (GENO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 2; Length 354;  
RESULT 1300  
ID ADJ76313 standard; protein; 363 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1565.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 8; Length 363;  
RESULT 1301  
ID ADX37611 standard; protein; 363 AA.  
DE Lung cancer related protein, SEQ ID 87.  
PN US2005048589-A1.  
PD 03-MAR-2005.  
PA (JEND/) JENDOUBI M.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 9; Length 363;  
RESULT 1302  
ID ABB78250 standard; protein; 652 AA.  
DE Amino acid sequence of a human heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GENO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 5; Length 652;  
RESULT 1303  
ID ABB78248 standard; protein; 841 AA.  
DE Amino acid sequence of a zebrafish heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GENO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 5; Length 841;  
RESULT 1304  
ID ADQ37103 standard; protein; 951 AA.  
DE Cell proliferation-related polypeptide #118.  
PN WO2004061122-A2.  
PD 22-JUL-2004.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 8; Length 951;

Best Local Similarity 26.0%; Pred. No. 59;  
RESULT 1305  
ID ABB78249 standard; protein; 977 AA.  
DE Amino acid sequence of a zebrafish heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GENO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 5; Length 977;  
RESULT 1306  
ID ABU54710 standard; protein; 1784 AA.  
DE Human CA125 protein amino terminal sequence.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 6; Length 1784;  
RESULT 1307  
ID ABU54858 standard; protein; 1794 AA.  
DE Human CA125 amino terminal domain.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 6; Length 1794;  
RESULT 1308  
ID ABU54707 standard; protein; 1821 AA.  
DE Human CA125 amino terminal domain.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 6; Length 1821;  
RESULT 1309  
ID AEB29721 standard; protein; 2448 AA.  
DE Human Mucin 5 (subtypes A and C).  
PN WO2005067667-A2.  
PD 28-JUL-2005.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 9; Length 2448;  
RESULT 1310  
ID AAE34702 standard; protein; 5877 AA.  
DE Human mucin (MUC-16B).  
PN WO200292836-A2.  
PD 21-NOV-2002.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 6; Length 5877;  
RESULT 1311  
ID ABU54721 standard; protein; 11721 AA.  
DE Human CA125 full length protein sequence.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 6; Length 11721;  
RESULT 1312  
ID ADP84155 standard; protein; 22157 AA.  
DE Human CA125 protein sequence SeqID 5.  
PN WO2004045553-A2.  
PD 03-JUN-2004.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match  
Best Local Similarity 7.5%; Score 85.5; DB 8; Length 22157;  
RESULT 1313  
ID ABB50001 standard; protein; 569 AA.  
DE Listeria monocytogenes protein #2705.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match  
Best Local Similarity 7.5%; Score 85; DB 5; Length 569;  
RESULT 1314  
ID ABB50001 standard; protein; 569 AA.  
DE Listeria monocytogenes protein #2705.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match  
Best Local Similarity 7.5%; Score 85; DB 5; Length 569;

RESULT 1314  
ID ABU32518 standard; protein; 569 AA.  
DE Protein encoded by Prokaryotic essential gene #18045.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (EULI-) ELITRA PHARM INC.  
Query Match 7.5%; Score 85; DB 6; Length 569;  
Best Local Similarity 22.9%; Pred. No. 33;  
RESULT 1315  
ID ABB55236 standard; protein; 627 AA.  
DE Lactococcus lactis protein yf1c.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 7.5%; Score 85; DB 5; Length 627;  
Best Local Similarity 21.5%; Pred. No. 38;  
RESULT 1316  
ID ADS29466 standard; protein; 627 AA.  
DE Bacterial polypeptide #18499.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.5%; Score 85; DB 8; Length 627;  
Best Local Similarity 21.5%; Pred. No. 38;  
RESULT 1317  
ID AG83274 standard; protein; 631 AA.  
DE Chlamydia trachomatis PmpH(N-term) fusion protein.  
PN WO200140474-A2.  
PD 07-JUN-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 7.5%; Score 85; DB 4; Length 631;  
Best Local Similarity 27.7%; Pred. No. 38;  
RESULT 1318  
ID ABB94245 standard; protein; 631 AA.  
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.  
PN WO200208267-A2.  
PD 31-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.5%; Score 85; DB 5; Length 631;  
Best Local Similarity 27.7%; Pred. No. 38;  
RESULT 1319  
ID ADD42755 standard; protein; 664 AA.  
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.  
PN WO2003041560-A2.  
PD 22-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.5%; Score 85; DB 7; Length 664;  
Best Local Similarity 27.7%; Pred. No. 41;  
RESULT 1320  
ID AAU38901 standard; protein; 1016 AA.  
DE C. trachomatis CT872 protein.  
PN WO200181379-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 7.5%; Score 85; DB 4; Length 1016;  
Best Local Similarity 27.7%; Pred. No. 72;  
RESULT 1321  
ID ABG91037 standard; protein; 1016 AA.  
DE Chlamydia trachomatis outer membrane protein H protein.  
PN WO200262380-A2.  
PD 15-AUG-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 7.5%; Score 85; DB 5; Length 1016;  
Best Local Similarity 27.7%; Pred. No. 72;  
RESULT 1322  
ID ADD42682 standard; protein; 1016 AA.  
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.  
PN WO2003041560-A2.  
PD 22-MAY-2003.

PA (CORI-) CORIXA CORP.  
Query Match 7.5%; Score 85; DB 7; Length 1016;  
Best Local Similarity 27.7%; Pred. No. 72;  
RESULT 1323  
ID ADD43800 standard; protein; 1016 AA.  
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 95.  
PN WO2003049762-A2.  
PD 19-JUN-2003.  
PA (CHIR-) CHIRON SPA.  
Query Match 7.5%; Score 85; DB 7; Length 1016;  
Best Local Similarity 27.7%; Pred. No. 72;  
RESULT 1324  
ID ADW29028 standard; protein; 1016 AA.  
DE C trachomatis polymorphic membrane protein (PmpH) Seq 22.  
PN WO2005002619-A2.  
PD 13-JAN-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 7.5%; Score 85; DB 9; Length 1016;  
Best Local Similarity 27.7%; Pred. No. 72;  
RESULT 1325  
ID AEA19092 standard; protein; 1016 AA.  
DE Chlamydia trachomatis protein - SEQ ID 95.  
PN US2005106162-A1.  
PD 19-MAY-2005.  
PA (GRAN/) GRANDI G.  
PA (RATT/) RATTI G.  
Query Match 7.5%; Score 85; DB 9; Length 1016;  
Best Local Similarity 27.7%; Pred. No. 72;  
RESULT 1326  
ID ABB60387 standard; protein; 1049 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7953.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.5%; Score 85; DB 4; Length 1049;  
Best Local Similarity 22.1%; Pred. No. 75;  
RESULT 1327  
ID ADX67527 standard; protein; 349 AA.  
DE Plant full length insert polypeptide seqid 38370.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 7.4%; Score 84.5; DB 8; Length 349;  
Best Local Similarity 25.0%; Pred. No. 19;  
RESULT 1328  
ID ABM88426 standard; protein; 494 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:6672.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 7.4%; Score 84.5; DB 7; Length 494;  
Best Local Similarity 24.2%; Pred. No. 31;  
RESULT 1329  
ID ADJ66747 standard; protein; 2234 AA.  
DE Human Muc16 GST fusion protein amino acid sequence SeqID20.  
PN WO2004005470-A2.  
PD 15-JAN-2004.  
PA (TMU-) IMMUNOGEN INC.  
Query Match 7.4%; Score 84.5; DB 8; Length 2234;  
Best Local Similarity 27.2%; Pred. No. 2.3e+02;  
RESULT 1330  
ID ADR72871 standard; protein; 22152 AA.  
DE Human ovarian cancer-related tumour marker CA125 protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 7.4%; Score 84.5; DB 8; Length 22152;  
Best Local Similarity 27.2%; Pred. No. 4.9e+03;

RESULT 1331  
ID AB11729 standard; protein; 216 AA.  
DE Cryptosporidium parvum Iowa isolate GP900, domain 2.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.4%; Score 84; DB 3; Length 216;  
Best Local Similarity 26.7%; Pred. No. 11;  
RESULT 1332  
ID AB11734 standard; protein; 216 AA.  
DE Cryptosporidium parvum NINC isolate GP900, domain 2.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.4%; Score 84; DB 3; Length 216;  
Best Local Similarity 26.7%; Pred. No. 11;  
RESULT 1333  
ID AB11726 standard; protein; 1837 AA.  
DE Cryptosporidium parvum Iowa isolate GP900.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.4%; Score 84; DB 5; Length 216;  
Best Local Similarity 26.7%; Pred. No. 11;  
RESULT 1334  
ID AA842164 standard; protein; 330 AA.  
DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.4%; Score 84; DB 3; Length 330;  
Best Local Similarity 27.5%; Pred. No. 20;  
RESULT 1335  
ID AB859598 standard; protein; 330 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 5586.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.4%; Score 84; DB 4; Length 330;  
Best Local Similarity 30.6%; Pred. No. 20;  
RESULT 1336  
ID AD061979 standard; protein; 335 AA.  
DE Transcription factor G2571, SEQ ID 446.  
PN WO2004031349-A2.  
PD 15-APR-2004.  
PA (MENND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 7.4%; Score 84; DB 8; Length 335;  
Best Local Similarity 26.4%; Pred. No. 20;  
RESULT 1337  
ID AE27053 standard; protein; 335 AA.  
DE Stress tolerant plant-related transcription factor protein SeqID894.  
PN WO2005047516-A2.  
PD 26-MAY-2005.  
PA (MENND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 7.4%; Score 84; DB 9; Length 335;  
Best Local Similarity 26.4%; Pred. No. 20;  
RESULT 1338  
ID AAB96091 standard; protein; 1362 AA.  
DE Putative P. abyssi amylopullulanase.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 7.4%; Score 84; DB 4; Length 1362;  
Best Local Similarity 26.5%; Pred. No. 1.3e+02;  
RESULT 1339  
ID AA48299 standard; protein; 1721 AA.  
DE Cryptosporidium parvum GP900 antigen.  
PN WO9806430-A1.  
PD 19-FEB-1998.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.4%; Score 84; DB 2; Length 1721;  
Best Local Similarity 26.7%; Pred. No. 1.8e+02;

RESULT 1340  
ID AB11727 standard; protein; 1721 AA.  
DE Portion of Cryptosporidium parvum NINC isolate GP900.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.4%; Score 84; DB 3; Length 1721;  
Best Local Similarity 26.7%; Pred. No. 1.8e+02;  
RESULT 1341  
ID ABJ04045 standard; protein; 1721 AA.  
DE C parvum GP900 protein fragment SEQ ID NO: 6.  
PN WO200194631-A1.  
PD 13-DEC-2001.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.4%; Score 84; DB 5; Length 1721;  
Best Local Similarity 26.7%; Pred. No. 1.8e+02;  
RESULT 1342  
ID AB11726 standard; protein; 1837 AA.  
DE Cryptosporidium parvum Iowa isolate GP900.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.4%; Score 84; DB 3; Length 1837;  
Best Local Similarity 26.7%; Pred. No. 2e+02;  
RESULT 1343  
ID ABJ04044 standard; protein; 1837 AA.  
DE C parvum GP900 protein fragment SEQ ID NO: 5.  
PN WO200194631-A1.  
PD 13-DEC-2001.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.4%; Score 84; DB 5; Length 1837;  
Best Local Similarity 26.7%; Pred. No. 2e+02;  
RESULT 1344  
ID AD707505 standard; protein; 2109 AA.  
DE Human colon-specific polypeptide (CSP) #22.  
PN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 7.4%; Score 84; DB 8; Length 2109;  
Best Local Similarity 31.5%; Pred. No. 2.4e+02;  
RESULT 1345  
ID AD707506 standard; protein; 2254 AA.  
DE Human colon-specific polypeptide (CSP) #23.  
PN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 7.4%; Score 84; DB 8; Length 2254;  
Best Local Similarity 31.5%; Pred. No. 2.6e+02;  
RESULT 1346  
ID AD707507 standard; protein; 2401 AA.  
DE Human colon-specific polypeptide (CSP) #24.  
PN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 7.4%; Score 84; DB 8; Length 2401;  
Best Local Similarity 31.5%; Pred. No. 2.8e+02;  
RESULT 1347  
ID AEB56507 standard; protein; 5858 AA.  
DE Radiochemotherapy response detection associated protein SEQ ID NO 82.  
PN WO2005073411-A1.  
PD 11-AUG-2005.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 7.4%; Score 84; DB 9; Length 5858;  
Best Local Similarity 31.5%; Pred. No. 9.3e+02;  
RESULT 1348  
ID ABU53165 standard; protein; 143 AA.  
DE Human testes-derived DRFZphtes3\_2all homologue #25.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 7.4%; Score 83.5; DB 4; Length 143;  
Best Local Similarity 30.7%; Pred. No. 7.4;  
RESULT 1349

ID ABU53163 standard; protein; 247 AA.  
 DE Human testes-derived DKF2phtes3\_2all homologue #23.  
 PN WO200112659-A2.  
 PD 22-FEB-2001.  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 Query Match 7.4%; Score 83.5; DB 4; Length 247;  
 Best Local Similarity 30.7%; Pred. No. 15;  
 RESULT 1350  
 ID ABU53158 standard; protein; 260 AA.  
 DE Human testes-derived DKF2phtes3\_2all homologue #18.  
 PN WO200112659-A2.  
 PD 22-FEB-2001.  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 Query Match 7.4%; Score 83.5; DB 4; Length 260;  
 Best Local Similarity 30.7%; Pred. No. 16;  
 RESULT 1351  
 ID ADX94171 standard; protein; 357 AA.  
 DE Plant full length insert polypeptide seqid 56835.  
 PN US2004034888-A1.  
 PD 19-FEB-2004.  
 PA (LIUJ/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S B.  
 PA (TABA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 Query Match 7.4%; Score 83.5; DB 8; Length 357;  
 Best Local Similarity 24.0%; Pred. No. 25;  
 RESULT 1352  
 ID ABU53157 standard; protein; 368 AA.  
 DE Human testes-derived DKF2phtes3\_2all homologue #17.  
 PN WO200112659-A2.  
 PD 22-FEB-2001.  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 Query Match 7.4%; Score 83.5; DB 4; Length 368;  
 Best Local Similarity 30.7%; Pred. No. 26;  
 RESULT 1353  
 ID ABU53156 standard; protein; 385 AA.  
 DE Human testes-derived DKF2phtes3\_2all homologue #16.  
 PN WO200112659-A2.  
 PD 22-FEB-2001.  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 Query Match 7.4%; Score 83.5; DB 4; Length 385;  
 Best Local Similarity 30.7%; Pred. No. 28;  
 RESULT 1354  
 ID ABU53159 standard; protein; 386 AA.  
 DE Human testes-derived DKF2phtes3\_2all homologue #19.  
 PN WO200112659-A2.  
 PD 22-FEB-2001.  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 Query Match 7.4%; Score 83.5; DB 4; Length 387;  
 Best Local Similarity 30.7%; Pred. No. 28;  
 RESULT 1355  
 ID ABU53161 standard; protein; 387 AA.  
 DE Human testes-derived DKF2phtes3\_2all homologue #21.  
 PN WO200112659-A2.  
 PD 22-FEB-2001.  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 Query Match 7.4%; Score 83.5; DB 4; Length 387;  
 Best Local Similarity 30.7%; Pred. No. 28;  
 RESULT 1356  
 ID AAM50241 standard; protein; 393 AA.  
 DE Wheat tyrosine decarboxylase.  
 PN US6297055-B1.  
 PD 02-OCT-2001.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 Query Match 7.4%; Score 83.5; DB 4; Length 393;  
 Best Local Similarity 26.5%; Pred. No. 28;  
 RESULT 1357  
 ID AAU76423 standard; protein; 393 AA.  
 DE Wheat tyrosine decarboxylase clone wr1.pk0059.g9.  
 PN US2002009801-A1.  
 PD 24-JAN-2002.

PA (FALC/) FALCO S C.  
 PA (PAMO/) FAMODU O O.  
 PA (OROZ/) OROZCO E R.  
 Query Match 7.4%; Score 83.5; DB 5; Length 393;  
 Best Local Similarity 26.5%; Pred. No. 28;  
 RESULT 1358  
 ID ABU53160 standard; protein; 395 AA.  
 DE Human testes-derived DKF2phtes3\_2all homologue #20.  
 PN WO200112659-A2.  
 PD 22-FEB-2001.  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 Query Match 7.4%; Score 83.5; DB 4; Length 395;  
 Best Local Similarity 30.7%; Pred. No. 29;  
 RESULT 1359  
 ID ABB10349 standard; protein; 553 AA.  
 DE Human cDNA SEQ ID NO: 657.  
 PN WO200154474-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 7.4%; Score 83.5; DB 4; Length 553;  
 Best Local Similarity 22.9%; Pred. No. 45;  
 RESULT 1360  
 ID ABP66936 standard; protein; 553 AA.  
 DE Human polypeptide SEQ ID NO 657.  
 PN US2002090672-A1.  
 PD 11-JUL-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (ROBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 7.4%; Score 83.5; DB 5; Length 553;  
 Best Local Similarity 22.9%; Pred. No. 45;  
 RESULT 1361  
 ID ABU53144 standard; protein; 717 AA.  
 DE Human testes-derived DKF2phtes3\_2all homologue #4.  
 PN WO200112659-A2.  
 PD 22-FEB-2001.  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 Query Match 7.4%; Score 83.5; DB 4; Length 717;  
 Best Local Similarity 30.7%; Pred. No. 63;  
 RESULT 1362  
 ID AAY54466 standard; protein; 788 AA.  
 DE Amino acid sequence of intestinal insect mucin isoform IIM14.  
 PN WO9967373-A2.  
 PD 29-DEC-1999.  
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.  
 Query Match 7.4%; Score 83.5; DB 3; Length 788;  
 Best Local Similarity 26.5%; Pred. No. 72;  
 RESULT 1363  
 ID AAY54467 standard; protein; 807 AA.  
 DE Amini acid sequence of intestinal insect mucin isoform IIM22.  
 PN WO9967373-A2.  
 PD 29-DEC-1999.  
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.  
 Query Match 7.4%; Score 83.5; DB 3; Length 807;  
 Best Local Similarity 26.5%; Pred. No. 74;  
 RESULT 1364  
 ID ABU62079 standard; protein; 4123 AA.  
 DE Human jelly belly (Jeb) protein.  
 PN US2003054485-A1.  
 PD 20-MAR-2003.  
 PA (SCOT/) SCOTT M P.  
 PA (WEIS/) WEISS J B.  
 Query Match 7.4%; Score 83.5; DB 7; Length 4123;  
 Best Local Similarity 22.7%; Pred. No. 6.5e+02;  
 RESULT 1365  
 ID ADH48718 standard; protein; 4219 AA.  
 DE NOV1 protein sequence, SEQ ID 2.  
 PN WO200268652-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 7.4%; Score 83.5; DB 5; Length 4219;  
 Best Local Similarity 22.7%; Pred. No. 6.7e+02;  
 RESULT 1366

ID AEA04533 standard; protein; 5178 AA.  
DE Human protein from gene under-expressed in cancer, MUC2.  
PN WO2005044990-A2.  
PD 19-MAY-2005.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 7.4%; Score 83.5; DB 9; Length 5178;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1367  
ID ANM24516 standard; protein; 5179 AA.  
DE C899P predicted amino acid sequence.  
PN WO2001497116-A2.  
PD 12-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 7.4%; Score 83.5; DB 4; Length 5179;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1368  
ID ABP55365 standard; protein; 5179 AA.  
DE Human colon tumour protein for clone C899P SEQ ID NO:1068.  
PN WO200283070-A2.  
PD 24-OCT-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.4%; Score 83.5; DB 6; Length 5179;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1369  
ID ABO07258 standard; protein; 5179 AA.  
DE Human p53 modifying protein, SEQ ID 218.  
PN WO200299122-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 7.4%; Score 83.5; DB 6; Length 5179;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1370  
ID ADP48091 standard; protein; 5179 AA.  
DE Human Protein NP\_024448, SEQ ID NO 13789.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.4%; Score 83.5; DB 7; Length 5179;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1371  
ID ADD44998 standard; protein; 5179 AA.  
DE Human Protein Q02817, SEQ ID NO 10430.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.4%; Score 83.5; DB 7; Length 5179;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1372  
ID ADQ29695 standard; protein; 5179 AA.  
DE Human colorectal cancer-associated protein #50.  
PN EPI439393-A2.  
PD 21-JUL-2004.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 7.4%; Score 83.5; DB 8; Length 5179;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1373  
ID ADQ80379 standard; protein; 5179 AA.  
DE Intestinal/tracheal mucin 2 protein.  
PN WO2004063709-A2.  
PD 29-JUL-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 7.4%; Score 83.5; DB 8; Length 5179;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1374  
ID AEA27639 standard; protein; 5179 AA.  
DE Human intestinal mucin.  
PN WO2005047321-A2.  
PD 26-MAY-2005.  
PA (UYCR-) UNIV CREIGHTON.

Query Match 7.4%; Score 83.5; DB 9; Length 5179;  
Best Local Similarity 30.7%; Pred. No. 8.8e+02;  
RESULT 1375  
ID ADN95228 standard; protein; 5737 AA.  
DE Human BEC/LEC-related protein sequence SeqID150.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 7.4%; Score 83.5; DB 7; Length 5737;  
Best Local Similarity 22.7%; Pred. No. 1e+03;  
RESULT 1376  
ID AAR07670 standard; protein; 166 AA.  
DE Intestinal mucin deduced from clone SMUC 40.  
PN WO9012892-A.  
PD 01-NOV-1990.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.3%; Score 83; DB 2; Length 166;  
Best Local Similarity 29.9%; Pred. No. 10;  
RESULT 1377  
ID AAW75700 standard; peptide; 409 AA.  
DE Vpr protein binding HHR23B amino acid sequence.  
PN WO9835234-A1.  
PD 13-AUG-1998.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.3%; Score 83; DB 2; Length 409;  
Best Local Similarity 28.6%; Pred. No. 34;  
RESULT 1378  
ID AAW68186 standard; protein; 409 AA.  
DE Vpr binding protein HHR23B amino acid sequence.  
PN WO9835032-A2.  
PD 13-AUG-1998.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 7.3%; Score 83; DB 2; Length 409;  
Best Local Similarity 28.6%; Pred. No. 34;  
RESULT 1379  
ID ABU07460 standard; protein; 409 AA.  
DE Protein differentially regulated in prostate cancer #63.  
PN WO200281638-A2.  
PD 17-OCT-2002.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 7.3%; Score 83; DB 6; Length 409;  
Best Local Similarity 28.6%; Pred. No. 34;  
RESULT 1380  
ID ADN03716 standard; protein; 409 AA.  
DE Antipsoriatic protein sequence #55.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 83; DB 8; Length 409;  
Best Local Similarity 28.6%; Pred. No. 34;  
RESULT 1381  
ID ADQ65876 standard; protein; 409 AA.  
DE Novel human protein sequence #849.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.3%; Score 83; DB 8; Length 409;  
Best Local Similarity 28.6%; Pred. No. 34;  
RESULT 1382  
ID ADW08718 standard; protein; 409 AA.  
DE Human protein which is down-regulated in HCV-infected tissue - SEQ ID 55.  
PN EPI493750-A2.  
PD 05-JAN-2005.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 7.3%; Score 83; DB 9; Length 409;  
Best Local Similarity 28.6%; Pred. No. 34;  
RESULT 1383  
ID ADV14438 standard; protein; 409 AA.  
DE PRO polypeptide SEQ ID NO 244.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 7.3%; Score 83; DB 9; Length 409;  
RESULT 1384  
ID AB861785 standard; protein; 471 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12147.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 7.3%; Score 83; DB 4; Length 471;  
RESULT 1385  
ID AD843566 standard; protein; 605 AA.  
DE Bacterial polypeptide #22016.  
FN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 7.3%; Score 83; DB 8; Length 605;  
RESULT 1386  
ID ADX97567 standard; protein; 2624 AA.  
DE Pancreatic cancer associated human protein, SEQ ID 115.  
FN EPI471075-A2.  
PD 27-OCT-2004.  
PA (HINZ/) HINZMANN B.  
PA (ROSE/) ROSENTHAL A.  
PA (PILA/) PILARSKY C.  
PA (DAHL/) DAHL E.  
PA (SPEC/) SPECHT T.  
PA (LICH/) LICHTNER R.  
Query Match  
Best Local Similarity 7.3%; Score 83; DB 8; Length 2624;  
RESULT 1387  
ID AAG34201 standard; protein; 280 AA.  
DE Zea mays protein fragment SEQ ID NO: 41576.  
FN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 7.3%; Score 82.5; DB 3; Length 280;  
RESULT 1388  
ID AAG40817 standard; protein; 346 AA.  
DE Zea mays protein fragment SEQ ID NO: 50697.  
FN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 7.3%; Score 82.5; DB 3; Length 346;  
RESULT 1389  
ID ADY11098 standard; protein; 463 AA.  
DE Plant full length insert polypeptide seqid 66913.  
FN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match  
Best Local Similarity 7.3%; Score 82.5; DB 8; Length 463;  
RESULT 1390  
ID AAG44071 standard; protein; 825 AA.  
DE Bacterial polypeptide #22501.  
FN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 7.3%; Score 82.5; DB 8; Length 825;

Best Local Similarity 24.8%; Pred. No. 96;  
RESULT 1391  
ID AB871012 standard; protein; 843 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 7.3%; Score 82.5; DB 4; Length 843;  
RESULT 1392  
ID AAW38272 standard; protein; 1085 AA.  
DE Bovine parathyroid cell calcium receptor 1 (BoPCar 1).  
FN US5688938-A.  
PD 18-NOV-1997.  
PA (BGMH ) BRIGHAM & WOMENS HOSPITAL.  
PA (NPSP-) NPS PHARM INC.  
Query Match  
Best Local Similarity 7.3%; Score 82.5; DB 2; Length 1085;  
RESULT 1393  
ID ABB69011 standard; protein; 1371 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33825.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 7.3%; Score 82.5; DB 4; Length 1371;  
RESULT 1394  
ID ABB60186 standard; protein; 1714 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7350.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 7.3%; Score 82.5; DB 4; Length 1714;  
RESULT 1395  
ID AAM21657 standard; protein; 89 AA.  
DE Peptide #8091 encoded by probe for measuring cervical gene expression.  
FN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 7.2%; Score 82; DB 4; Length 89;  
RESULT 1396  
ID ABB44016 standard; peptide; 89 AA.  
DE Peptide #11522 encoded by human foetal liver single exon probe.  
FN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 7.2%; Score 82; DB 4; Length 89;  
RESULT 1397  
ID AAM37960 standard; protein; 89 AA.  
DE Peptide #11997 encoded by probe for measuring placental gene expression.  
FN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 7.2%; Score 82; DB 4; Length 89;  
RESULT 1398  
ID ABB26922 standard; protein; 89 AA.  
DE Protein #8921 encoded by probe for measuring heart cell gene expression.  
FN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 7.2%; Score 82; DB 4; Length 89;  
RESULT 1399  
ID AAM77746 standard; protein; 89 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 38052.  
FN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 7.2%; Score 82; DB 4; Length 89;

Best Local Similarity 28.9%; Pred. No. 5.5;  
 RESULT 1400  
 ID AAM65031 standard; protein; 89 AA.  
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 37136.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 7.2%; Score 82; DB 4; Length 89;  
 Best Local Similarity 28.9%; Pred. No. 5.5;  
 RESULT 1401  
 ID ABG59403 standard; peptide; 89 AA.  
 DE Human liver peptide, SEQ ID NO 38051.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 7.2%; Score 82; DB 4; Length 89;  
 Best Local Similarity 28.9%; Pred. No. 5.5;  
 RESULT 1402  
 ID ABG46774 standard; peptide; 89 AA.  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 36439.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 7.2%; Score 82; DB 5; Length 89;  
 Best Local Similarity 28.9%; Pred. No. 5.5;  
 RESULT 1403  
 ID ABG67754 standard; protein; 339 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 30054.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 7.2%; Score 82; DB 4; Length 339;  
 Best Local Similarity 25.4%; Pred. No. 33;  
 RESULT 1404  
 ID ADQ18080 standard; protein; 477 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 897.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 7.2%; Score 82; DB 8; Length 477;  
 Best Local Similarity 32.1%; Pred. No. 52;  
 RESULT 1405  
 ID ABG70759 standard; protein; 553 AA.  
 DE T. maritima endoglucanase protein.  
 PN US2002120118-A1.  
 PD 29-AUG-2002.  
 PA (SHOR/) SHORT J M.  
 PA (LAMD/) LAM D E.  
 PA (MATH/) MATHUR E J.  
 Query Match 7.2%; Score 82; DB 5; Length 553;  
 Best Local Similarity 28.2%; Pred. No. 63;  
 RESULT 1406  
 ID AAM34999 standard; protein; 628 AA.  
 DE Archaeobacterium AEP11a endoglucanase.  
 PN WO9744361-A1.  
 PD 27-NOV-1997.  
 PA (RECO-) RECOMBINANT BIOTECNOLOGY INC.  
 Query Match 7.2%; Score 82; DB 2; Length 628;  
 Best Local Similarity 28.2%; Pred. No. 75;  
 RESULT 1407  
 ID ADA55053 standard; protein; 637 AA.  
 DE Human protein, SEQ ID 2621.  
 PN EPI293569-A2.  
 PD 19-MAR-2003.  
 PA (HELIX-) RES ASSOC BIOTECHNOLOGY.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 7.2%; Score 82; DB 6; Length 637;  
 Best Local Similarity 24.2%; Pred. No. 76;  
 RESULT 1408  
 ID AAE29654 standard; protein; 667 AA.  
 DE Human membrane-associated protein HUMAP-11.  
 PN WO2000605054-A2.  
 PD 02-NOV-2000.

PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 7.2%; Score 82; DB 3; Length 667;  
 Best Local Similarity 24.2%; Pred. No. 81;  
 RESULT 1409  
 ID AAM34985 standard; protein; 841 AA.  
 DE Archaeobacterial thermostable endoglucanase.  
 PN WO9744361-A1.  
 PD 27-NOV-1997.  
 PA (RECO-) RECOMBINANT BIOTECNOLOGY INC.  
 Query Match 7.2%; Score 82; DB 2; Length 841;  
 Best Local Similarity 28.2%; Pred. No. 1.1e+02;  
 RESULT 1410  
 ID AAE22234 standard; protein; 995 AA.  
 DE Sequence encoded by ILTV gp60 gene.  
 PN WO9203554-A.  
 PD 05-MAR-1992.  
 PA (WEBS-) WEBSTER A PTY LTD.  
 Query Match 7.2%; Score 82; DB 2; Length 995;  
 Best Local Similarity 31.7%; Pred. No. 1.4e+02;  
 RESULT 1411  
 ID ADM47185 standard; protein; 1671 AA.  
 DE Neurexin III-alpha membrane-bound type I precursor like NOVX 3a protein.  
 PN WO2003083039-A2.  
 PD 09-OCT-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 7.2%; Score 82; DB 7; Length 1671;  
 Best Local Similarity 24.2%; Pred. No. 2.7e+02;  
 RESULT 1412  
 ID ABU23564 standard; protein; 386 AA.  
 DE Protein encoded by Prokaryotic essential gene #9091.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 7.2%; Score 81.5; DB 6; Length 386;  
 Best Local Similarity 22.0%; Pred. No. 44;  
 RESULT 1413  
 ID AEM87947 standard; protein; 525 AA.  
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:6193.  
 PN WO2003008540-A2.  
 PD 30-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 7.2%; Score 81.5; DB 7; Length 525;  
 Best Local Similarity 20.7%; Pred. No. 66;  
 RESULT 1414  
 ID ABO58564 standard; protein; 800 AA.  
 DE Human genome derived single exon protein #4798.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Query Match 7.2%; Score 81.5; DB 8; Length 800;  
 Best Local Similarity 35.8%; Pred. No. 1.2e+02;  
 RESULT 1415  
 ID ADX96680 standard; protein; 929 AA.  
 DE Plant full length insert polypeptide seqid 59344.  
 PN US2004034888-A1.  
 PD 19-FEB-2004.  
 PA (LIUJ/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABAJ/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 Query Match 7.2%; Score 81.5; DB 8; Length 929;  
 Best Local Similarity 27.9%; Pred. No. 1.4e+02;  
 RESULT 1416  
 ID AAY59288 standard; protein; 957 AA.  
 DE Human MUC11 polypeptide.  
 PN WO200004142-A1.  
 PD 27-JAN-2000.  
 PA (CCUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
 PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.

Query Match  
Best Local Similarity 7.2%; Score 81.5; DB 3; Length 957;  
RESULT 1417  
ID AAM24513 standard; protein; 957 AA.  
DE C900P predicted amino acid sequence.  
PN WO200149716-A2.  
PD 12-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.2%; Score 81.5; DB 4; Length 957;  
RESULT 1418  
ID ABP5362 standard; protein; 957 AA.  
DE Human colon tumour protein for clone C900P SEQ ID NO:1065.  
PN WO200283070-A2.  
PD 24-OCT-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.2%; Score 81.5; DB 6; Length 957;  
RESULT 1419  
ID AEA20406 standard; protein; 1004 AA.  
DE Novel human polypeptide SEQ ID NO 1100.  
PN WO2005049806-A2.  
PD 02-JUN-2005.  
PA (NUVE-) NUVELO INC.  
Query Match  
Best Local Similarity 7.2%; Score 81.5; DB 9; Length 1004;  
RESULT 1420  
ID AEA20405 standard; protein; 1032 AA.  
DE Novel human polypeptide SEQ ID NO 1099.  
PN WO2005049806-A2.  
PD 02-JUN-2005.  
PA (NUVE-) NUVELO INC.  
Query Match  
Best Local Similarity 7.2%; Score 81.5; DB 9; Length 1032;  
RESULT 1421  
ID ADC31682 standard; protein; 1205 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1764.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.2%; Score 81.5; DB 7; Length 1205;  
RESULT 1422  
ID ABB69973 standard; protein; 1354 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 36711.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 7.2%; Score 81.5; DB 4; Length 1354;  
RESULT 1423  
ID AAU50934 standard; protein; 176 AA.  
DE Propionibacterium acnes immunogenic protein #11830.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 4; Length 176;  
RESULT 1424  
ID ABM47453 standard; protein; 176 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12129.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 6; Length 176;  
RESULT 1425  
ID AAY93912 standard; protein; 289 AA.  
DE A human hyaluronan-binding protein, designated OB-HABP.  
PN WO200039166-A1.  
PD 06-JUL-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (AMNA-) AMERICAN NAT RED CROSS.

Query Match  
Best Local Similarity 7.1%; Score 81; DB 3; Length 289;  
RESULT 1426  
ID ABB64749 standard; protein; 294 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 21039.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 4; Length 294;  
RESULT 1427  
ID AAR60563 standard; protein; 862 AA.  
DE Yeast 2.6 kD agglutination gene FLO1S.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SAPB-) SAPPORO BREWERIES.  
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 2; Length 862;  
RESULT 1428  
ID AAR58754 standard; protein; 894 AA.  
DE S. cerevisiae FLO1.  
PN WO9418330-A1.  
PD 18-AUG-1994.  
PA (UNIL-) UNILEVER PLC.  
PA (UNIL-) UNILEVER NV.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 2; Length 894;  
RESULT 1429  
ID AAR47578 standard; protein; 894 AA.  
DE Flocculation protein of *Saccharomyces cerevisiae*.  
PN WO9401567-A1.  
PD 20-JAN-1994.  
PA (UNIL-) UNILEVER PLC.  
PA (UNIL-) UNILEVER NV.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 2; Length 894;  
RESULT 1430  
ID ADE58456 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4331.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1431  
ID ADE58468 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4343.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1432  
ID ADE58460 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4335.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1433  
ID ADE58464 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4339.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1434  
ID ADE58466 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4335.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1435  
ID ADE58468 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4339.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1436  
ID ADE58466 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4339.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1437  
ID ADE58468 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4339.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1438  
ID ADE58468 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4339.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1439  
ID ADE58468 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4339.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 7.1%; Score 81; DB 7; Length 1031;  
RESULT 1440  
ID ADE58468 standard; protein; 1031 AA.  
DE Rat Protein AAK52670, SEQ ID NO 4339.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.



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RESULT 1434
ID ADE58472 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4347.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.1%; Score 81; DB 7; Length 1031;
Best Local Similarity 20.9%; Pred. No. 1.8e+02;
RESULT 1435
ID ADE58476 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4351.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.1%; Score 81; DB 7; Length 1031;
Best Local Similarity 20.9%; Pred. No. 1.8e+02;
RESULT 1436
ID ADS44054 standard; protein; 1128 AA.
DE Bacterial polypeptide #22484.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 81; DB 8; Length 1128;
Best Local Similarity 22.8%; Pred. No. 2e+02;
RESULT 1437
ID AAR60562 standard; protein; 1537 AA.
DE Yeast 4.7 kD agglutination gene FLO1L.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB ) SAPPOPO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGERILABORATORIUM.
Query Match 7.1%; Score 81; DB 2; Length 1537;
Best Local Similarity 21.8%; Pred. No. 3.1e+02;
RESULT 1438
ID ADP87475 standard; protein; 1537 AA.
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN WO2004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 7.1%; Score 81; DB 8; Length 1537;
Best Local Similarity 21.8%; Pred. No. 3.1e+02;
RESULT 1439
ID ADN18745 standard; protein; 1537 AA.
DE Bacterial polypeptide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 81; DB 8; Length 1537;
Best Local Similarity 21.8%; Pred. No. 3.1e+02;
RESULT 1440
ID ADN18921 standard; protein; 1569 AA.
DE Human mucin glycoprotein, MUC6.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.1%; Score 81; DB 8; Length 1569;
Best Local Similarity 25.5%; Pred. No. 3.2e+02;
RESULT 1441
ID ADN18882 standard; protein; 1609 AA.
DE Bacterial polypeptide #1535.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 81; DB 8; Length 1609;
Best Local Similarity 22.4%; Pred. No. 3.3e+02;
RESULT 1442
ID ADN18914 standard; protein; 2240 AA.
DE Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.1%; Score 81; DB 8; Length 2240;
Best Local Similarity 25.5%; Pred. No. 5.1e+02;
RESULT 1443
ID ADR18913 standard; protein; 2258 AA.
DE Human mucin-like protein, SCS0004, variant SEQ ID 3.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.1%; Score 81; DB 8; Length 2258;
Best Local Similarity 25.5%; Pred. No. 5.2e+02;
RESULT 1444
ID ADR18915 standard; protein; 2264 AA.
DE His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.1%; Score 81; DB 8; Length 2264;
Best Local Similarity 25.5%; Pred. No. 5.2e+02;
RESULT 1445
ID AB869480 standard; protein; 2977 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35232.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 7.1%; Score 81; DB 4; Length 2977;
Best Local Similarity 18.8%; Pred. No. 7.5e+02;
RESULT 1446
ID ABP07042 standard; protein; 128 AA.
DE Human ORFX protein sequence SEQ ID NO:14066.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 7.1%; Score 80.5; DB 5; Length 128;
Best Local Similarity 33.8%; Pred. No. 13;
RESULT 1447
ID ADP46369 standard; protein; 148 AA.
DE Rat Protein CAA34901, SEQ ID NO 12049.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.1%; Score 80.5; DB 7; Length 148;
Best Local Similarity 23.5%; Pred. No. 15;
RESULT 1448
ID ABU26248 standard; protein; 323 AA.
DE Protein encoded by Prokaryotic essential gene #11775.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 80.5; DB 6; Length 323;
Best Local Similarity 27.1%; Pred. No. 43;
RESULT 1449
ID ABP28528 standard; protein; 540 AA.
DE Streptococcus polypeptide SEQ ID NO 6232.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.1%; Score 80.5; DB 5; Length 540;
Best Local Similarity 22.5%; Pred. No. 86;
RESULT 1450
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ID ADUG9670 standard; protein; 540 AA.  
DE S agalactiae hyperimmune serum reactive antigen seqid 365.  
PN WO200409242-A2.  
PD 18-NOV-2004.  
PA (INTE-) INTERCELL AG. 7.1%; Score 80.5; DB 8; Length 540;  
Query Match 22.5%; Pred. No. 86;  
Best Local Similarity 22.5%; Pred. No. 86;  
RESULT 1451  
ID ADV8602 standard; protein; 540 AA.  
DE Streptococcus agalactiae protein sequence, SEQ ID 996.  
PN FR2824074-A1.  
PD 31-OCT-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 7.1%; Score 80.5; DB 8; Length 540;  
Best Local Similarity 22.5%; Pred. No. 86;  
RESULT 1452  
ID ADV79855 standard; protein; 540 AA.  
DE Streptococcus agalactiae protein, SEQ ID 996.  
PN WO200292818-A2.  
PD 21-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 7.1%; Score 80.5; DB 8; Length 540;  
Best Local Similarity 22.5%; Pred. No. 86;  
RESULT 1453  
ID ADV82007 standard; protein; 540 AA.  
DE Streptococcus agalactiae protein, SEQ ID 3148.  
PN WO200292818-A2.  
PD 21-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 7.1%; Score 80.5; DB 8; Length 540;  
Best Local Similarity 22.5%; Pred. No. 86;  
RESULT 1454  
ID ABE57757 standard; protein; 1167 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 63.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 7.1%; Score 80.5; DB 4; Length 1167;  
Best Local Similarity 28.2%; Pred. No. 2.4e+02;  
RESULT 1455  
ID AAR77036 standard; protein; 52 AA.  
DE Human brain-enriched hyaluronan binding protein PTR1 domain.  
PN WO9527785-A1.  
PD 19-OCT-1995.  
PA (UYIA) UNIV YALE.  
Query Match 7.0%; Score 80; DB 2; Length 52;  
Best Local Similarity 35.0%; Pred. No. 4.2;  
RESULT 1456  
ID ABP63646 standard; protein; 89 AA.  
DE Human ORF16.  
PN US2002082206-A1.  
PD 27-JUN-2002.  
PA (LEAC) LEACH M D.  
PA (MEHR) MEHRABAN P.  
PA (CONL) CONLEY P B.  
PA (TOPP) TOPPER J N.  
PA (LAWD) LAW D.  
Query Match 7.0%; Score 80; DB 5; Length 89;  
Best Local Similarity 32.6%; Pred. No. 8.7;  
RESULT 1457  
ID ABO79758 standard; protein; 95 AA.  
DE Pseudomonas aeruginosa polypeptide #11933.  
PN US551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.0%; Score 80; DB 7; Length 95;  
Best Local Similarity 28.3%; Pred. No. 9.4;  
RESULT 1458  
ID ADX73466 standard; protein; 169 AA.  
DE Plant full length insert polypeptide seqid 42832.

PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ) LIU J.  
PA (ZHOU) ZHOU Y.  
PA (KOVA) KOVALIC D K.  
PA (SCRE) SCREEN S E.  
PA (TABA) TABASKA J E.  
PA (CAOY) CAO Y.  
Query Match 7.0%; Score 80; DB 8; Length 169;  
Best Local Similarity 23.2%; Pred. No. 20;  
RESULT 1459  
ID ADR09088 standard; protein; 272 AA.  
DE Human protein useful for treating neurological disease Seq 2594.  
PN EPI447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.0%; Score 80; DB 8; Length 272;  
Best Local Similarity 23.4%; Pred. No. 38;  
RESULT 1460  
ID ADF58702 standard; protein; 351 AA.  
DE Human polypeptide sequence SEQ ID NO:1110.  
PN WO2003080795-A2.  
PD 02-OCT-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 80; DB 7; Length 351;  
Best Local Similarity 23.4%; Pred. No. 54;  
RESULT 1461  
ID ADY08994 standard; protein; 365 AA.  
DE Plant full length insert polypeptide seqid 64809.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ) LIU J.  
PA (ZHOU) ZHOU Y.  
PA (KOVA) KOVALIC D K.  
PA (SCRE) SCREEN S E.  
PA (TABA) TABASKA J E.  
PA (CAOY) CAO Y.  
Query Match 7.0%; Score 80; DB 8; Length 365;  
Best Local Similarity 22.2%; Pred. No. 57;  
RESULT 1462  
ID ABB66171 standard; protein; 449 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 25305.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 7.0%; Score 80; DB 4; Length 449;  
Best Local Similarity 23.9%; Pred. No. 75;  
RESULT 1463  
ID AAY01077 standard; protein; 473 AA.  
DE H. insolens Cel6A fungal cellulase protien sequence.  
PN WO9901544-A1.  
PD 14-JAN-1999.  
PA (NOVO) NOVO-NORDISK AS.  
Query Match 7.0%; Score 80; DB 2; Length 473;  
Best Local Similarity 28.1%; Pred. No. 80;  
RESULT 1464  
ID ADY24635 standard; protein; 575 AA.  
DE Plant full length insert polypeptide seqid 72419.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ) LIU J.  
PA (ZHOU) ZHOU Y.  
PA (KOVA) KOVALIC D K.  
PA (SCRE) SCREEN S E.  
PA (TABA) TABASKA J E.  
PA (CAOY) CAO Y.  
Query Match 7.0%; Score 80; DB 8; Length 575;  
Best Local Similarity 18.8%; Pred. No. 1e+02;  
RESULT 1465  
ID ADN19351 standard; protein; 725 AA.  
DE Bacterial polypeptide #2004.  
PN US2003233675-A1.  
PD 18-DEC-2003.

PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.0%; Score 80; DB 8; Length 725;  
Best Local Similarity 27.2%; Pred. No. 1.4e+02;  
RESULT 1466  
ID ABU09610 standard; protein; 729 AA.  
DE Mouse retinoic acid-regulated nuclear matrix-associated protein.  
PN US200303485-A1.  
PD 02-JAN-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 7.0%; Score 80; DB 6; Length 729;  
Best Local Similarity 20.6%; Pred. No. 1.4e+02;  
RESULT 1467  
ID ABG23210 standard; protein; 791 AA.  
DE Novel human diagnostic protein #23201.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 80; DB 4; Length 791;  
Best Local Similarity 23.6%; Pred. No. 1.6e+02;  
RESULT 1468  
ID ADS12299 standard; protein; 791 AA.  
DE Human therapeutic contig protein - SEQ ID 2536.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 7.0%; Score 80; DB 8; Length 791;  
Best Local Similarity 23.6%; Pred. No. 1.6e+02;  
RESULT 1469  
ID AAG70752 standard; protein; 881 AA.  
DE S cerevisiae apoptosis associated protein YUL070C.  
PN WO200102550-A2.  
PD 11-JAN-2001.  
PA (JANC) JANSSEN PHARM NV.  
Query Match 7.0%; Score 80; DB 4; Length 881;  
Best Local Similarity 23.6%; Pred. No. 1.8e+02;  
RESULT 1470  
ID AEA08149 standard; protein; 4262 AA.  
DE Human mucin 17 (MUC17SEC) protein - SEQ ID 4.  
PN US2005100925-A1.  
PD 12-MAY-2005.  
PA (BATR/) BATRA S.  
PA (MONI/) MONIAUX N.  
Query Match 7.0%; Score 80; DB 9; Length 4262;  
Best Local Similarity 24.2%; Pred. No. 1.5e+03;  
RESULT 1471  
ID AEA08148 standard; protein; 4493 AA.  
DE Human mucin 17 protein - SEQ ID 3.  
PN US2005100925-A1.  
PD 12-MAY-2005.  
PA (BATR/) BATRA S.  
PA (MONI/) MONIAUX N.  
Query Match 7.0%; Score 80; DB 9; Length 4493;  
Best Local Similarity 24.2%; Pred. No. 1.6e+03;  
RESULT 1472  
ID ABU54861 standard; protein; 10431 AA.  
DE Human CA125 amino terminal extension.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 7.0%; Score 80; DB 6; Length 10431;  
Best Local Similarity 22.3%; Pred. No. 5e+03;  
RESULT 1473  
ID ADY53881 standard; protein; 114 AA.  
DE Candida albicans glycosylphosphatidylinositol-anchored protein- SEQ ID 1.  
PN WO2005021789-A1.  
PD 10-MAR-2005.  
PA (INSP) INST PASTEUR.  
Query Match 7.0%; Score 79.5; DB 9; Length 114;  
Best Local Similarity 28.0%; Pred. No. 13;

RESULT 1474  
ID ABU53162 standard; protein; 277 AA.  
DE Human testes-derived DKFZp385\_2a11 homologue #22.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 7.0%; Score 79.5; DB 4; Length 277;  
Best Local Similarity 29.4%; Pred. No. 44;  
RESULT 1475  
ID ABG01510 standard; protein; 320 AA.  
DE Novel human diagnostic protein #1501.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 79.5; DB 4; Length 320;  
Best Local Similarity 25.7%; Pred. No. 53;  
RESULT 1476  
ID ABO62076 standard; protein; 324 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8593.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.0%; Score 79.5; DB 7; Length 324;  
Best Local Similarity 21.3%; Pred. No. 54;  
RESULT 1477  
ID ABG07923 standard; protein; 366 AA.  
DE Novel human diagnostic protein #7914.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 79.5; DB 4; Length 366;  
Best Local Similarity 25.7%; Pred. No. 64;  
RESULT 1478  
ID ABB63033 standard; protein; 583 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15891.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 7.0%; Score 79.5; DB 4; Length 583;  
Best Local Similarity 23.5%; Pred. No. 1.2e+02;  
RESULT 1479  
ID AAU38948 standard; protein; 583 AA.  
DE Drosophila G-protein coupled receptor, GCPR #26.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 7.0%; Score 79.5; DB 4; Length 583;  
Best Local Similarity 23.5%; Pred. No. 1.2e+02;  
RESULT 1480  
ID ADC35826 standard; protein; 583 AA.  
DE Drosophila G-protein coupled receptor seq id 28.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 7.0%; Score 79.5; DB 7; Length 583;  
Best Local Similarity 23.5%; Pred. No. 1.2e+02;  
RESULT 1481  
ID ABU53155 standard; protein; 692 AA.  
DE Human testes-derived DKFZp385\_2a11 homologue #15.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 7.0%; Score 79.5; DB 4; Length 692;  
Best Local Similarity 29.4%; Pred. No. 1.5e+02;  
RESULT 1482  
ID ABB63128 standard; protein; 796 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16176.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 7.0%; Score 79.5; DB 4; Length 796;  
Best Local Similarity 26.3%; Pred. No. 1.8e+02;  
RESULT 1483

ID ABB49326 standard; protein; 860 AA.  
DE Listeria monocytogenes protein #2030.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 7.0%; Score 79.5; DB 5; Length 860;  
Best Local Similarity 20.3%; Pred. No. 2e+02;  
RESULT 1484  
ID ABB32996 standard; protein; 860 AA.  
DE Protein encoded by Prokaryotic essential gene #18523.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.0%; Score 79.5; DB 6; Length 860;  
Best Local Similarity 20.3%; Pred. No. 2e+02;  
RESULT 1485  
ID ABB71072 standard; protein; 875 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40008.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.0%; Score 79.5; DB 4; Length 875;  
Best Local Similarity 29.5%; Pred. No. 2e+02;  
RESULT 1486  
ID AAW00634 standard; protein; 985 AA.  
DE ILTV glycoprotein g60.  
PN WO9508622-A1.  
PD 30-MAR-1995.  
PA (SYTR ) SYNTRO CORP.  
Query Match 7.0%; Score 79.5; DB 2; Length 985;  
Best Local Similarity 30.9%; Pred. No. 2.4e+02;  
RESULT 1487  
ID AAW06786 standard; protein; 985 AA.  
DE ILTV glycoprotein g60.  
PN WO9628396-A1.  
PD 26-SEP-1996.  
PA (SYTR ) SYNTRO CORP.  
Query Match 7.0%; Score 79.5; DB 2; Length 985;  
Best Local Similarity 30.9%; Pred. No. 2.4e+02;  
RESULT 1488  
ID AAY41092 standard; protein; 1114 AA.  
DE Peptide Seq ID No: 34 of WO9945111.  
PN WO9945111-A1.  
PD 10-SEP-1999.  
PA (ICOS-) ICOS CORP.  
Query Match 7.0%; Score 79.5; DB 2; Length 1114;  
Best Local Similarity 20.8%; Pred. No. 2.8e+02;  
RESULT 1489  
ID AAB15730 standard; protein; 1114 AA.  
DE Protein encoded by cDNA generated from RACE3.3 and clone 3.3 sequences.  
PN WO200052039-A2.  
PD 08-SEP-2000.  
PA (ICOS-) ICOS CORP.  
Query Match 7.0%; Score 79.5; DB 3; Length 1114;  
Best Local Similarity 20.8%; Pred. No. 2.8e+02;  
RESULT 1490  
ID AAY41086 standard; protein; 1123 AA.  
DE Human lectomedin-lb beta polypeptide.  
PN WO9945111-A1.  
PD 10-SEP-1999.  
PA (ICOS-) ICOS CORP.  
Query Match 7.0%; Score 79.5; DB 2; Length 1123;  
Best Local Similarity 20.8%; Pred. No. 2.9e+02;  
RESULT 1491  
ID AAB15724 standard; protein; 1123 AA.  
DE Human lectomedin-lb beta.  
PN WO200052039-A2.  
PD 08-SEP-2000.  
PA (ICOS-) ICOS CORP.  
Query Match 7.0%; Score 79.5; DB 3; Length 1123;  
Best Local Similarity 20.8%; Pred. No. 2.9e+02;  
RESULT 1492  
ID AAY41085 standard; protein; 1177 AA.

DE Human lectomedin-lalpha.  
PN WO9945111-A1.  
PD 10-SEP-1999.  
PA (ICOS-) ICOS CORP.  
Query Match 7.0%; Score 79.5; DB 2; Length 1177;  
Best Local Similarity 20.8%; Pred. No. 3e+02;  
RESULT 1493  
ID AAB15723 standard; protein; 1177 AA.  
DE Human lectomedin-lalpha.  
PN WO200052039-A2.  
PD 08-SEP-2000.  
PA (ICOS-) ICOS CORP.  
Query Match 7.0%; Score 79.5; DB 3; Length 1177;  
Best Local Similarity 20.8%; Pred. No. 3e+02;  
RESULT 1494  
ID ADD46682 standard; protein; 1318 AA.  
DE Human Protein CAC19796, SEQ ID NO 12367.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.0%; Score 79.5; DB 7; Length 1318;  
Best Local Similarity 20.8%; Pred. No. 3.5e+02;  
RESULT 1495  
ID ADE55337 standard; protein; 1318 AA.  
DE Human Protein CAC19796, SEQ ID NO 1151.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.0%; Score 79.5; DB 7; Length 1318;  
Best Local Similarity 20.8%; Pred. No. 3.5e+02;  
RESULT 1496  
ID AAY41087 standard; protein; 1403 AA.  
DE Human lectomedin-Ig gamma polypeptide.  
PN WO9945111-A1.  
PD 10-SEP-1999.  
PA (ICOS-) ICOS CORP.  
Query Match 7.0%; Score 79.5; DB 2; Length 1403;  
Best Local Similarity 20.8%; Pred. No. 3.8e+02;  
RESULT 1497  
ID AAB15725 standard; protein; 1403 AA.  
DE Human lectomedin-Ig gamma CDNA.  
PN WO200052039-A2.  
PD 08-SEP-2000.  
PA (ICOS-) ICOS CORP.  
Query Match 7.0%; Score 79.5; DB 3; Length 1403;  
Best Local Similarity 20.8%; Pred. No. 3.8e+02;  
RESULT 1498  
ID ABP81675 standard; protein; 1403 AA.  
DE Human latrophilin-2 protein SEQ ID NO:526.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 7.0%; Score 79.5; DB 6; Length 1403;  
Best Local Similarity 20.8%; Pred. No. 3.8e+02;  
RESULT 1499  
ID ADD89067 standard; protein; 1403 AA.  
DE TAT254.  
PN WO2003057160-A2.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 79.5; DB 7; Length 1403;  
Best Local Similarity 20.8%; Pred. No. 3.8e+02;  
RESULT 1500  
ID ADN95548 standard; protein; 1403 AA.  
DE Human BEC/LSC-related protein sequence SeqID471.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 7.0%; Score 79.5; DB 7; Length 1403;  
Best Local Similarity 20.8%; Pred. No. 3.8e+02;



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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:13:31 ; Search time 37.3585 Seconds  
(without alignments)  
2460.550 Million cell updates/sec

Perfect score: 1136  
Sequence: 1 TTRLLVQGSRLRAEELSTQVS.....TEPFEVNEKAAFKNEAAAGFGG 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 15

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Database : Published Applications AA Main:
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6: /cgn2_6/ptodata/1/pubpaa/US11 PUBCOMB.pcp:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
3	1136	100.0	322	3	US-09-905-291A-201		Sequence 201, Appl
93	1136	100.0	322	4	US-10-223-085-32		Sequence 32, Appl
94	1136	100.0	322	4	US-10-223-084-32		Sequence 32, Appl
95	1136	100.0	322	4	US-10-223-088-32		Sequence 32, Appl
96	1136	100.0	322	4	US-10-223-090-32		Sequence 32, Appl
98	1136	100.0	322	4	US-10-223-087-32		Sequence 32, Appl
101	1136	100.0	322	4	US-10-223-083-32		Sequence 32, Appl
102	1136	100.0	322	4	US-10-079-111-1		Sequence 1, Appl
103	1136	100.0	322	4	US-10-223-089-32		Sequence 32, Appl
108	1136	100.0	322	4	US-10-299-976-201		Sequence 201, Appl
136	1136	100.0	322	4	US-10-063-742-6		Sequence 6, Appl
211	1136	100.0	322	4	US-10-299-937-201		Sequence 201, Appl
214	1136	100.0	322	4	US-10-223-081-32		Sequence 32, Appl
224	1136	100.0	322	4	US-10-223-082-32		Sequence 32, Appl
230	1136	100.0	322	4	US-10-298-993-201		Sequence 201, Appl
231	1136	100.0	322	4	US-10-305-654-32		Sequence 32, Appl
232	1136	100.0	322	4	US-10-448-923-201		Sequence 201, Appl
233	1136	100.0	322	4	US-10-449-656-201		Sequence 201, Appl
234	1136	100.0	322	4	US-10-448-713-201		Sequence 201, Appl
235	1136	100.0	322	4	US-10-425-447-201		Sequence 201, Appl
236	1136	100.0	322	4	US-10-081-056-32		Sequence 32, Appl
238	1136	100.0	322	4	US-10-215-371-201		Sequence 201, Appl
239	1136	100.0	322	4	US-10-797-366-201		Sequence 201, Appl
240	1136	100.0	322	4	US-10-771-187-201		Sequence 201, Appl
241	1136	100.0	322	5	US-10-972-317-6		Sequence 6, Appl
242	1136	100.0	322	5	US-10-963-467-201		Sequence 201, Appl
243	1136	100.0	322	5	US-10-978-255-201		Sequence 201, Appl
244	1136	100.0	322	5	US-10-820-474A-64		Sequence 64, Appl







1307	83.5	7.4	357	4	US-10-425-114-56835	Sequence 56835, A	1380	79.5	7.0	583	4	US-10-270-333-78	Sequence 78, Appl
1308	83.5	7.4	357	4	US-10-425-115-267262	Sequence 267262,	1381	79.5	7.0	583	6	US-11-097-143-15891	Sequence 15891, A
1309	83.5	7.4	393	3	US-09-846-590B-14	Sequence 14, Appl	1382	79.5	7.0	796	6	US-11-097-143-16176	Sequence 16176, A
1310	83.5	7.4	553	3	US-09-764-835-657	Sequence 657, App	1383	79.5	7.0	860	4	US-10-282-122A-60920	Sequence 60920, A
1311	83.5	7.4	591	4	US-10-437-963-161046	Sequence 161046,	1384	79.5	7.0	875	6	US-11-097-143-40008	Sequence 40008, A
1312	83.5	7.4	615	4	US-10-239-818-14	Sequence 14, Appl	1385	79.5	7.0	985	3	US-09-994-064-6	Sequence 6, Appl
1313	83.5	7.4	4123	4	US-10-213-509-5	Sequence 5, Appl	1386	79.5	7.0	985	3	US-09-994-064-66	Sequence 66, Appl
1314	83.5	7.4	4819	4	US-10-085-198-2	Sequence 2, Appl	1387	79.5	7.0	985	3	US-09-993-777-6	Sequence 6, Appl
1315	83.5	7.4	5179	3	US-09-922-217-1068	Sequence 1068, Ap	1388	79.5	7.0	985	3	US-09-993-777-66	Sequence 66, Appl
1316	83.5	7.4	5179	3	US-09-833-263-1068	Sequence 1068, Ap	1389	79.5	7.0	985	5	US-10-836-383-6	Sequence 66, Appl
1317	83.5	7.4	5179	4	US-10-025-380-1068	Sequence 1068, Ap	1390	79.5	7.0	985	5	US-10-836-383-66	Sequence 66, Appl
1318	83.5	7.4	5179	4	US-10-734-564-121	Sequence 121, App	1391	79.5	7.0	1216	4	US-10-437-963-148212	Sequence 148212,
1319	83	7.3	471	6	US-11-097-143-13147	Sequence 1247, A	1392	79.5	7.0	1403	4	US-10-225-567A-526	Sequence 526, App
1320	83	7.3	605	3	US-09-801-368-428	Sequence 428, App	1393	79.5	7.0	1403	4	US-10-331-496A-71	Sequence 71, Appl
1321	83	7.3	605	4	US-10-369-493-22016	Sequence 22016, A	1394	79.5	7.0	1441	5	US-10-732-923-1652	Sequence 1652, Ap
1322	82.5	7.3	463	4	US-10-425-114-66913	Sequence 66913, A	1395	79.5	7.0	1441	5	US-10-732-923-1653	Sequence 1653, Ap
1323	82.5	7.3	825	4	US-10-425-115-322413	Sequence 322413,	1396	79.5	7.0	1459	4	US-10-188-186-100	Sequence 100, App
1324	82.5	7.3	463	4	US-10-369-493-23501	Sequence 23501,	1397	79.5	7.0	1486	6	US-11-097-143-4767	Sequence 4767, Ap
1325	82.5	7.3	843	6	US-11-097-143-38828	Sequence 38828, A	1398	79	7.0	162	4	US-10-437-963-145598	Sequence 145598,
1326	82.5	7.3	1371	6	US-11-097-143-33825	Sequence 33825, A	1399	79	7.0	195	6	US-11-097-143-34818	Sequence 34818, A
1327	82.5	7.3	1714	6	US-11-097-143-7350	Sequence 7350, Ap	1400	79	7.0	323	4	US-10-425-114-59856	Sequence 59856, A
1328	82	7.2	89	3	US-09-864-761-42220	Sequence 42220, A	1401	79	7.0	352	3	US-09-934-455-118	Sequence 118, App
1329	82	7.2	339	6	US-11-097-143-30054	Sequence 30054, A	1402	79	7.0	352	4	US-10-278-173-110	Sequence 110, App
1330	82	7.2	477	5	US-10-723-860-897	Sequence 897, App	1403	79	7.0	352	4	US-10-225-066A-112	Sequence 112, App
1331	82	7.2	477	5	US-10-756-149-4935	Sequence 4935, Ap	1404	79	7.0	352	4	US-10-225-067-20	Sequence 20, Appl
1332	82	7.2	553	3	US-09-888-224-2	Sequence 2, Appl	1405	79	7.0	352	4	US-10-374-780A-2052	Sequence 2052, Ap
1333	82	7.2	637	4	US-10-094-749-2621	Sequence 749, Ap	1406	79	7.0	352	4	US-10-412-699B-450	Sequence 450, App
1334	82	7.2	1039	5	US-10-732-923-8770	Sequence 8770, Ap	1407	79	7.0	352	5	US-10-225-066A-112	Sequence 112, App
1335	82	7.2	1489	4	US-10-437-963-138442	Sequence 138442,	1408	79	7.0	425	4	US-10-435-115-227109	Sequence 227109,
1336	82	7.2	1671	4	US-10-187-975-18	Sequence 18, Appl	1409	79	7.0	629	6	US-11-097-143-5313	Sequence 5313, Ap
1337	81.5	7.2	186	4	US-10-437-963-186467	Sequence 186467,	1410	79	7.0	629	6	US-11-097-143-29106	Sequence 29106, A
1338	81.5	7.2	352	4	US-10-424-599-195846	Sequence 195846,	1411	79	7.0	820	4	US-10-437-963-155777	Sequence 155777,
1339	81.5	7.2	386	4	US-10-282-122A-51488	Sequence 51488, A	1412	79	7.0	1605	5	US-10-732-923-18432	Sequence 18432, A
1340	81.5	7.2	792	3	US-09-802-207-27	Sequence 27, Appl	1413	79	7.0	2156	5	US-10-732-923-18431	Sequence 18431, A
1341	81.5	7.2	800	4	US-10-029-386-32198	Sequence 32198, A	1414	79	7.0	2616	6	US-11-097-143-21459	Sequence 21459, A
1342	81.5	7.2	929	4	US-10-425-114-59344	Sequence 59344, A	1415	78.5	6.9	133	4	US-10-424-599-161524	Sequence 161524,
1343	81.5	7.2	957	3	US-09-922-217-1065	Sequence 1065, Ap	1416	78.5	6.9	252	5	US-10-868-381-36	Sequence 36, Appl
1344	81.5	7.2	957	3	US-09-833-263-1065	Sequence 1065, Ap	1417	78.5	6.9	569	4	US-10-108-260A-4361	Sequence 4361, Ap
1345	81.5	7.2	957	4	US-10-025-380-1065	Sequence 1065, Ap	1418	78.5	6.9	585	5	US-10-868-381-56	Sequence 56, Appl
1346	81.5	7.2	1354	6	US-11-097-143-36711	Sequence 36711, A	1419	78.5	6.9	585	5	US-10-868-381-57	Sequence 57, Appl
1347	81.5	7.2	1500	4	US-10-437-963-118360	Sequence 118360,	1420	78.5	6.9	586	5	US-10-635-211-2	Sequence 2, Appl
1348	81	7.1	260	4	US-10-460-513-3	Sequence 3, Appl	1421	78.5	6.9	590	3	US-09-957-187-12	Sequence 12, Appl
1349	81	7.1	260	5	US-10-897-911-3	Sequence 3, Appl	1422	78.5	6.9	590	6	US-11-058-709-12	Sequence 12, Appl
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	202	17.8	691	6	US-10-995-561-617
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12	196.5	17.3	535	6	US-10-995-561-610
13	196	17.3	361	6	US-10-995-561-612
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15	196	17.3	395	6	US-10-995-561-614
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21	119	10.5	457	6	US-10-986-501-110
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23	112	9.9	721	6	US-11-128-059-88
24	112	9.9	897	6	US-10-453-372-208
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273	66	758	7	US-11-087-099-251	Sequence 251, App	349	65	5.7	1992	7	US-11-013-759-13	Sequence 13, Appl
274	66	780	7	US-11-087-099-1109	Sequence 1109, A	350	65	5.7	2047	7	US-11-013-759-4	Sequence 4, Appli
275	66	823	7	US-11-087-099-11109	Sequence 323, App	351	65	5.7	2047	7	US-11-013-759-9	Sequence 9, Appli
276	66	1052	7	US-11-124-367A-323	Sequence 323, App	352	64.5	5.7	160	6	US-10-533-811-13	Sequence 13, Appl
277	66	1061	7	US-11-000-463-347	Sequence 347, App	353	64.5	5.7	223	7	US-11-087-099-7197	Sequence 7197, Ap
278	66	1061	7	US-11-124-367A-325	Sequence 325, App	354	64.5	5.7	250	7	US-11-096-568A-3195	Sequence 3195, Ap
279	66	1091	7	US-11-000-463-348	Sequence 348, App	355	64.5	5.7	367	7	US-11-072-512-2763	Sequence 2763, Ap
280	66	1122	7	US-11-191-374-3	Sequence 3, Appli	356	64.5	5.7	370	7	US-11-096-568A-3216	Sequence 3216, Ap
281	66	1122	7	US-11-191-375-3	Sequence 3, Appli	357	64.5	5.7	370	7	US-11-096-568A-3217	Sequence 3217, Ap
282	66	1122	7	US-11-191-588-3	Sequence 1622, Ap	358	64.5	5.7	371	6	US-10-467-657-1926	Sequence 1926, Ap
283	66	1338	6	US-10-821-234-1622	Sequence 23, Appl	359	64.5	5.7	378	7	US-11-087-099-8872	Sequence 8872, Ap
284	66	1338	7	US-11-109-156-23	Sequence 23, Appli	360	64.5	5.7	378	7	US-11-087-099-11183	Sequence 11183, A
285	66	1338	7	US-11-075-047A-2	Sequence 2, Appli	361	64.5	5.7	393	7	US-11-096-568A-3215	Sequence 3215, Ap
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287	66	1428	7	US-11-124-367A-320	Sequence 320, App	363	64.5	5.7	482	6	US-10-821-234-972	Sequence 972, App
288	66	2011	7	US-11-080-991-56	Sequence 56, Appl	364	64.5	5.7	519	7	US-11-087-099-5406	Sequence 5406, Ap
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290	65.5	175	7	US-11-087-099-6466	Sequence 6466, Ap	366	64.5	5.7	2910	7	US-11-087-084-2	Sequence 2, Appli
291	65.5	208	6	US-10-973-1158-510	Sequence 510, App	367	64.5	5.7	2910	7	US-11-087-085-2	Sequence 2, Appli
292	65.5	257	7	US-11-096-568A-25250	Sequence 25250, A	368	64	5.6	131	7	US-11-096-568A-12238	Sequence 12238, A
293	65.5	362	7	US-11-256-548-3	Sequence 3, Appli	369	64	5.6	145	7	US-11-152-601-43	Sequence 43, Appl
294	65.5	436	6	US-11-024-959-394	Sequence 394, App	370	64	5.6	187	7	US-11-096-568A-11277	Sequence 11277, A
295	65.5	445	6	US-10-467-657-5092	Sequence 5092, Ap	371	64	5.6	198	7	US-11-087-099-11173	Sequence 11173, A
296	65.5	472	7	US-11-165-211-7	Sequence 7, Appli	372	64	5.6	262	7	US-11-096-568A-11276	Sequence 11276, A
297	65.5	472	7	US-11-165-226-7	Sequence 7, Appli	373	64	5.6	263	7	US-11-096-568A-9712	Sequence 9712, Ap
298	65.5	485	7	US-11-096-568A-26552	Sequence 26552, A	374	64	5.6	266	7	US-11-096-568A-11275	Sequence 11275, A
299	65.5	541	7	US-11-201-916-17	Sequence 17, Appl	375	64	5.6	276	7	US-11-096-568A-30981	Sequence 30981, A
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301	65.5	618	7	US-11-087-099-6625	Sequence 6625, Ap	377	64	5.6	336	6	US-10-453-372-640	Sequence 640, App
302	65.5	644	7	US-11-087-099-11826	Sequence 11826, A	378	64	5.6	336	7	US-11-096-568A-30980	Sequence 30980, A
303	65.5	707	7	US-11-072-512-3162	Sequence 3162, Ap	379	64	5.6	346	7	US-11-096-568A-30979	Sequence 30979, A
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308	65.5	3100	6	US-11-235-732-7	Sequence 7, Appli	384	64	5.6	387	6	US-10-895-064-611	Sequence 611, App
309	65.5	3567	6	US-10-453-372-1112	Sequence 1112, Ap	385	64	5.6	387	7	US-11-123-741-611	Sequence 611, App
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312	65	235	7	US-11-159-597-2	Sequence 2, Appli	388	64	5.6	388	7	US-11-096-568A-27930	Sequence 27930, A
313	65	235	7	US-11-219-359-5	Sequence 5, Appli	389	64	5.6	389	7	US-11-096-568A-27929	Sequence 27929, A
314	65	244	7	US-11-052-554A-60	Sequence 60, Appli	390	64	5.6	446	7	US-11-087-099-8235	Sequence 8235, Ap
315	65	248	7	US-11-096-568A-13135	Sequence 13135, A	391	64	5.6	537	7	US-11-087-099-4695	Sequence 4695, Ap
316	65	253	7	US-11-096-568A-21716	Sequence 21716, A	392	64	5.6	619	6	US-10-999-886-3	Sequence 3, Appli
317	65	379	7	US-11-087-099-10889	Sequence 10889, A	393	64	5.6	640	6	US-11-098-686-4	Sequence 4, Appli
318	65	380	7	US-11-087-099-4525	Sequence 4525, Ap	394	64	5.6	648	7	US-11-098-686-10873	Sequence 10873, A
319	65	380	7	US-11-087-099-4810	Sequence 4810, Ap	395	64	5.6	756	6	US-10-055-877-138	Sequence 188, App
320	65	449	6	US-10-973-1158-224	Sequence 224, App	396	64	5.6	825	7	US-11-087-099-1341	Sequence 1341, Ap
321	65	509	7	US-11-008-727-16	Sequence 16, Appl	397	64	5.6	997	7	US-11-080-991-50	Sequence 50, Appl
322	65	512	7	US-11-108-172-1093	Sequence 1093, Ap	398	64	5.6				

398	64	5.6	999	7	US-11-113-424-36	Sequence 36, Appl	471	63	5.5	1966	6	US-10-480-330-22	Sequence 22, Appl
399	64	5.6	1078	7	US-11-096-568A-30451	Sequence 30451, A	472	63	5.5	1966	6	US-10-480-330-24	Sequence 24, Appl
400	64	5.6	1116	7	US-11-096-568A-30450	Sequence 30450, A	473	63	5.5	1966	6	US-10-480-330-26	Sequence 26, Appl
401	64	5.6	1123	7	US-11-096-568A-30449	Sequence 30449, A	474	63	5.5	1966	6	US-10-480-330-28	Sequence 28, Appl
402	64	5.6	1198	6	US-10-453-375-4	Sequence 4, Appl	475	63	5.5	2105	7	US-11-052-554A-173	Sequence 173, Appl
403	64	5.6	1445	7	US-11-169-041-181	Sequence 181, Appl	476	62.5	5.5	146	6	US-10-467-657-5594	Sequence 5594, Appl
404	64	5.6	1574	7	US-11-212-443-179	Sequence 179, Appl	477	62.5	5.5	158	7	US-11-096-568A-7142	Sequence 7142, Appl
405	64	5.6	1978	7	US-11-212-443-60	Sequence 60, Appl	478	62.5	5.5	298	7	US-11-080-091-9	Sequence 9, Appl
406	63.5	5.6	224	7	US-11-096-568A-7141	Sequence 7141, Appl	479	62.5	5.5	342	6	US-10-980-388-118	Sequence 118, Appl
407	63.5	5.6	256	7	US-11-096-568A-7140	Sequence 7140, Appl	480	62.5	5.5	342	7	US-11-174-816-18	Sequence 18, Appl
408	63.5	5.6	273	7	US-11-096-568A-22109	Sequence 22109, A	481	62.5	5.5	342	7	US-11-174-819-71	Sequence 71, Appl
409	63.5	5.6	304	7	US-11-080-091-10	Sequence 10, Appl	482	62.5	5.5	345	7	US-11-087-177-21	Sequence 21, Appl
410	63.5	5.6	335	7	US-11-087-099-4668	Sequence 4668, Appl	483	62.5	5.5	362	7	US-11-080-091-12	Sequence 12, Appl
411	63.5	5.6	343	7	US-11-080-091-4	Sequence 4, Appl	484	62.5	5.5	404	7	US-11-096-568A-28877	Sequence 28877, A
412	63.5	5.6	345	7	US-11-087-177-19	Sequence 19, Appl	485	62.5	5.5	432	7	US-11-124-367A-326	Sequence 326, A
413	63.5	5.6	358	7	US-11-096-568A-21943	Sequence 21943, A	486	62.5	5.5	442	7	US-11-102-621-136	Sequence 126, Appl
414	63.5	5.6	375	7	US-11-096-568A-21942	Sequence 21942, A	487	62.5	5.5	446	7	US-11-096-568A-28876	Sequence 28876, A
415	63.5	5.6	397	7	US-11-230-180-6	Sequence 6, Appl	488	62.5	5.5	489	7	US-11-096-568A-32213	Sequence 32213, A
416	63.5	5.6	446	7	US-11-102-621-138	Sequence 138, Appl	489	62.5	5.5	513	6	US-10-641-678-66	Sequence 67, Appl
417	63.5	5.6	458	7	US-11-096-568A-21941	Sequence 21941, A	490	62.5	5.5	514	6	US-10-641-678-66	Sequence 67, Appl
418	63.5	5.6	492	7	US-11-098-686-11360	Sequence 11360, A	491	62.5	5.5	539	7	US-11-096-568A-32212	Sequence 32212, A
419	63.5	5.6	541	6	US-11-201-916-14	Sequence 14, Appl	492	62.5	5.5	542	7	US-11-074-176-30	Sequence 30, Appl
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422	63.5	5.6	1009	6	US-10-912-971-16	Sequence 16, Appl	495	62.5	5.5	577	7	US-11-124-368A-232	Sequence 232, Appl
423	63.5	5.6	1053	6	US-10-517-939-52	Sequence 52, Appl	496	62.5	5.5	585	7	US-11-108-172-1067	Sequence 1067, Appl
424	63.5	5.6	1315	6	US-10-995-561-630	Sequence 630, Appl	497	62.5	5.5	915	7	US-11-156-084-119	Sequence 119, Appl
425	63.5	5.6	1392	7	US-11-069-834-58	Sequence 58, Appl	498	62.5	5.5	965	7	US-11-113-424-2	Sequence 2, Appl
426	63.5	5.6	2000	7	US-11-069-834-56	Sequence 56, Appl	499	62.5	5.5	1162	6	US-10-451-375-3	Sequence 3, Appl
427	63.5	5.6	2145	7	US-11-087-099-10331	Sequence 10331, A	500	62.5	5.5	1980	7	US-11-179-624-3	Sequence 3, Appl
428	63.5	5.6	2176	7	US-11-193-561-25	Sequence 25, Appl	501	62.5	5.5	2304	6	US-10-330-773-310	Sequence 310, Appl
429	63.5	5.6	2176	7	US-11-193-771-25	Sequence 25, Appl	502	62.5	5.5	2367	7	US-11-051-453-42	Sequence 42, Appl
430	63.5	5.6	2176	7	US-11-193-789-25	Sequence 25, Appl	503	62.5	5.5	2591	6	US-10-453-372-718	Sequence 718, Appl
431	63.5	5.6	2176	7	US-11-193-806-25	Sequence 25, Appl	504	62.5	5.5	2602	6	US-10-453-372-716	Sequence 716, Appl
432	63.5	5.6	2176	7	US-11-193-857-25	Sequence 25, Appl	505	62.5	5.5	2617	6	US-10-453-372-666	Sequence 666, Appl
433	63.5	5.6	2296	6	US-10-995-561-633	Sequence 633, Appl	506	62.5	5.5	2617	6	US-10-453-372-734	Sequence 734, Appl
434	63.5	5.6	2296	7	US-11-193-561-23	Sequence 23, Appl	507	62.5	5.5	2617	6	US-10-453-372-736	Sequence 736, Appl
435	63.5	5.6	2296	7	US-11-193-771-23	Sequence 23, Appl	508	62.5	5.5	2617	6	US-10-453-372-738	Sequence 738, Appl
436	63.5	5.6	2296	7	US-11-193-789-23	Sequence 23, Appl	509	62.5	5.5	2617	6	US-10-453-372-740	Sequence 740, Appl
437	63.5	5.6	2296	7	US-11-193-806-23	Sequence 23, Appl	510	62.5	5.5	2617	6	US-10-453-372-742	Sequence 742, Appl
438	63.5	5.6	2296	7	US-11-193-857-23	Sequence 23, Appl	511	62.5	5.5	2617	6	US-10-453-372-744	Sequence 744, Appl
439	63.5	5.6	3487	7	US-11-087-099-10423	Sequence 10423, A	512	62.5	5.5	2617	6	US-10-453-372-746	Sequence 746, Appl
440	63	5.5	163	7	US-11-096-568A-9622	Sequence 9622, Appl	513	62.5	5.5	2617	6	US-10-453-372-748	Sequence 748, Appl
441	63	5.5	173	7	US-11-096-568A-9621	Sequence 9621, Appl	514	62.5	5.5	2617	6	US-10-453-372-750	Sequence 750, Appl
442	63	5.5	176	7	US-11-096-568A-9620	Sequence 9620, Appl	515	62.5	5.5	2617	6	US-10-453-372-751	Sequence 751, Appl
443	63	5.5	192	7	US-11-072-512-3585	Sequence 3585, Appl	516	62.5	5.5	2871	7	US-11-169-041-131	Sequence 131, Appl
444	63	5.5	309	7	US-11-037-243-118	Sequence 118, Appl	517	62.5	5.5	3002	6	US-10-821-234-916	Sequence 916, Appl
445	63	5.5	336	7	US-11-087-099-11933	Sequence 11933, A	518	62.5	5.5	3011	6	US-10-985-205-3	Sequence 3, Appl
446	63	5.5	359	7	US-11-087-099-7177	Sequence 7177, Appl	519	62.5	5.5	3487	7	US-11-087-099-9068	Sequence 9068, Appl
447	63	5.5	362	7	US-11-087-099-7379	Sequence 7379, Appl	520	62	5.5	165	6	US-10-821-234-1539	Sequence 1539, Appl
448	63	5.5	363	7	US-11-087-099-9842	Sequence 9842, Appl	521	62	5.5	233	7	US-11-096-568A-18993	Sequence 18993, A
449	63	5.5	471	7	US-11-087-099-8817	Sequence 8817, Appl	522	62	5.5	291	7	US-11-096-568A-6790	Sequence 6790, Appl
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451	63	5.5	581	7	US-11-236-198-7	Sequence 7, Appl	524	62	5.5	341	7	US-11-240-769-72	Sequence 72, Appl
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453	63	5.5	610	7	US-11-096-568A-33959	Sequence 33959, A	526	62	5.5	341	7	US-11-151-868-2	Sequence 2, Appl
454	63	5.5	694	7	US-11-096-568A-29818	Sequence 29818, A	527	62	5.5	362	7	US-11-096-568A-25696	Sequence 25696, A
455	63	5.5	706	7	US-11-087-099-4237	Sequence 4237, Appl	528	62	5.5	370	7	US-11-096-568A-6789	Sequence 6789, Appl
456	63	5.5	717	7	US-11-096-568A-28799	Sequence 28799, A	529	62	5.5	379	7	US-11-087-099-8218	Sequence 8218, Appl
457	63	5.5	738	6	US-10-880-881-23	Sequence 23, Appl	530	62	5.5	395	7	US-11-096-568A-25695	Sequence 25695, A
458	63	5.5	902	7	US-11-182-016-36	Sequence 36, Appl	531	62	5.5	395	7	US-11-124-367A-322	Sequence 322, Appl
459	63	5.5	1083	7	US-11-113-751-40	Sequence 40, Appl	532	62	5.5	447	6	US-10-641-678-58	Sequence 58, Appl
460	63	5.5	1328	6	US-10-480-330-30	Sequence 30, Appl	533	62	5.5	489	7	US-11-264-728-4	Sequence 4, Appl
461	63	5.5	1965	6	US-10-480-330-4	Sequence 4, Appl	534	62	5.5	532	7	US-11-087-099-8860	Sequence 8860, Appl
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465	63	5.5	1966	6	US-10-480-330-10	Sequence 10, Appl	538	62	5.5	764	7	US-11-072-512-2379	Sequence 2379, Appl
466	63	5.5	1966	6	US-10-480-330-12	Sequence 12, Appl	539	62	5.5	871	7	US-11-087-099-6053	Sequence 6053, Appl
467	63	5.5	1966	6	US-10-480-330-14	Sequence 14, Appl	540	62	5.5	896	7	US-11-087-099-6053	Sequence 10311, A
468	63	5.5	1966	6	US-10-480-330-16	Sequence 16, Appl	541	62	5.5	925	7	US-11-024-959-518	Sequence 518, Appl
469	63	5.5	1966	6	US-10-480-330-18	Sequence 18, Appl	542	62	5.5	1001	6	US-10-330-773-510	Sequence 510, Appl
470	63	5.5	1966	6	US-10-480-330-20	Sequence 20, Appl	543	61.5	5.4	235	7	US-11-126-126-16	Sequence 16, Appl

544	61.5	5.4	239	7	US-11-096-568A-14888	Sequence 14888, A	617	61	5.4	1751	7	US-11-018-868-16	Sequence 16, Appl
545	61.5	5.4	240	7	US-11-096-568A-4927	Sequence 4927, Ap	618	61	5.4	2214	7	US-11-080-991-94	Sequence 94, Appl
546	61.5	5.4	246	7	US-11-096-568A-4926	Sequence 4926, Ap	619	60.5	5.3	53	7	US-11-096-568A-6179	Sequence 6179, Ap
547	61.5	5.4	251	7	US-11-096-568A-14887	Sequence 14887, A	620	60.5	5.3	101	7	US-11-096-568A-26972	Sequence 26972, A
548	61.5	5.4	296	7	US-11-196-475-22	Sequence 22, Appl	621	60.5	5.3	132	7	US-11-087-099-3992	Sequence 3992, Ap
549	61.5	5.4	340	6	US-10-501-035-354	Sequence 354, App	622	60.5	5.3	154	6	US-10-475-075-802	Sequence 802, App
550	61.5	5.4	342	7	US-11-008-570-45	Sequence 45, Appl	623	60.5	5.3	245	7	US-11-186-284-157	Sequence 167, App
551	61.5	5.4	370	7	US-11-096-568A-6444	Sequence 6444, Ap	624	60.5	5.3	261	7	US-11-096-568A-18389	Sequence 17990, A
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554	61.5	5.4	381	6	US-10-821-234-1342	Sequence 1342, Ap	627	60.5	5.3	279	7	US-11-096-568A-8112	Sequence 8112, Ap
555	61.5	5.4	393	7	US-11-196-475-114	Sequence 114, App	628	60.5	5.3	283	7	US-11-096-568A-8111	Sequence 8111, Ap
556	61.5	5.4	431	7	US-11-096-568A-6443	Sequence 6443, Ap	629	60.5	5.3	290	7	US-11-096-568A-18388	Sequence 18388, A
557	61.5	5.4	441	7	US-11-196-475-120	Sequence 120, App	630	60.5	5.3	342	7	US-11-096-568A-8110	Sequence 8110, Ap
558	61.5	5.4	454	7	US-11-196-475-116	Sequence 116, App	631	60.5	5.3	348	7	US-11-174-751-19	Sequence 19, Appl
559	61.5	5.4	455	7	US-11-096-568A-29406	Sequence 29406, A	632	60.5	5.3	343	6	US-10-793-626-1626	Sequence 1626, Ap
560	61.5	5.4	455	7	US-11-096-568A-29757	Sequence 29757, A	633	60.5	5.3	343	6	US-10-793-626-1626	Sequence 1626, Ap
561	61.5	5.4	459	7	US-11-096-568A-29405	Sequence 29405, A	634	60.5	5.3	343	6	US-10-793-626-1626	Sequence 1626, Ap
562	61.5	5.4	461	7	US-11-132-283-6	Sequence 6, Appl	635	60.5	5.3	444	7	US-11-004-590-232	Sequence 232, App
563	61.5	5.4	461	7	US-11-182-946-4	Sequence 4, Appl	636	60.5	5.3	473	7	US-11-096-568A-148	Sequence 148, App
564	61.5	5.4	468	7	US-11-096-568A-6442	Sequence 6442, Ap	637	60.5	5.3	476	7	US-11-024-959-385	Sequence 385, App
565	61.5	5.4	510	6	US-10-641-678-43	Sequence 43, Appl	638	60.5	5.3	477	7	US-11-024-959-385	Sequence 385, App
566	61.5	5.4	511	6	US-10-641-678-42	Sequence 42, Appl	639	60.5	5.3	510	7	US-11-096-568A-147	Sequence 147, App
567	61.5	5.4	540	6	US-10-641-678-44	Sequence 44, Appl	640	60.5	5.3	511	7	US-11-096-568A-146	Sequence 146, App
568	61.5	5.4	549	7	US-11-096-568A-33577	Sequence 33577, A	641	60.5	5.3	524	7	US-11-087-099-12268	Sequence 12268, A
569	61.5	5.4	588	7	US-11-196-475-122	Sequence 122, App	642	60.5	5.3	545	7	US-11-201-916-34	Sequence 34, Appl
570	61.5	5.4	731	7	US-11-098-686-10415	Sequence 10415, A	643	60.5	5.3	545	7	US-11-201-916-34	Sequence 34, Appl
571	61.5	5.4	2015	7	US-11-052-554A-374	Sequence 374, App	644	60.5	5.3	858	6	US-10-995-561-852	Sequence 852, App
572	61	5.4	149	7	US-11-096-568A-7117	Sequence 7117, Ap	645	60.5	5.3	862	7	US-11-051-720-1443	Sequence 854, App
573	61	5.4	154	7	US-11-096-568A-11923	Sequence 11923, A	646	60.5	5.3	964	7	US-11-137-465-58	Sequence 1443, Ap
574	61	5.4	202	7	US-11-096-568A-7116	Sequence 7116, Ap	647	60.5	5.3	965	7	US-11-147-047-51	Sequence 58, Appl
575	61	5.4	244	7	US-11-096-568A-9713	Sequence 9713, Ap	648	60.5	5.3	1007	7	US-11-051-720-1445	Sequence 51, Appl
576	61	5.4	246	7	US-11-052-554A-50	Sequence 50, Appl	649	60.5	5.3	1120	7	US-11-051-720-1733	Sequence 1733, Ap
577	61	5.4	265	7	US-11-087-099-5324	Sequence 5324, Ap	650	60.5	5.3	1137	6	US-10-995-561-851	Sequence 70, Appl
578	61	5.4	273	7	US-11-087-099-2523	Sequence 2523, Ap	651	60.5	5.3	1178	6	US-10-995-561-851	Sequence 851, App
579	61	5.4	288	7	US-11-052-554A-353	Sequence 353, App	652	60.5	5.3	1263	6	US-10-485-517-127	Sequence 127, App
580	61	5.4	293	7	US-11-096-568A-15588	Sequence 15588, A	653	60.5	5.3	1305	7	US-11-051-720-1370	Sequence 1370, Ap
581	61	5.4	295	7	US-11-096-568A-30519	Sequence 30519, A	654	60.5	5.3	1337	7	US-11-112-304A-33	Sequence 33, Appl
582	61	5.4	297	7	US-11-096-568A-15587	Sequence 15587, A	655	60.5	5.3	1637	6	US-10-821-234-1204	Sequence 1204, Ap
583	61	5.4	315	7	US-11-096-568A-21620	Sequence 21620, A	656	60.5	5.3	1995	7	US-11-069-834-60	Sequence 60, Appl
584	61	5.4	317	6	US-10-674-767-2	Sequence 2, Appl	657	60.5	5.3	2244	7	US-11-131-263-9	Sequence 9, Appl
585	61	5.4	329	7	US-11-096-568A-30518	Sequence 30518, A	658	60.5	5.3	2244	7	US-11-131-263-18	Sequence 18, Appl
586	61	5.4	330	7	US-11-096-568A-21618	Sequence 21618, A	659	60.5	5.3	2244	7	US-11-131-263-30	Sequence 30, Appl
587	61	5.4	336	7	US-11-096-568A-15586	Sequence 15586, A	660	60.5	5.3	2314	7	US-11-013-759-11	Sequence 11, Appl
588	61	5.4	332	7	US-11-124-367A-265	Sequence 265, App	661	60	5.3	5291	7	US-11-052-554A-281	Sequence 281, App
589	61	5.4	352	7	US-11-124-367A-265	Sequence 267, App	662	60	5.3	1109	6	US-10-517-696-115	Sequence 115, App
590	61	5.4	379	7	US-11-087-099-1412	Sequence 1412, Ap	663	60	5.3	112	7	US-11-096-568A-7599	Sequence 7599, Ap
591	61	5.4	379	7	US-11-087-099-5014	Sequence 5014, Ap	664	60	5.3	142	7	US-11-186-284-105	Sequence 105, App
592	61	5.4	380	7	US-11-087-099-5011	Sequence 5011, Ap	665	60	5.3	150	6	US-10-467-657-2040	Sequence 2040, Ap
593	61	5.4	424	7	US-11-024-959-8556	Sequence 8556, Ap	666	60	5.3	195	7	US-11-096-568A-21216	Sequence 21216, A
594	61	5.4	424	7	US-11-024-959-499	Sequence 499, App	667	60	5.3	246	7	US-11-073-226-1	Sequence 1, Appl
595	61	5.4	472	7	US-11-165-211-6	Sequence 6, Appl	668	60	5.3	264	7	US-11-087-099-772	Sequence 772, App
596	61	5.4	472	7	US-11-165-226-6	Sequence 6, Appl	669	60	5.3	289	7	US-11-087-099-8567	Sequence 8567, Ap
597	61	5.4	473	7	US-11-096-568A-21002	Sequence 21002, A	670	60	5.3	305	7	US-11-087-099-2861	Sequence 2861, Ap
598	61	5.4	474	7	US-11-096-568A-21001	Sequence 21001, A	671	60	5.3	316	6	US-10-517-696-126	Sequence 126, App
599	61	5.4	523	7	US-11-087-099-6081	Sequence 6081, Ap	672	60	5.3	324	7	US-11-087-099-4866	Sequence 4866, Ap
600	61	5.4	557	7	US-11-096-568A-21000	Sequence 21000, A	673	60	5.3	324	7	US-11-087-099-8018	Sequence 8018, Ap
601	61	5.4	560	7	US-11-018-868-40	Sequence 40, Appl	674	60	5.3	324	7	US-11-087-099-9180	Sequence 9180, Ap
602	61	5.4	569	7	US-11-096-568A-30517	Sequence 30517, A	675	60	5.3	325	6	US-11-087-099-11267	Sequence 11267, A
603	61	5.4	600	7	US-11-072-512-3397	Sequence 3397, Ap	676	60	5.3	330	7	US-10-517-696-148	Sequence 148, App
604	61	5.4	645	7	US-11-072-512-3418	Sequence 3418, Ap	677	60	5.3	336	6	US-10-517-696-153	Sequence 153, App
605	61	5.4	665	7	US-11-124-368A-289	Sequence 289, App	678	60	5.3	339	7	US-11-087-099-6189	Sequence 6189, Ap
606	61	5.4	685	7	US-11-072-512-2916	Sequence 2916, Ap	679	60	5.3	342	7	US-11-087-099-10231	Sequence 10231, A
607	61	5.4	713	6	US-10-330-773-668	Sequence 668, App	680	60	5.3	348	7	US-11-087-099-7041	Sequence 7041, Ap
608	61	5.4	843	7	US-11-129-104-89	Sequence 89, Appl	681	60	5.3	350	6	US-10-517-696-125	Sequence 125, App
609	61	5.4	897	7	US-11-137-465-35	Sequence 35, Appl	682	60	5.3	361	7	US-11-087-099-2191	Sequence 2191, Ap
610	61	5.4	899	7	US-11-124-368A-290	Sequence 290, App	683	60	5.3	361	6	US-10-517-696-129	Sequence 129, App
611	61	5.4	980	6	US-10-330-773-507	Sequence 507, App	684	60	5.3	372	6	US-10-517-696-150	Sequence 150, App
612	61	5.4	1071	6	US-10-467-657-1654	Sequence 1654, Ap	685	60	5.3	379	6	US-11-087-099-8485	Sequence 8485, Ap
613	61	5.4	1439	7	US-11-124-368A-291	Sequence 291, App	686	60	5.3	379	7	US-11-087-099-11680	Sequence 11680, A
614	61	5.4	1493	7	US-11-183-136-26	Sequence 26, Appl	687	60	5.3	380	7	US-11-087-099-6231	Sequence 6231, Ap
615	61	5.4	1613	7	US-11-108-528-84	Sequence 84, Appl	688	60	5.3	380	7	US-11-087-099-8371	Sequence 8371, Ap
616	61	5.4	1751	7	US-11-103-957-45	Sequence 45, Appl	689	60	5.3	388	7	US-11-072-512-3454	Sequence 3454, Ap



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691	60	5.3	396	6	US-10-517-696-147	Sequence 147, App	764	59.5	5.2	481	7	US-11-031-206-76	Sequence 76, Appl
692	60	5.3	398	6	US-10-517-696-136	Sequence 136, App	765	59.5	5.2	487	7	US-11-096-568A-22133	Sequence 22133, A
693	60	5.3	409	6	US-10-517-696-149	Sequence 149, App	766	59.5	5.2	519	7	US-11-096-568A-22132	Sequence 22132, A
694	60	5.3	412	6	US-11-096-568A-21231	Sequence 21231, A	767	59.5	5.2	534	7	US-11-055-822-268	Sequence 268, App
695	60	5.3	420	6	US-10-517-696-141	Sequence 141, App	768	59.5	5.2	553	7	US-11-055-822-266	Sequence 266, App
696	60	5.3	431	6	US-10-821-234-1285	Sequence 1285, Ap	769	59.5	5.2	575	7	US-11-096-568A-27577	Sequence 27577, A
697	60	5.3	435	6	US-11-072-512-3499	Sequence 3499, Ap	770	59.5	5.2	583	7	US-11-024-959-268	Sequence 268, App
698	60	5.3	450	7	US-11-177-648-27	Sequence 27, Appl	771	59.5	5.2	625	7	US-11-072-512-3210	Sequence 3210, Ap
699	60	5.3	462	7	US-11-177-648-92	Sequence 92, Appl	772	59.5	5.2	690	7	US-11-098-686-10811	Sequence 10811, A
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701	60	5.3	462	7	US-11-177-648-94	Sequence 94, Appl	774	59.5	5.2	722	6	US-11-098-686-10811	Sequence 6, Appl
702	60	5.3	462	7	US-11-177-648-95	Sequence 95, Appl	775	59.5	5.2	726	7	US-11-096-568A-2446	Sequence 2446, Ap
703	60	5.3	463	6	US-10-517-696-121	Sequence 121, App	776	59.5	5.2	727	7	US-11-096-568A-2445	Sequence 2445, Ap
704	60	5.3	475	6	US-10-501-035-309	Sequence 309, App	777	59.5	5.2	816	7	US-11-143-980-67	Sequence 67, Appl
705	60	5.3	475	6	US-10-517-696-117	Sequence 117, App	778	59.5	5.2	836	7	US-11-096-568A-2444	Sequence 2444, Ap
706	60	5.3	483	6	US-10-517-696-132	Sequence 132, App	779	59.5	5.2	874	7	US-11-087-099-10263	Sequence 10263, A
707	60	5.3	484	6	US-10-517-696-130	Sequence 130, App	780	59.5	5.2	1075	7	US-11-100-640-12	Sequence 12, Appl
708	60	5.3	485	6	US-10-517-696-142	Sequence 142, App	781	59.5	5.2	1230	7	US-11-087-099-8922	Sequence 8922, Ap
709	60	5.3	491	7	US-11-072-512-3243	Sequence 3243, Ap	782	59.5	5.2	1230	7	US-11-087-099-8922	Sequence 2, Appl
710	60	5.3	492	6	US-10-517-696-111	Sequence 131, App	783	59.5	5.2	1402	6	US-10-971-982-2	Sequence 340, App
711	60	5.3	517	6	US-10-517-696-144	Sequence 144, App	784	59.5	5.2	1678	7	US-11-124-367A-340	Sequence 341, App
712	60	5.3	524	6	US-10-517-696-132	Sequence 128, App	785	59.5	5.2	1678	7	US-11-124-367A-341	Sequence 1641, Ap
713	60	5.3	533	7	US-11-147-047-33	Sequence 33, Appl	786	59.5	5.2	1970	6	US-10-821-234-1641	Sequence 305, App
714	60	5.3	548	7	US-11-052-554A-324	Sequence 324, App	787	59.5	5.2	2801	7	US-11-124-368A-305	Sequence 433, App
715	60	5.3	611	6	US-10-517-939-156	Sequence 156, App	788	59.5	5.2	2801	7	US-11-124-367A-433	Sequence 306, App
716	60	5.3	614	6	US-10-517-696-128	Sequence 128, App	789	59.5	5.2	2896	7	US-11-124-368A-306	Sequence 434, App
717	60	5.3	728	6	US-10-530-340-14	Sequence 14, Appl	790	59.5	5.2	2896	7	US-11-124-367A-434	Sequence 304, App
718	60	5.3	755	6	US-11-037-243-82	Sequence 82, Appl	791	59.5	5.2	3256	7	US-11-124-368A-304	Sequence 432, App
719	60	5.3	756	6	US-10-055-877-34	Sequence 34, Appl	792	59.5	5.2	3256	7	US-11-124-367A-432	Sequence 9005, Ap
720	60	5.3	756	6	US-10-055-877-187	Sequence 187, App	793	59.5	5.2	3488	7	US-11-087-099-9005	Sequence 20920, A
721	60	5.3	756	6	US-10-055-877-189	Sequence 189, App	794	59	5.2	126	7	US-11-096-568A-20920	Sequence 20919, A
722	60	5.3	761	6	US-10-485-517-282	Sequence 257, App	795	59	5.2	130	7	US-11-096-568A-20919	Sequence 2471, Ap
723	60	5.3	771	7	US-11-147-047-34	Sequence 34, Appl	796	59	5.2	132	7	US-11-072-512-2471	Sequence 1418, Ap
724	60	5.3	813	7	US-11-096-568A-31851	Sequence 31851, A	797	59	5.2	135	7	US-11-096-568A-1418	Sequence 1417, Ap
725	60	5.3	830	6	US-10-055-877-32	Sequence 32, Appl	798	59	5.2	208	7	US-11-128-440-6	Sequence 6, Appl
726	60	5.3	851	7	US-11-096-568A-31850	Sequence 31850, A	799	59	5.2	214	7	US-11-096-568A-1416	Sequence 1416, App
727	60	5.3	902	7	US-11-096-568A-31849	Sequence 31849, A	800	59	5.2	217	7	US-11-186-284-165	Sequence 165, App
728	60	5.3	1000	7	US-11-098-686-10907	Sequence 10907, A	801	59	5.2	220	7	US-11-096-568A-21946	Sequence 21946, A
729	60	5.3	1103	7	US-11-096-568A-27585	Sequence 27585, A	802	59	5.2	264	7	US-11-096-568A-8571	Sequence 8571, Ap
730	60	5.3	1143	7	US-11-096-568A-27584	Sequence 27584, A	803	59	5.2	265	7	US-11-096-568A-8570	Sequence 8570, Ap
731	60	5.3	1615	6	US-10-055-877-145	Sequence 145, App	804	59	5.2	270	7	US-11-008-727-24	Sequence 24, Appl
732	60	5.3	1613	7	US-11-108-528-86	Sequence 86, Appl	805	59	5.2	281	7	US-11-087-177-3	Sequence 3, Appl
733	60	5.3	1637	6	US-10-055-877-144	Sequence 144, App	806	59	5.2	284	7	US-11-096-568A-20740	Sequence 20740, A
734	60	5.3	1694	7	US-11-052-554A-83	Sequence 83, Appl	807	59	5.2	290	7	US-11-087-099-4115	Sequence 4115, Ap
735	60	5.3	16990	7	US-11-175-689-7	Sequence 7, Appl	808	59	5.2	292	6	US-10-770-726-53	Sequence 53, Appl
736	59.5	5.2	152	7	US-11-096-568A-7426	Sequence 7426, Ap	809	59	5.2	307	7	US-11-096-568A-28007	Sequence 28007, A
737	59.5	5.2	162	7	US-11-096-568A-7425	Sequence 7425, Ap	810	59	5.2	314	7	US-11-096-568A-20739	Sequence 20739, A
738	59.5	5.2	180	7	US-11-096-568A-7424	Sequence 7424, Ap	811	59	5.2	322	7	US-11-087-099-8944	Sequence 8944, Ap
739	59.5	5.2	181	7	US-11-087-099-9675	Sequence 9675, Ap	812	59	5.2	322	7	US-11-087-099-6769	Sequence 6769, Ap
740	59.5	5.2	181	7	US-11-096-568A-12137	Sequence 12137, A	813	59	5.2	332	6	US-10-467-657-3868	Sequence 3868, Ap
741	59.5	5.2	188	7	US-11-087-099-9413	Sequence 9413, Ap	814	59	5.2	332	6	US-10-467-657-7154	Sequence 7154, Ap
742	59.5	5.2	236	7	US-11-096-568A-22845	Sequence 22845, A	815	59	5.2	332	6	US-11-096-568A-26084	Sequence 26084, A
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745	59.5	5.2	298	7	US-11-096-568A-35290	Sequence 35290, A	818	59	5.2	357	7	US-11-087-099-11841	Sequence 7, Appl
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748	59.5	5.2	312	6	US-10-986-501-124	Sequence 124, App	821	59	5.2	363	7	US-11-087-099-2464	Sequence 4705, Ap
749	59.5	5.2	313	6	US-10-485-517-123	Sequence 123, App	822	59	5.2	369	7	US-11-087-099-4705	Sequence 1251, Ap
750	59.5	5.2	313	6	US-10-485-517-293	Sequence 293, App	823	59	5.2	379	7	US-11-087-099-1251	Sequence 7723, Ap
751	59.5	5.2	316	7	US-11-152-811-4	Sequence 4, Appl	824	59	5.2	379	7	US-11-087-099-7723	Sequence 10588, A
752	59.5	5.2	316	7	US-11-072-512-2455	Sequence 2455, Ap	825	59	5.2	380	7	US-11-087-099-10588	Sequence 369, App
753	59.5	5.2	317	7	US-11-096-568A-12521	Sequence 12521, A	826	59	5.2	384	7	US-11-052-554A-369	Sequence 33509, A
754	59.5	5.2	335	7	US-11-087-099-1878	Sequence 1878, Ap	827	59	5.2	388	7	US-11-096-568A-33508	Sequence 33508, A
755	59.5	5.2	342	7	US-11-008-570-47	Sequence 47, Appl	828	59	5.2	396	7	US-11-096-568A-33507	Sequence 33507, A
756	59.5	5.2	347	6	US-10-821-234-1379	Sequence 1379, Ap	829	59	5.2	405	7	US-11-096-568A-28005	Sequence 28005, A
757	59.5	5.2	375	7	US-11-087-099-7023	Sequence 7023, Ap	830	59	5.2	433	7	US-11-196-475-180	Sequence 180, App
758	59.5	5.2	462	7	US-11-072-512-2209	Sequence 2209, Ap	831	59	5.2	440	7	US-11-196-475-178	Sequence 178, App
759	59.5	5.2	462	7	US-11-096-568A-30639	Sequence 30639, A	832	59	5.2	452	6	US-10-641-678-50	Sequence 50, Appl
760	59.5	5.2	476	7	US-11-055-822-540	Sequence 540, App	833	59	5.2	461	7	US-11-183-205-32	Sequence 32, Appl
761	59.5	5.2	476	7	US-11-055-822-542	Sequence 542, App	834	59	5.2	462	7	US-11-177-648-96	Sequence 96, Appl
762	59.5	5.2	476	7	US-11-055-822-1122	Sequence 1122, Ap	835	59	5.2				

836	59	5.2	492	6	US-10-501-035-359	Sequence 359, App	909	58.5	5.1	810	6	US-10-453-372-1116	Sequence 1116, App
837	59	5.2	494	6	US-10-793-626-36	Sequence 36, App	910	58.5	5.1	820	6	US-10-491-468-14	Sequence 14, App
838	59	5.2	499	7	US-11-096-568A-32028	Sequence 32028, A	911	58.5	5.1	820	7	US-11-165-819-1	Sequence 1, App
839	59	5.2	515	6	US-10-517-696-1114	Sequence 114, App	912	58.5	5.1	821	7	US-11-096-568A-30426	Sequence 30426, A
840	59	5.2	524	6	US-10-517-696-1113	Sequence 113, App	913	58.5	5.1	825	7	US-11-096-568A-29626	Sequence 29626, A
841	59	5.2	525	7	US-11-098-686-10993	Sequence 10993, A	914	58.5	5.1	895	7	US-11-124-367A-313	Sequence 313, App
842	59	5.2	531	7	US-11-008-727-18	Sequence 18, App	915	58.5	5.1	941	7	US-11-124-367A-315	Sequence 315, App
843	59	5.2	533	7	US-11-072-512-3224	Sequence 3224, App	916	58.5	5.1	941	7	US-11-124-367A-315	Sequence 109, App
844	59	5.2	564	7	US-11-151-601-25	Sequence 25, App	917	58.5	5.1	1236	6	US-10-873-528-109	Sequence 626, App
845	59	5.2	564	7	US-11-186-284-139	Sequence 199, App	918	58.5	5.1	1498	6	US-10-501-035-226	Sequence 22, App
846	59	5.2	576	6	US-10-530-340-12	Sequence 12, App	919	58.5	5.1	1532	7	US-11-212-443-62	Sequence 42, App
847	59	5.2	579	7	US-11-072-512-2360	Sequence 2360, App	920	58.5	5.1	2059	7	US-11-087-100-4	Sequence 4, App
848	59	5.2	586	7	US-11-054-281-93	Sequence 93, App	921	58.5	5.1	2059	7	US-11-087-084-4	Sequence 4, App
849	59	5.2	592	7	US-11-087-099-912	Sequence 912, App	922	58.5	5.1	2059	7	US-11-087-085-4	Sequence 4, App
850	59	5.2	626	7	US-11-072-512-2827	Sequence 2827, App	923	58	5.1	3623	6	US-10-995-561-593	Sequence 593, App
851	59	5.2	663	7	US-11-087-099-3211	Sequence 3211, App	924	58	5.1	121	7	US-11-096-568A-20921	Sequence 20921, A
852	59	5.2	681	7	US-11-096-568A-2501	Sequence 2501, App	925	58	5.1	132	7	US-11-100-338-51	Sequence 51, App
853	59	5.2	696	7	US-11-256-548-23	Sequence 23, App	926	58	5.1	187	7	US-11-096-568A-32157	Sequence 32157, A
854	59	5.2	703	7	US-11-063-695-4	Sequence 4, App	927	58	5.1	246	6	US-10-467-657-2424	Sequence 2424, App
855	59	5.2	720	7	US-11-256-548-6	Sequence 6, App	928	58	5.1	251	7	US-11-096-568A-18174	Sequence 18174, A
856	59	5.2	728	7	US-11-087-099-9526	Sequence 9526, App	929	58	5.1	261	7	US-11-087-099-8985	Sequence 8985, App
857	59	5.2	735	7	US-11-087-099-8719	Sequence 8719, App	930	58	5.1	292	6	US-10-858-730-18	Sequence 18, App
858	59	5.2	856	6	US-10-510-947-8	Sequence 8, App	931	58	5.1	327	6	US-10-055-877-183	Sequence 35, App
859	59	5.2	856	7	US-11-042-988-13	Sequence 13, App	932	58	5.1	339	6	US-10-498-026-35	Sequence 36, App
860	59	5.2	856	7	US-11-135-235-1	Sequence 1, App	933	58	5.1	345	7	US-11-072-512-3496	Sequence 3496, App
861	59	5.2	932	7	US-11-188-743-18	Sequence 17, App	934	58	5.1	352	7	US-11-087-099-5875	Sequence 5875, App
862	59	5.2	932	7	US-11-188-743-18	Sequence 18, App	935	58	5.1	361	7	US-11-087-099-4996	Sequence 4996, App
863	59	5.2	932	7	US-11-183-294-18	Sequence 18, App	936	58	5.1	364	6	US-10-481-935A-201	Sequence 201, App
864	59	5.2	1121	7	US-11-087-099-10482	Sequence 10482, A	937	58	5.1	375	7	US-11-096-568A-23618	Sequence 23618, A
865	59	5.2	1203	7	US-11-096-568A-33183	Sequence 33183, A	938	58	5.1	379	7	US-11-087-099-3007	Sequence 3007, App
866	59	5.2	1344	7	US-11-072-512-2452	Sequence 2452, App	939	58	5.1	379	7	US-11-087-099-3480	Sequence 3480, App
867	59	5.2	1372	7	US-11-096-568A-33182	Sequence 33182, A	940	58	5.1	379	7	US-11-087-099-4624	Sequence 4624, App
868	59	5.2	1395	6	US-11-096-568A-33181	Sequence 33181, A	941	58	5.1	379	7	US-11-087-099-8557	Sequence 8557, App
869	59	5.2	1690	6	US-10-330-773-389	Sequence 389, App	942	58	5.1	389	7	US-11-087-099-1556	Sequence 1556, App
870	59	5.2	2426	6	US-11-203-806A-11	Sequence 11, App	943	58	5.1	406	6	US-10-821-234-1521	Sequence 1521, App
871	59	5.2	2432	6	US-10-821-234-899	Sequence 899, App	944	58	5.1	422	7	US-11-087-099-11257	Sequence 11257, A
872	58.5	5.1	146	6	US-10-821-234-1225	Sequence 1225, App	945	58	5.1	441	7	US-11-024-959-280	Sequence 280, App
873	58.5	5.1	190	7	US-11-096-568A-631	Sequence 631, App	946	58	5.1	441	7	US-11-024-959-281	Sequence 281, App
874	58.5	5.1	196	6	US-10-967-527A-27	Sequence 27, App	947	58	5.1	462	7	US-11-177-648-97	Sequence 97, App
875	58.5	5.1	207	7	US-11-096-568A-6266	Sequence 6266, App	948	58	5.1	497	7	US-11-072-512-3603	Sequence 3603, App
876	58.5	5.1	209	7	US-11-096-568A-630	Sequence 630, App	949	58	5.1	557	6	US-10-821-234-895	Sequence 895, App
877	58.5	5.1	237	7	US-11-096-568A-6265	Sequence 6265, App	950	58	5.1	590	7	US-11-087-099-10675	Sequence 10675, A
878	58.5	5.1	253	7	US-11-096-568A-15019	Sequence 15019, A	951	58	5.1	590	7	US-11-096-568A-10460	Sequence 10460, A
879	58.5	5.1	258	7	US-11-096-568A-149	Sequence 149, App	952	58	5.1	624	6	US-10-467-657-338	Sequence 338, App
880	58.5	5.1	262	7	US-11-096-568A-6264	Sequence 6264, App	954	58	5.1	690	6	US-10-973-115B-306	Sequence 306, App
881	58.5	5.1	277	7	US-11-096-568A-10326	Sequence 10326, A	955	58	5.1	714	7	US-11-121-419-17	Sequence 17, App
882	58.5	5.1	284	7	US-11-096-568A-6263	Sequence 6263, App	956	58	5.1	717	7	US-11-050-857-954	Sequence 954, App
883	58.5	5.1	293	7	US-11-096-568A-12293	Sequence 12293, A	957	58	5.1	717	7	US-11-051-720-1895	Sequence 1695, App
884	58.5	5.1	299	7	US-11-072-512-2792	Sequence 2792, App	958	58	5.1	754	6	US-10-467-962B-63	Sequence 63, App
885	58.5	5.1	300	7	US-11-096-568A-10325	Sequence 10325, A	959	58	5.1	787	7	US-11-087-099-10681	Sequence 10681, A
886	58.5	5.1	308	7	US-11-072-512-3398	Sequence 3398, App	960	58	5.1	1033	6	US-10-921-415-1	Sequence 1, App
887	58.5	5.1	316	7	US-11-096-568A-28013	Sequence 28013, A	961	58	5.1	1165	7	US-11-192-219-2	Sequence 2, App
888	58.5	5.1	325	7	US-11-096-568A-24112	Sequence 24112, A	962	58	5.1	1165	7	US-11-202-330-4	Sequence 4, App
889	58.5	5.1	367	7	US-11-096-568A-31466	Sequence 31466, A	963	58	5.1	1263	7	US-11-076-163-3	Sequence 3, App
890	58.5	5.1	373	7	US-11-096-568A-24111	Sequence 24111, A	964	58	5.1	1362	7	US-11-043-693-33	Sequence 33, App
891	58.5	5.1	369	7	US-11-096-568A-24110	Sequence 24110, A	965	58	5.1	1725	6	US-10-766-317-8	Sequence 8, App
892	58.5	5.1	409	7	US-11-096-568A-7532	Sequence 7532, App	966	58	5.1	7465	7	US-11-087-099-7521	Sequence 7521, App
893	58.5	5.1	461	7	US-11-096-568A-22134	Sequence 22134, A	967	58	5.1	122	7	US-11-087-099-6151	Sequence 6151, App
894	58.5	5.1	486	7	US-11-057-012-11	Sequence 11, App	968	57.5	5.1	176	6	US-10-401-386B-10	Sequence 10, App
895	58.5	5.1	496	7	US-11-182-016-33	Sequence 33, App	969	57.5	5.1	180	6	US-10-511-988-2	Sequence 2, App
896	58.5	5.1	500	7	US-11-087-100-8	Sequence 8, App	970	57.5	5.1	191	7	US-11-096-568A-24831	Sequence 24831, A
897	58.5	5.1	500	7	US-11-087-084-8	Sequence 8, App	971	57.5	5.1	221	7	US-11-096-568A-12499	Sequence 12499, A
898	58.5	5.1	500	7	US-11-087-085-8	Sequence 8, App	972	57.5	5.1	227	6	US-10-977-334-7	Sequence 7, App
899	58.5	5.1	530	7	US-11-124-367A-314	Sequence 314, App	973	57.5	5.1	234	6	US-10-401-386B-8	Sequence 8, App
900	58.5	5.1	540	7	US-11-212-443-167	Sequence 167, App	974	57.5	5.1	238	7	US-11-096-568A-3196	Sequence 3196, App
901	58.5	5.1	621	7	US-11-087-099-2170	Sequence 2170, App	975	57.5	5.1	238	7	US-11-096-568A-3198	Sequence 3198, App
902	58.5	5.1	654	7	US-11-096-568A-30428	Sequence 30428, A	976	57.5	5.1	245	7	US-11-096-568A-21710	Sequence 21710, A
903	58.5	5.1	667	7	US-11-206-416-13	Sequence 13, App	977	57.5	5.1	253	7	US-11-096-568A-9854	Sequence 9854, App
904	58.5	5.1	740	7	US-11-124-367A-293	Sequence 293, App	978	57.5	5.1	261	7	US-11-138-242A-8	Sequence 8, App
905	58.5	5.1	760	7	US-11-124-367A-292	Sequence 292, App	979	57.5	5.1	261	7	US-11-138-242A-10	Sequence 10, App
906	58.5	5.1	761	7	US-11-212-443-22	Sequence 22, App	980	57.5	5.1	261	7	US-11-150-066-8	Sequence 8, App
907	58.5	5.1	801	7	US-11-052-554A-166	Sequence 166, App	981	57.5	5.1	261	7	US-11-150-066-8	Sequence 10, App
908	58.5	5.1	807	7	US-11-096-568A-30427	Sequence 30427, A	982	57.5	5.1	261	7	US-11-150-066-10	Sequence 10, App

983	57.5	5.1	261	7	US-11-033-039-358	Sequence 358, App	1057	57	5.0	219	7	US-11-096-568A-18567	Sequence 18567, A
984	57.5	5.1	261	7	US-11-155-288-10	Sequence 10, Appl	1058	57	5.0	220	6	US-10-330-773-16	Sequence 16, Appl
985	57.5	5.1	267	6	US-10-506-443A-38	Sequence 38, Appl	1059	57	5.0	220	6	US-10-330-773-16	Sequence 18, Appl
986	57.5	5.1	269	6	US-10-401-366B-2	Sequence 2, Appl	1060	57	5.0	226	7	US-11-104-111-18	Sequence 18, Appl
987	57.5	5.1	271	6	US-10-714-887-48	Sequence 48, Appl	1061	57	5.0	226	7	US-11-096-568A-2890	Sequence 2890, Ap
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990	57.5	5.1	286	7	US-11-087-099-268	Sequence 268, App	1064	57	5.0	241	7	US-11-064-774A-127	Sequence 127, App
991	57.5	5.1	291	7	US-11-041-095-60	Sequence 60, Appl	1065	57	5.0	241	7	US-11-075-400-20	Sequence 20, Appl
992	57.5	5.1	293	7	US-11-096-568A-12504	Sequence 12504, A	1066	57	5.0	241	7	US-11-211-724-4	Sequence 4, Appl
993	57.5	5.1	306	6	US-10-793-626-574	Sequence 574, App	1067	57	5.0	241	7	US-11-143-462-4	Sequence 4, Appl
994	57.5	5.1	306	6	US-10-793-626-2490	Sequence 2490, Ap	1068	57	5.0	241	7	US-11-129-076-3	Sequence 3, Appl
995	57.5	5.1	306	6	US-10-793-626-2640	Sequence 2640, Ap	1069	57	5.0	241	7	US-11-076-427A-20	Sequence 20, Appl
996	57.5	5.1	313	7	US-11-096-568A-10470	Sequence 10470, A	1070	57	5.0	241	7	US-11-233-119-6	Sequence 6, Appl
997	57.5	5.1	319	7	US-11-096-568A-10469	Sequence 10469, A	1071	57	5.0	241	7	US-11-075-047A-101	Sequence 101, App
998	57.5	5.1	324	7	US-11-096-568A-10468	Sequence 10468, A	1072	57	5.0	242	7	US-11-096-568A-25373	Sequence 25373, A
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1000	57.5	5.1	339	7	US-11-096-568A-6831	Sequence 6831, Ap	1074	57	5.0	254	6	US-10-510-386-146	Sequence 178, App
1001	57.5	5.1	341	7	US-11-096-568A-21708	Sequence 21708, A	1075	57	5.0	270	7	US-11-096-568A-9107	Sequence 9107, Ap
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1005	57.5	5.1	406	7	US-11-107-028-7	Sequence 7, Appl	1079	57	5.0	285	7	US-11-087-099-6222	Sequence 6222, Ap
1006	57.5	5.1	418	6	US-10-873-528-72	Sequence 72, Appl	1080	57	5.0	289	7	US-11-096-568A-9106	Sequence 9106, Ap
1007	57.5	5.1	421	7	US-11-096-568A-6829	Sequence 6829, Ap	1081	57	5.0	289	7	US-11-096-568A-9108	Sequence 9108, Ap
1008	57.5	5.1	427	7	US-11-087-099-9452	Sequence 9452, Ap	1083	57	5.0	299	6	US-10-973-115B-366	Sequence 366, App
1009	57.5	5.1	444	7	US-11-004-590-233	Sequence 233, App	1084	57	5.0	299	7	US-11-000-463-275	Sequence 275, App
1010	57.5	5.1	446	7	US-11-102-621-136	Sequence 136, App	1085	57	5.0	299	7	US-11-000-463-747	Sequence 747, App
1011	57.5	5.1	446	7	US-11-102-621-137	Sequence 137, App	1086	57	5.0	299	7	US-11-000-463-748	Sequence 748, App
1012	57.5	5.1	446	7	US-11-102-621-139	Sequence 139, App	1087	57	5.0	299	7	US-11-173-037-7	Sequence 7, Appl
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1014	57.5	5.1	470	7	US-11-087-099-5620	Sequence 5620, Ap	1089	57	5.0	311	7	US-11-096-568A-5368	Sequence 5368, Ap
1015	57.5	5.1	493	7	US-11-096-568A-11657	Sequence 11657, A	1090	57	5.0	324	7	US-11-096-568A-9105	Sequence 9105, Ap
1016	57.5	5.1	497	7	US-11-087-099-809	Sequence 809, App	1091	57	5.0	334	7	US-11-096-568A-6230	Sequence 6230, Ap
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1020	57.5	5.1	633	7	US-11-096-568A-2566	Sequence 2566, Ap	1095	57	5.0	341	7	US-11-099-691-6	Sequence 6, Appl
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1022	57.5	5.1	673	7	US-11-102-240-16	Sequence 16, Appl	1098	57	5.0	344	6	US-10-878-556A-123	Sequence 123, App
1023	57.5	5.1	673	7	US-11-103-195-16	Sequence 16, Appl	1099	57	5.0	344	7	US-11-016-564-13	Sequence 13, Appl
1024	57.5	5.1	674	7	US-11-096-568A-2565	Sequence 2565, Ap	1100	57	5.0	344	7	US-11-087-099-6649	Sequence 6649, Ap
1025	57.5	5.1	674	7	US-11-096-568A-2564	Sequence 2564, Ap	1101	57	5.0	345	7	US-11-087-099-6649	Sequence 4, Appl
1026	57.5	5.1	723	6	US-10-467-657-1916	Sequence 1916, Ap	1102	57	5.0	349	7	US-11-100-352-4	Sequence 9, Appl
1027	57.5	5.1	753	7	US-11-037-243-68	Sequence 68, Appl	1103	57	5.0	356	6	US-11-016-564-9	Sequence 4740, Ap
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1029	57.5	5.1	799	6	US-10-493-909-8	Sequence 8, Appl	1105	57	5.0	357	7	US-11-120-308-188	Sequence 34179, A
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1031	57.5	5.1	836	7	US-11-154-227-105	Sequence 105, App	1107	57	5.0	372	7	US-11-096-568A-5366	Sequence 5366, Ap
1032	57.5	5.1	904	7	US-11-154-227-97	Sequence 97, Appl	1108	57	5.0	378	7	US-11-096-568A-33265	Sequence 33265, A
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1034	57.5	5.1	1126	7	US-11-110-480-9	Sequence 9, Appl	1110	57	5.0	379	7	US-11-087-099-2694	Sequence 2694, Ap
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1036	57.5	5.1	1126	7	US-11-110-480-27	Sequence 27, Appl	1112	57	5.0	379	7	US-11-033-030-38	Sequence 38, Appl
1037	57.5	5.1	1126	7	US-11-110-480-37	Sequence 37, Appl	1113	57	5.0	380	7	US-11-087-099-5234	Sequence 5234, Ap
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1039	57.5	5.1	1126	7	US-11-110-480-59	Sequence 59, Appl	1115	57	5.0	396	7	US-11-087-099-3134	Sequence 3134, Ap
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1041	57.5	5.1	1126	7	US-11-110-480-88	Sequence 88, Appl	1117	57	5.0	406	7	US-11-096-568A-9725	Sequence 9725, Ap
1042	57.5	5.1	1218	7	US-11-052-554A-123	Sequence 123, App	1118	57	5.0	417	7	US-11-096-568A-6229	Sequence 6229, Ap
1043	57.5	5.1	1544	6	US-10-453-372-1186	Sequence 1186, Ap	1119	57	5.0	425	7	US-11-096-568A-6228	Sequence 6228, Ap
1044	57.5	5.1	1680	6	US-10-517-939-362	Sequence 362, App	1120	57	5.0	428	7	US-11-072-512-3675	Sequence 3675, Ap
1045	57.5	5.1	1806	7	US-11-096-568A-17179	Sequence 17179, A	1121	57	5.0	430	7	US-11-087-099-9088	Sequence 9088, Ap
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1047	57	5.0	1127	6	US-10-467-657-5334	Sequence 5334, Ap	1123	57	5.0	442	6	US-10-501-035-386	Sequence 386, App
1048	57	5.0	150	6	US-10-330-773-20	Sequence 20, Appl	1124	57	5.0	446	7	US-11-117-667-2	Sequence 2, Appl
1049	57	5.0	166	7	US-11-096-568A-30224	Sequence 30224, A	1125	57	5.0	450	7	US-11-096-568A-10802	Sequence 10802, A
1050	57	5.0	177	7	US-11-096-568A-17177	Sequence 17177, A	1126	57	5.0	461	7	US-11-096-568A-30898	Sequence 30898, A
1051	57	5.0	181	7	US-11-096-568A-25375	Sequence 25375, A	1127	57	5.0	481	7	US-11-096-568A-10801	Sequence 10801, A
1052	57	5.0	184	7	US-11-096-568A-5864	Sequence 5864, Ap	1128	57	5.0	482	7	US-11-087-099-6811	Sequence 6811, Ap
1053	57	5.0	195	7	US-11-096-568A-5863	Sequence 5863, Ap	1129	57	5.0	490	6	US-10-973-115B-356	Sequence 356, App
1054	57	5.0	204	7	US-11-098-686-10454	Sequence 10454, A	1130	57	5.0	492	7	US-11-096-568A-30897	Sequence 30897, A
1055	57	5.0	214	7	US-11-031-206-66	Sequence 66, Appl	1131	57	5.0	495	7	US-11-096-568A-30896	Sequence 30896, A
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1134	57	5.0	509	6	US-11-096-568A-29814	Sequence 29814, A	1208	56.5	5.0	382	7	US-11-087-099-8409	Sequence 8409, Ap
1135	57	5.0	526	6	US-10-490-824-3	Sequence 3, Appl1	1209	56.5	5.0	390	7	US-11-087-099-8409	Sequence 8409, Ap
1136	57	5.0	530	6	US-11-054-281-94	Sequence 94, Appl1	1210	56.5	5.0	397	6	US-10-793-626-644	Sequence 644, App
1137	57	5.0	536	6	US-10-641-678-61	Sequence 61, Appl1	1211	56.5	5.0	403	7	US-11-096-568A-29313	Sequence 29313, A
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1139	57	5.0	552	7	US-11-087-099-10920	Sequence 10920, A	1213	56.5	5.0	407	7	US-11-096-568A-33132	Sequence 33132, A
1140	57	5.0	558	7	US-11-096-568A-32065	Sequence 32065, A	1214	56.5	5.0	410	7	US-11-096-568A-4872	Sequence 4872, Ap
1141	57	5.0	572	6	US-11-096-568A-10461	Sequence 10461, A	1215	56.5	5.0	423	7	US-11-096-568A-29312	Sequence 29312, A
1143	57	5.0	575	6	US-10-973-115B-128	Sequence 128, App	1216	56.5	5.0	424	7	US-11-087-099-5546	Sequence 5546, Ap
1144	57	5.0	625	7	US-11-096-568A-32064	Sequence 32064, A	1217	56.5	5.0	425	7	US-11-087-099-1247	Sequence 1247, Ap
1145	57	5.0	651	7	US-11-052-554A-111	Sequence 111, App	1218	56.5	5.0	425	7	US-11-096-568A-4871	Sequence 4871, Ap
1146	57	5.0	670	6	US-10-995-561-528	Sequence 528, App	1219	56.5	5.0	431	6	US-10-821-234-1065	Sequence 1065, Ap
1147	57	5.0	693	6	US-10-714-995-24	Sequence 24, Appl1	1220	56.5	5.0	437	6	US-10-967-648A-2	Sequence 2, Appl1
1148	57	5.0	728	6	US-10-517-969-112	Sequence 112, App	1221	56.5	5.0	442	7	US-11-102-621-124	Sequence 124, App
1149	57	5.0	769	7	US-11-188-743-15	Sequence 15, Appl1	1222	56.5	5.0	442	7	US-11-102-621-125	Sequence 125, App
1150	57	5.0	808	7	US-11-087-099-7073	Sequence 7073, Ap	1223	56.5	5.0	442	7	US-11-102-621-127	Sequence 127, App
1151	57	5.0	832	7	US-11-098-686-10182	Sequence 10182, A	1224	56.5	5.0	442	7	US-11-102-621-128	Sequence 128, App
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1156	57	5.0	1116	7	US-11-156-084-118	Sequence 118, App	1229	56.5	5.0	503	7	US-11-098-686-10362	Sequence 10362, A
1157	57	5.0	1126	7	US-11-113-751-32	Sequence 32, Appl1	1230	56.5	5.0	507	6	US-10-467-657-1612	Sequence 1612, Ap
1158	57	5.0	1129	6	US-10-995-561-705	Sequence 705, App	1231	56.5	5.0	508	7	US-11-072-512-3333	Sequence 3233, Ap
1159	57	5.0	1129	6	US-10-995-561-706	Sequence 706, App	1232	56.5	5.0	512	7	US-11-096-568A-33131	Sequence 33131, A
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1162	57	5.0	1255	7	US-11-050-857-487	Sequence 487, App	1235	56.5	5.0	569	7	US-11-096-568A-6975	Sequence 6975, Ap
1163	57	5.0	1255	7	US-11-043-806-398	Sequence 398, App	1236	56.5	5.0	596	7	US-11-087-099-2777	Sequence 2777, Ap
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1170	57	5.0	1398	6	US-10-995-561-662	Sequence 662, App	1243	56.5	5.0	737	6	US-10-055-877-156	Sequence 156, App
1171	57	5.0	1954	6	US-10-995-561-660	Sequence 660, App	1244	56.5	5.0	749	6	US-10-453-372-800	Sequence 800, App
1172	57	5.0	1972	6	US-10-995-561-664	Sequence 664, App	1245	56.5	5.0	750	6	US-10-467-657-88	Sequence 88, Appl1
1173	57	5.0	2072	6	US-10-995-561-666	Sequence 666, App	1246	56.5	5.0	755	6	US-10-467-657-6342	Sequence 6342, Ap
1174	57	5.0	2086	7	US-11-128-059-82	Sequence 82, Appl1	1247	56.5	5.0	755	6	US-10-517-939-330	Sequence 330, App
1175	57	5.0	2087	7	US-11-075-185-28	Sequence 28, Appl1	1248	56.5	5.0	756	7	US-11-188-743-20	Sequence 20, Appl1
1176	57	5.0	2292	6	US-10-330-773-907	Sequence 907, App	1249	56.5	5.0	756	7	US-11-183-294-22	Sequence 22, Appl1
1177	56.5	5.0	126	7	US-11-041-471-10	Sequence 10, Appl1	1250	56.5	5.0	774	6	US-10-055-877-191	Sequence 191, App
1178	56.5	5.0	135	7	US-11-096-568A-16110	Sequence 16110, A	1251	56.5	5.0	837	6	US-10-501-035-345	Sequence 345, App
1179	56.5	5.0	152	7	US-11-089-266-4	Sequence 4, Appl1	1252	56.5	5.0	882	6	US-10-453-372-60	Sequence 60, Appl1
1180	56.5	5.0	164	7	US-11-096-568A-3342	Sequence 3342, Ap	1253	56.5	5.0	884	6	US-10-453-372-58	Sequence 58, Appl1
1181	56.5	5.0	175	7	US-11-096-568A-16109	Sequence 16109, A	1254	56.5	5.0	1048	6	US-10-912-580-6	Sequence 6, Appl1
1182	56.5	5.0	196	7	US-11-096-568A-16108	Sequence 16108, A	1255	56.5	5.0	1048	6	US-10-912-581-1	Sequence 1, Appl1
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1184	56.5	5.0	220	7	US-11-096-568A-21253	Sequence 21253, A	1257	56.5	5.0	1208	6	US-10-330-773-244	Sequence 244, App
1185	56.5	5.0	221	7	US-11-112-481C-2	Sequence 2, Appl1	1258	56.5	5.0	1438	6	US-10-453-372-796	Sequence 796, App
1186	56.5	5.0	229	7	US-11-096-568A-19426	Sequence 3, Appl1	1259	56.5	5.0	3104	6	US-10-453-372-34	Sequence 34, Appl1
1187	56.5	5.0	233	7	US-11-096-568A-29421	Sequence 29421, A	1260	56.5	5.0	3104	6	US-10-453-372-62	Sequence 62, Appl1
1188	56.5	5.0	248	7	US-11-096-568A-19425	Sequence 19425, A	1261	56.5	5.0	3104	6	US-10-453-372-64	Sequence 64, Appl1
1189	56.5	5.0	251	7	US-11-054-515-976	Sequence 976, App	1262	56.5	5.0	3130	6	US-10-453-372-42	Sequence 42, Appl1
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1193	56.5	5.0	261	7	US-11-150-066-3	Sequence 3, Appl1	1266	56	4.9	121	7	US-11-087-099-7475	Sequence 7475, Ap
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1195	56.5	5.0	262	7	US-11-087-099-5951	Sequence 5951, Ap	1268	56	4.9	167	7	US-11-087-099-2931	Sequence 2931, Ap
1196	56.5	5.0	265	7	US-11-096-568A-22358	Sequence 22358, A	1269	56	4.9	202	7	US-11-096-568A-11688	Sequence 11688, A
1197	56.5	5.0	266	7	US-11-009-063-35	Sequence 35, Appl1	1270	56	4.9	233	7	US-11-128-900-15	Sequence 15, Appl1
1198	56.5	5.0	281	7	US-11-096-568A-19424	Sequence 19424, A	1271	56	4.9	233	7	US-11-128-900-67	Sequence 67, Appl1
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1200	56.5	5.0	326	7	US-11-207-626A-19	Sequence 19, Appl1	1273	56	4.9	249	7	US-11-072-512-2195	Sequence 2195, Ap
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1203	56.5	5.0	353	6	US-10-999-866-31	Sequence 31, Appl1	1276	56	4.9	257	7	US-11-072-175-234	Sequence 234, App
1204	56.5	5.0	354	6	US-10-935-005B-62	Sequence 62, Appl1	1277	56	4.9	262	7	US-11-096-568A-21488	Sequence 21488, A
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1281	56	4.9	303	7	US-11-096-568A-21487	Sequence 21487, A	1354	56	4.9	1593	7	US-11-149-003-4	Sequence 4, Appli
1282	56	4.9	305	6	US-10-502-972-4	Sequence 4, Appli	1355	56	4.9	1628	7	US-11-149-003-2	Sequence 2, Appli
1283	56	4.9	305	7	US-11-087-099-6451	Sequence 6451, Ap	1356	56	4.9	1839	7	US-11-087-099-9631	Sequence 9631, Ap
1284	56	4.9	305	7	US-11-096-568A-11194	Sequence 11194, A	1357	56	4.9	2362	7	US-11-096-568A-31778	Sequence 31778, A
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1286	56	4.9	338	7	US-11-207-626A-29	Sequence 29, Appl	1359	56	4.9	2433	7	US-11-096-568A-31777	Sequence 31777, A
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1288	56	4.9	340	7	US-11-096-568A-237	Sequence 237, App	1361	56	4.9	14130	7	US-11-175-689-9	Sequence 9, Appli
1289	56	4.9	345	7	US-11-096-568A-234	Sequence 234, App	1362	55.5	4.9	114	7	US-11-100-553B-35	Sequence 35, Appl
1290	56	4.9	345	7	US-11-096-568A-34448	Sequence 34448, A	1363	55.5	4.9	136	7	US-11-049-536-36	Sequence 36, Appl
1291	56	4.9	346	7	US-11-008-570-48	Sequence 48, Appl	1364	55.5	4.9	136	7	US-11-096-568A-31481	Sequence 31481, A
1292	56	4.9	349	7	US-11-096-568A-10641	Sequence 10641, A	1365	55.5	4.9	141	7	US-11-096-568A-4518	Sequence 4518, Ap
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1294	56	4.9	355	7	US-11-096-568A-23509	Sequence 23509, A	1367	55.5	4.9	171	7	US-11-096-568A-13784	Sequence 13784, A
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1296	56	4.9	369	7	US-11-096-568A-6733	Sequence 6733, Ap	1369	55.5	4.9	200	7	US-11-096-568A-16604	Sequence 16604, A
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1298	56	4.9	386	7	US-11-072-512-2777	Sequence 2777, Ap	1371	55.5	4.9	214	7	US-11-102-621-129	Sequence 129, App
1299	56	4.9	389	7	US-11-096-568A-28493	Sequence 28493, A	1372	55.5	4.9	220	7	US-11-096-568A-245	Sequence 245, App
1300	56	4.9	392	6	US-10-453-372-632	Sequence 632, App	1373	55.5	4.9	224	7	US-11-096-568A-15262	Sequence 15262, A
1301	56	4.9	392	6	US-10-453-372-634	Sequence 634, App	1374	55.5	4.9	232	7	US-11-096-568A-244	Sequence 244, App
1302	56	4.9	396	6	US-10-453-372-620	Sequence 620, App	1375	55.5	4.9	232	7	US-11-096-568A-246	Sequence 246, App
1303	56	4.9	396	7	US-11-087-099-7884	Sequence 7884, Ap	1376	55.5	4.9	238	7	US-11-096-568A-27672	Sequence 27672, A
1304	56	4.9	403	7	US-11-169-041-185	Sequence 185, App	1377	55.5	4.9	239	7	US-11-096-568A-16153	Sequence 16153, A
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1306	56	4.9	438	7	US-11-087-099-10527	Sequence 10527, A	1379	55.5	4.9	244	7	US-11-090-878-68	Sequence 68, Appl
1307	56	4.9	442	6	US-10-453-372-618	Sequence 618, App	1380	55.5	4.9	244	7	US-11-090-878-69	Sequence 69, Appl
1308	56	4.9	442	6	US-10-453-372-626	Sequence 626, App	1381	55.5	4.9	250	6	US-10-948-429A-10	Sequence 10, Appl
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1310	56	4.9	442	6	US-10-453-372-630	Sequence 630, App	1383	55.5	4.9	251	7	US-11-054-515-991	Sequence 991, App
1311	56	4.9	442	6	US-10-453-372-636	Sequence 636, App	1384	55.5	4.9	252	6	US-10-512-184-28	Sequence 28, Appl
1312	56	4.9	442	6	US-10-877-346-19	Sequence 19, Appl	1385	55.5	4.9	277	7	US-11-096-568A-1871	Sequence 1871, Ap
1313	56	4.9	442	6	US-10-877-346-21	Sequence 21, Appl	1386	55.5	4.9	277	7	US-11-096-568A-27199	Sequence 27199, A
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1315	56	4.9	442	6	US-10-877-346-55	Sequence 55, Appl	1388	55.5	4.9	291	7	US-11-096-568A-26427	Sequence 26427, A
1316	56	4.9	442	6	US-10-877-346-56	Sequence 56, App	1389	55.5	4.9	291	7	US-11-096-568A-32907	Sequence 32907, A
1317	56	4.9	442	7	US-11-096-568A-20632	Sequence 20632, A	1390	55.5	4.9	292	7	US-11-096-568A-17208	Sequence 17208, A
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1319	56	4.9	459	6	US-10-821-234-896	Sequence 896, App	1392	55.5	4.9	311	7	US-11-087-099-5603	Sequence 5603, Ap
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462	71	6.2	610	1	US-08-135-929A-11	Sequence 11, Appl	535	69	6.1	2035	4	PCT-US93-11721-5	
463	71	6.2	610	1	US-08-234-265A-11	Sequence 11, Appl	536	69	6.1	2045	2	Sequence 10491, A	
464	71	6.2	1014	2	US-09-078-347A-3	Sequence 3, Appli	537	68.5	6.0	256	2	Sequence 14185, A	
465	71	6.2	1014	2	US-09-596-248D-25	Sequence 25, Appl	538	68.5	6.0	291	2	Sequence 45280, A	









977	64	5.6	1445	1	US-08-015-986A-2	Sequence 2, Appli	1050	63.5	5.6	1466	2	US-09-262-537-20	Sequence 20, Appli
978	64	5.6	1445	1	US-08-446-363-2	Sequence 2, Appli	1051	63.5	5.6	1469	2	US-09-262-537-58	Sequence 58, Appli
979	64	5.6	1474	2	US-09-302-626B-179	Sequence 179, App	1052	63.5	5.6	1471	2	US-08-811-519-1	Sequence 1, Appli
980	64	5.6	1978	2	US-09-302-626B-60	Sequence 60, Appl	1053	63.5	5.6	1475	2	US-09-538-092-1160	Sequence 1160, Ap
981	64	5.6	2781	2	US-09-698-295-10	Sequence 10, Appl	1054	63.5	5.6	1478	2	US-09-949-016-8315	Sequence 8315, Ap
982	64	5.6	2307	2	US-09-698-295-1	Sequence 1, Appli	1055	63.5	5.6	1535	2	US-08-755-587-185	Sequence 185, App
983	63.5	5.6	83	2	US-09-252-991A-21499	Sequence 21499, A	1056	63.5	5.6	1841	2	US-09-477-962-99	Sequence 99, Appl
984	63.5	5.6	179	2	US-09-252-991A-26797	Sequence 26797, A	1057	63.5	5.6	1979	2	US-09-949-016-8468	Sequence 8468, Ap
985	63.5	5.6	210	2	US-09-270-767-33951	Sequence 33951, A	1058	63.5	5.6	2231	1	US-08-153-799-16	Sequence 16, Appl
986	63.5	5.6	216	2	US-09-270-767-48168	Sequence 48168, A	1059	63.5	5.6	2940	2	US-10-226-629A-13	Sequence 13, Appl
987	63.5	5.6	264	2	US-09-107-532A-4916	Sequence 4916, A	1060	63	5.5	26	1	US-08-450-360-12	Sequence 12, Appl
988	63.5	5.6	264	1	US-08-463-115-93	Sequence 93, Appl	1061	63	5.5	128	2	US-08-845-258-41	Sequence 41, Appl
989	63.5	5.6	264	1	US-08-465-388-93	Sequence 93, Appl	1062	63	5.5	128	2	US-08-930-571-41	Sequence 41, Appl
990	63.5	5.6	319	2	US-08-832-399-2	Sequence 2, Appli	1063	63	5.5	128	2	US-08-723-142A-41	Sequence 41, Appl
991	63.5	5.6	319	2	US-09-372-498-2	Sequence 2, Appli	1064	63	5.5	128	2	US-09-528-784A-41	Sequence 41, Appl
992	63.5	5.6	338	2	US-09-807-933B-7	Sequence 7, Appli	1065	63	5.5	128	2	US-09-569-098A-41	Sequence 41, Appl
993	63.5	5.6	347	2	US-09-252-991A-19498	Sequence 19498, A	1066	63	5.5	133	2	US-09-252-991A-23872	Sequence 23872, A
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998	63.5	5.6	399	1	US-08-926-922-5	Sequence 5, Appli	1071	63	5.5	191	1	US-08-253-155A-39	Sequence 39, Appl
999	63.5	5.6	399	2	US-09-253-682-5	Sequence 5, Appli	1072	63	5.5	192	2	US-10-104-047-3585	Sequence 3585, Ap
1000	63.5	5.6	399	2	US-09-527-657-5	Sequence 5, Appli	1073	63	5.5	202	2	US-09-252-991A-20995	Sequence 20995, A
1001	63.5	5.6	399	2	US-09-892-100-5	Sequence 5, Appli	1074	63	5.5	204	2	US-09-248-796A-16962	Sequence 16962, A
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1004	63.5	5.6	423	2	US-09-826-509-537	Sequence 537, App	1077	63	5.5	248	2	US-09-533-029A-22	Sequence 22, Appl
1005	63.5	5.6	423	2	US-09-674-330A-4	Sequence 4, Appli	1078	63	5.5	291	6	5194600-2	Patent No. 5194600
1006	63.5	5.6	423	2	US-09-674-330A-9	Sequence 9, Appli	1079	63	5.5	302	2	US-09-252-991A-21231	Sequence 21231, A
1007	63.5	5.6	428	1	US-09-134-000C-6457	Sequence 6457, Ap	1080	63	5.5	306	2	US-09-189-060B-68	Sequence 68, Appl
1008	63.5	5.6	447	1	US-08-450-360-4	Sequence 4, Appli	1081	63	5.5	309	2	US-09-248-796A-25339	Sequence 25339, A
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1015	63.5	5.6	465	2	US-08-723-142A-30	Sequence 30, Appl	1088	63	5.5	422	2	US-09-949-016-8251	Sequence 8251, Ap
1016	63.5	5.6	465	2	US-09-528-784A-30	Sequence 30, Appl	1089	63	5.5	424	1	US-08-419-414-2	Sequence 2, Appli
1017	63.5	5.6	465	2	US-09-569-098A-30	Sequence 30, Appl	1090	63	5.5	435	2	US-09-949-016-9133	Sequence 9133, Ap
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1021	63.5	5.6	468	2	US-09-187-906-2	Sequence 2, Appli	1094	63	5.5	454	2	US-09-949-016-9823	Sequence 9823, Ap
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1023	63.5	5.6	468	2	US-09-388-316C-21	Sequence 21, Appl	1096	63	5.5	456	2	US-08-648-650A-4	Sequence 4, Appli
1024	63.5	5.6	486	1	US-09-489-407-2	Sequence 2, Appli	1097	63	5.5	457	2	US-09-183-266A-4	Sequence 4, Appli
1025	63.5	5.6	486	1	US-08-450-360-2	Sequence 2, Appli	1098	63	5.5	463	2	US-09-248-796A-14184	Sequence 14184, A
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1035	63.5	5.6	699	2	US-10-237-551-254	Sequence 254, App	1108	63	5.5	888	2	US-09-248-796A-18627	Sequence 18627, A
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1037	63.5	5.6	918	2	US-09-200-650E-1	Sequence 1, Appli	1110	63	5.5	1065	2	US-09-538-092-84	Sequence 84, Appl
1038	63.5	5.6	973	1	US-08-162-809-10	Sequence 10, Appl	1111	63	5.5	1557	2	US-09-410-551B-27	Sequence 27, Appl
1039	63.5	5.6	988	1	US-08-162-809A-14	Sequence 14, Appl	1112	63	5.5	1557	2	US-09-940-316B-27	Sequence 27, Appl
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1048	63.5	5.6	1339	2	US-09-949-016-10448	Sequence 10448, A	1121	63	5.5	2628	1	US-08-570-311-14	Sequence 14, Appl
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1124	62.5	5.5	99	2	US-09-270-767-58460	Sequence 58460, A	1197	62.5	5.5	457	2	US-09-949-016-8178	Sequence 8178, A
1125	62.5	5.5	100	2	US-08-469-260A-396	Sequence 396, App	1198	62.5	5.5	458	2	US-09-631-220-2	Sequence 2, Appl
1126	62.5	5.5	100	2	US-08-488-446-396	Sequence 396, App	1199	62.5	5.5	462	1	US-08-552-383-2	Sequence 2, Appl
1127	62.5	5.5	100	2	US-08-467-344A-396	Sequence 396, App	1200	62.5	5.5	462	1	US-08-095-728B-4	Sequence 4, Appl
1128	62.5	5.5	100	2	US-08-424-550B-396	Sequence 396, App	1201	62.5	5.5	462	4	PCT-US92-02320A-4	Sequence 4, Appl
1129	62.5	5.5	113	2	US-09-899-082B-111	Sequence 111, App	1202	62.5	5.5	478	2	US-09-134-000C-3709	Sequence 3709, Ap
1130	62.5	5.5	113	2	US-09-899-082B-112	Sequence 112, App	1203	62.5	5.5	491	2	US-09-270-767-44430	Sequence 44430, A
1131	62.5	5.5	159	2	US-09-248-796A-21631	Sequence 21631, A	1204	62.5	5.5	513	1	US-08-676-166A-5	Sequence 5, Appl
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1133	62.5	5.5	170	2	US-09-252-991A-28550	Sequence 28550, A	1206	62.5	5.5	540	2	US-09-134-000C-3745	Sequence 3745, Ap
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1136	62.5	5.5	187	1	US-07-853-985A-2	Sequence 2, Appl	1209	62.5	5.5	593	1	US-08-722-806A-2	Sequence 2, Appl
1137	62.5	5.5	187	1	US-07-681-703B-2	Sequence 2, Appl	1210	62.5	5.5	593	1	US-09-337-028-2	Sequence 2, Appl
1138	62.5	5.5	187	1	US-08-184-236-2	Sequence 2, Appl	1211	62.5	5.5	593	2	US-09-537-877-2	Sequence 2, Appl
1139	62.5	5.5	187	1	US-08-407-410B-2	Sequence 2, Appl	1212	62.5	5.5	601	1	US-08-606-288-7	Sequence 7, Appl
1140	62.5	5.5	187	1	US-08-485-500-2	Sequence 2, Appl	1213	62.5	5.5	601	1	US-08-606-288-10	Sequence 10, Appl
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1144	62.5	5.5	252	2	US-09-270-767-43125	Sequence 43125, A	1217	62.5	5.5	613	2	US-10-446-468-3	Sequence 3, Appl
1145	62.5	5.5	257	2	US-09-902-540-15102	Sequence 15102, A	1218	62.5	5.5	635	1	US-08-571-758-10	Sequence 10, Appl
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1147	62.5	5.5	325	1	US-08-233-788A-55	Sequence 55, Appl	1220	62.5	5.5	635	1	US-08-909-983-10	Sequence 10, Appl
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1149	62.5	5.5	331	2	US-09-467-638-5	Sequence 5, Appl	1222	62.5	5.5	797	4	PCT-US92-02320A-2	Sequence 2, Appl
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1152	62.5	5.5	362	1	US-08-415-751-5	Sequence 5, Appl	1225	62.5	5.5	875	1	US-08-571-758-8	Sequence 8, Appl
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1155	62.5	5.5	367	2	US-09-643-596B-54	Sequence 54, Appl	1228	62.5	5.5	877	1	US-08-916-917-2	Sequence 2, Appl
1156	62.5	5.5	367	2	US-10-099-278-54	Sequence 54, Appl	1229	62.5	5.5	877	1	US-08-972-631-2	Sequence 2, Appl
1157	62.5	5.5	371	2	US-09-378-088A-64	Sequence 64, Appl	1230	62.5	5.5	877	1	US-08-972-632-2	Sequence 2, Appl
1158	62.5	5.5	371	2	US-09-643-596B-64	Sequence 64, Appl	1231	62.5	5.5	877	1	US-08-972-630-2	Sequence 2, Appl
1159	62.5	5.5	371	2	US-10-099-278-64	Sequence 64, Appl	1232	62.5	5.5	877	1	US-08-672-211-2	Sequence 2, Appl
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1161	62.5	5.5	385	2	US-08-633-993A-11	Sequence 11, Appl	1234	62.5	5.5	1011	2	US-08-850-328-5	Sequence 5, Appl
1162	62.5	5.5	385	2	US-08-844-188-11	Sequence 11, Appl	1235	62.5	5.5	1075	1	US-08-993-228-19	Sequence 19, Appl
1163	62.5	5.5	385	2	US-09-378-088A-11	Sequence 11, Appl	1236	62.5	5.5	1232	2	US-09-248-796A-14563	Sequence 14563, A
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1165	62.5	5.5	385	2	US-09-378-088A-116	Sequence 116, App	1238	62.5	5.5	1416	2	US-10-071-035-404	Sequence 404, App
1166	62.5	5.5	385	2	US-09-548-334A-11	Sequence 11, Appl	1239	62.5	5.5	1416	2	US-10-206-576-404	Sequence 404, App
1167	62.5	5.5	385	2	US-09-563-269-8	Sequence 8, Appl	1240	62.5	5.5	1448	2	US-10-071-035-402	Sequence 402, App
1168	62.5	5.5	385	2	US-09-547-621-11	Sequence 11, Appl	1241	62.5	5.5	1448	2	US-10-206-576-402	Sequence 402, App
1169	62.5	5.5	385	2	US-09-643-596B-11	Sequence 11, Appl	1242	62.5	5.5	1577	1	US-08-793-824-2	Sequence 2, Appl
1170	62.5	5.5	385	2	US-09-643-596B-68	Sequence 68, Appl	1243	62.5	5.5	1769	2	US-09-949-016-8280	Sequence 8280, Ap
1171	62.5	5.5	385	2	US-09-643-596B-116	Sequence 116, App	1244	62.5	5.5	1769	2	US-09-949-016-8281	Sequence 8281, Ap
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; APPLICANT: Wood, William, I.
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; FILE REFERENCE: 10466-14
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; OTHER INFORMATION: Synthetic protein
US-09-907-794A-201

Query Match 100.0%; Score 1136; DB 2; Length 322;
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; APPLICANT: Ferrara, Napoleone
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; ORGANISM: Artificial sequence
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; OTHER INFORMATION: Synthetic protein
US-09-907-794A-201

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; Sequence 201, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 201  
;; LENGTH: 322  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic protein  
US-09-905-125A-201

Query Match 100.0%; Score 1136; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.7e-115;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKACRLGLSLAGKQV 60  
Db 16 TTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKACRLGLSLAGKQV 75

Qy 61 TALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120  
Db 76 TALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135

Qy 121 TNSCIPRIITTKDPIENTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 180  
Db 136 TNSCIPRIITTKDPIENTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 195

Qy 181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAGFGG 220  
Db 196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAGFGG 235

RESULT 4  
US-09-902-775A-201  
; Sequence 201, Application US/09902775A  
; Patent No. 6686451  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: 10466-14  
;; CURRENT APPLICATION NUMBER: US/09/902,775A  
;; CURRENT FILING DATE: 2001-07-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: 2000-02-22  
;; PRIOR APPLICATION NUMBER: US 60/143,048  
;; PRIOR FILING DATE: 1999-07-07  
;; PRIOR APPLICATION NUMBER: US 60/145,698  
;; PRIOR FILING DATE: 1999-07-26  
;; PRIOR APPLICATION NUMBER: US 60/146,222  
;; PRIOR FILING DATE: 1999-07-28  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/20944  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
;; PRIOR FILING DATE: 1999-11-29  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 201  
;; LENGTH: 322  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic protein  
US-09-902-775A-201

Query Match 100.0%; Score 1136; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.7e-115;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKACRLGLSLAGKQV 60  
Db 16 TTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKACRLGLSLAGKQV 75

Qy 61 TALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120  
Db 76 TALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135

Qy 121 TNSCIPRIITTKDPIENTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 180  
Db 136 TNSCIPRIITTKDPIENTQTATQTEFIVSDTSYVASPYSTIPAPTTTPAPASTSIPR 195

Qy 181 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAGFGG 220  
Db 196 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAGFGG 235

RESULT 5  
US-09-906-700-201  
; Sequence 201, Application US/09906700  
; Patent No. 6723535  
; GENERAL INFORMATION:

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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-906-700-201

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Query Match      100.0%; Score 1136; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTRLVQGLRAEELISQVSCRIMGITLVSKKANQQLNFTKEACRLLGLSLAGKQOVE 60
Db      16  TTRLVQGLRAEELISQVSCRIMGITLVSKKANQQLNFTKEACRLLGLSLAGKQOVE 75

QY     61  TALKASFETCSYGVWGDGFVVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120
Db      76  TALKASFETCSYGVWGDGFVVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135

QY     121 TNSCIPEIITTKDPIFNQTATQTTFEFIVSDTSVSPYSTIPATTPPAPASTSIPR 180
Db      136 TNSCIPEIITTKDPIFNQTATQTTFEFIVSDTSVSPYSTIPATTPPAPASTSIPR 195

QY     181 RKKLICVTEVFMEITSTMSTETETEPFVENKAAFNKAAGFGG 220
Db      196 RKKLICVTEVFMEITSTMSTETETEPFVENKAAFNKAAGFGG 235

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## RESULT 6

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US-09-903-603A-201
; Sequence 201, Application US/09903603A
; Patent No. 6767955
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
; US-09-903-603A-201

Query Match          100.0%; Score 1136; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLVQGSRAEELSIOVSCRIMGITLVSKKANQQLNFTFAKACRLGLSLAGKQDVE 60
Db 16 TTRLVQGSRAEELSIOVSCRIMGITLVSKKANQQLNFTFAKACRLGLSLAGKQDVE 75

Qy 61 TALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120
Db 76 TALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135

Qy 121 TNSCIPEIITTKDPIFNQTQTATQTEFTVSDTSYVASPYSTIPAPTTTPAPASTSIPR 180
Db 136 TNSCIPEIITTKDPIFNQTQTATQTEFTVSDTSYVASPYSTIPAPTTTPAPASTSIPR 195

Qy 181 RKKLICVTEVFMETSTWSTETEPFVENKAAFKNEAAGFGG 220
Db 196 RKKLICVTEVFMETSTWSTETEPFVENKAAFKNEAAGFGG 235
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## RESULT 7

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US-09-904-920A-201
; Sequence 201, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.

Query Match          100.0%; Score 1136; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLVQGSRAEELSIOVSCRIMGITLVSKKANQQLNFTFAKACRLGLSLAGKQDVE 60
Db 16 TTRLVQGSRAEELSIOVSCRIMGITLVSKKANQQLNFTFAKACRLGLSLAGKQDVE 75

Qy 61 TALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120
Db 76 TALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135

Qy 121 TNSCIPEIITTKDPIFNQTQTATQTEFTVSDTSYVASPYSTIPAPTTTPAPASTSIPR 180
Db 136 TNSCIPEIITTKDPIFNQTQTATQTEFTVSDTSYVASPYSTIPAPTTTPAPASTSIPR 195

Qy 181 RKKLICVTEVFMETSTWSTETEPFVENKAAFKNEAAGFGG 220
Db 196 RKKLICVTEVFMETSTWSTETEPFVENKAAFKNEAAGFGG 235

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
; US-09-904-920A-201
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
; US-09-904-920A-201
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RESULT 8
US-09-909-064-201
; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-909-064-201

Query Match      100.0%; Score 1136; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTRLVQGLRAEELSIQVSCRIMGITLVSKKANQQLNFTKEACRLLGLSLAGKQOVE 60
Db      16  TTRLVQGLRAEELSIQVSCRIMGITLVSKKANQQLNFTKEACRLLGLSLAGKQOVE 75

QY      61  TALKASFTCSYGVWGDGFVVISRISPNPKCGKKGVGVLWIKVPVSRQFAAYCYNSSDTW 120
Db      76  TALKASFTCSYGVWGDGFVVISRISPNPKCGKKGVGVLWIKVPVSRQFAAYCYNSSDTW 135

QY      121 TNSCIPELIITTKDPIFNQTATQTTEFIVSDTYSVASPYSTIPAPTTTPPAPASTSIPR 180
Db      136 TNSCIPELIITTKDPIFNQTATQTTEFIVSDTYSVASPYSTIPAPTTTPPAPASTSIPR 195

QY      181 RKKLICVTEVFMETSTMTSTETEPFVENKAAFKNEAAGFGG 220
Db      196 RKKLICVTEVFMETSTMTSTETEPFVENKAAFKNEAAGFGG 235

RESULT 9
US-09-905-381A-201
; Sequence 201, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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, PRIOR APPLICATION NUMBER: PCT/US99/21090
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/21547
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/23089
, PRIOR FILING DATE: 1999-10-05
, PRIOR APPLICATION NUMBER: PCT/US99/28214
, PRIOR FILING DATE: 1999-11-29
, PRIOR APPLICATION NUMBER: PCT/US99/28313
, PRIOR FILING DATE: 1999-11-30
, PRIOR APPLICATION NUMBER: PCT/US99/28564
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/28565
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: 1999-12-16
, PRIOR APPLICATION NUMBER: PCT/US99/30911
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 201
, LENGTH: 322
, TYPE: PRT
, ORGANISM: Artificial sequence
, FEATURE:
, OTHER INFORMATION: Synthetic protein
US-09-905-381a-201

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Query Match	100.0%;	Score 1136;	DB 2;	Length 322;
Best Local Similarity	100.0%;	Pred. No. 2.7e-115;		
Matches 220;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	TTRLVQGSRAEELSIQVSRIMGITLVSKKANQQLNPTAEKACRLGLSLAGKQVE	60	
Db	16	TTRLVQGSRAEELSIQVSRIMGITLVSKKANQQLNPTAEKACRLGLSLAGKQVE	75	
Qy	61	TALKASFETCSYGGWGDGFVVISRISNPCKGKNGVGVLWKVPVSRQFAAYCYNSSDWT	120	
Db	76	TALKASFETCSYGGWGDGFVVISRISNPCKGKNGVGVLWKVPVSRQFAAYCYNSSDWT	135	
Qy	121	TNSCIPEIITTKDPIENTQTATQTEFTVSDTSYVASPYSTTTPAPTPPPAPASTSI	180	
Db	136	TNSCIPEIITTKDPIENTQTATQTEFTVSDTSYVASPYSTTTPAPTPPPAPASTSI	195	
Qy	181	RKLLCVTEVFMETSTMSTETEPFVFNKAAPKNEAAGFGG	220	
Db	196	RKLLCVTEVFMETSTMSTETEPFVFNKAAPKNEAAGFGG	235	

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RESULT 10
US-09-906-618-201
; Sequence 201, Application US/09906618
; Patent No. 6828146
;
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-906-618-201

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Query Match      100.0%; Score 1136; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]



Qy 181 RKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGG 220  
Db 196 RKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGG 235

RESULT 11

US-09-906-646-201  
; Sequence 201, Application US/09906646  
; Patent No. 6852848  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/906,646  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-09-906-646-201

Query Match 100.0%; Score 1136; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.7e-115;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTRLLVQSLRAEELSIVQSCRIMGITLVSKKANQQLNFTTEAKEACRLGLSLAGKQDVE 60  
Db 16 TTRLLVQSLRAEELSIVQSCRIMGITLVSKKANQQLNFTTEAKEACRLGLSLAGKQDVE 75  
Qy 61 TALKASRETCSYGMVGDFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120  
Db 76 TALKASRETCSYGMVGDFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135  
Qy 121 TNSCIPRIITTKDPINFNTQTATQTTEFTIVSDTSYVASPYSTIPAPTTTPPAPASTSIPR 180  
Db 136 TNSCIPRIITTKDPINFNTQTATQTTEFTIVSDTSYVASPYSTIPAPTTTPPAPASTSIPR 195  
Qy 181 RKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGG 220  
Db 196 RKKLICVTEVFMETSTMSTETEPFVENKAAAFKNEAAGFGG 235

RESULT 12

US-09-904-462-201  
; Sequence 201, Application US/09904462  
; Patent No. 6878807  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/904,462  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/665,350  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698

APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,736A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-15  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 201  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-904-462-201

Query Match 100.0%; Score 1136; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2,7e-115;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLLVQGSRLAEELSIQVSCRMGITLVSKKANQQLNFTTEAKACRLGLSLAGKQDVE 60  
Db 16 TTRLLVQGSRLAEELSIQVSCRMGITLVSKKANQQLNFTTEAKACRLGLSLAGKQDVE 75  
Qy 61 TALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120  
Db 76 TALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135  
Qy 121 TNSCIPEIITTKDPIFNTQTATQTEFIVSDTYSVASPYSTIPAPTTTPAPASTSIPR 180  
Db 136 TNSCIPEIITTKDPIFNTQTATQTEFIVSDTYSVASPYSTIPAPTTTPAPASTSIPR 195  
Qy 181 RKKLICVTEVEMETSTWSTETEPFVKNKAAPKNEAGFGG 220  
Db 196 RKKLICVTEVEMETSTWSTETEPFVKNKAAPKNEAGFGG 235

RESULT 13

US-09-902-736A-201  
Sequence 201, Application US/09902736A  
Patent No. 6894148  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.

Query Match 100.0%; Score 1136; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2,7e-115;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLLVQGSRLAEELSIQVSCRMGITLVSKKANQQLNFTTEAKACRLGLSLAGKQDVE 60  
Db 16 TTRLLVQGSRLAEELSIQVSCRMGITLVSKKANQQLNFTTEAKACRLGLSLAGKQDVE 75  
Qy 61 TALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120  
Db 76 TALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135

QY 121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR 180  
Db 136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR 195  
QY 181 RKKLICVTEVFMETSTMSTETETPPFVENKAAAFKNEAAGFGG 220  
Db 196 RKKLICVTEVFMETSTMSTETETPPFVENKAAAFKNEAAGFGG 235

RESULT 14

US-09-906-722A-201  
; Sequence 201, Application US/09906722A  
; Patent No. 6946262  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: GNE.1618P2C61  
; CURRENT APPLICATION NUMBER: US/09/906,722A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-09-906-722A-201

Query Match 100.0%; Score 1136; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.7e-115;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTRLLVQGSLEAEELSIQVSCRIMGITILVSKKANQQLNFTTEAKEACRLGLSLAGKQOVE 60  
Db 16 TTRLLVQGSLEAEELSIQVSCRIMGITILVSKKANQQLNFTTEAKEACRLGLSLAGKQOVE 75  
QY 61 TALKASPETCSYGVWGDGFVVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120  
Db 76 TALKASPETCSYGVWGDGFVVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 135  
QY 121 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR 180  
Db 136 TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR 195  
QY 181 RKKLICVTEVFMETSTMSTETETPPFVENKAAAFKNEAAGFGG 220  
Db 196 RKKLICVTEVFMETSTMSTETETPPFVENKAAAFKNEAAGFGG 235

RESULT 15

US-09-949-016-7765  
; Sequence 7765, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7765  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7765

Query Match 100.0%; Score 1136; DB 2; Length 344;  
Best Local Similarity 100.0%; Pred. No. 3e-115;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTRLLVQGSLEAEELSIQVSCRIMGITILVSKKANQQLNFTTEAKEACRLGLSLAGKQOVE 60  
Db 38 TTRLLVQGSLEAEELSIQVSCRIMGITILVSKKANQQLNFTTEAKEACRLGLSLAGKQOVE 97  
QY 61 TALKASPETCSYGVWGDGFVVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 120  
Db 98 TALKASPETCSYGVWGDGFVVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTW 157

Qy 121 TNSCIPEIITTKDPIFNQTQTTFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 180  
Db |||||  
Qy 158 TNSCIPEIITTKDPIFNQTQTTFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR 217  
Db |||||  
Qy 181 RKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGG 220  
Db |||||  
Qy 218 RKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGG 257  
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Job time : 22.566 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:07:29 ; Search time 13.7123 Seconds  
(without alignments)  
2147.153 Million cell updates/sec

Title: US-10-063-510-6\_COPY\_17\_322

Perfect score: 1575

Sequence: 1 TRLVQGLRAEELSIQVSC.....NPESKSPSKTIVRCLEAEV 306

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR\_80.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	229	14.5	363	2 A37009	CD44 homolog membr
2	222.5	14.1	362	2 A30901	lymphocyte adhesio
3	222	14.1	365	2 A34424	CD44 membrane glyco
4	217.5	13.8	362	2 A35616	T-cell surface glyco
5	217	13.8	503	2 B38745	cell adhesion mole
6	208.5	13.2	366	2 A53286	cell-surface glyco
7	205	13.0	361	2 JH0417	cell adhesion mole
8	202	12.8	351	2 S45305	CD44 antigen precu
9	202	12.8	742	2 A47195	lymphocyte homing
10	199.5	12.7	426	2 JH0518	lymphocyte homing
11	199.5	12.7	493	2 S13530	CD44E protein, epi
12	198	12.6	395	2 I77371	CD44R5 - human
13	196.5	12.5	699	2 I37369	epican - human
14	186	11.8	359	2 S24240	lymphocyte surface
15	148.5	9.4	2109	1 I50431	aggreccan precursor
16	145.5	9.2	3562	2 A47171	chondroitin sulfat
17	145	9.2	277	2 A41735	hyaluronate-bindin
18	145	9.2	1069	2 T42681	hypothetical prote
19	144	9.1	275	2 JC6506	tumor necrosis fac
20	143	9.1	2327	2 T42630	aggreccan - bovine
21	137	8.7	276	2 A47290	TSG-6 homolog p84
22	131.5	8.3	2124	2 A28452	proteoglycan core
23	131	8.3	2132	1 A55182	aggreccan precursor
24	130.5	8.3	883	2 S57653	brevican precursor
25	130.5	8.3	883	2 S49126	brevican precursor
26	130.5	8.3	2415	1 A39086	aggreccan precursor
27	128.5	8.2	912	2 A54423	aggreccan precursor
28	121	7.7	1340	2 A39808	proteoglycan core
29	116	7.4	2397	1 A55535	versican precursor

aggreccan - pig (fr  
versican precursor  
versican precursor  
neurocan precursor  
brain link protein  
glycoprotein 1 pre  
dihydropolamide a  
LDL receptor 2 pre  
versican precursor  
proteoglycan link  
hypothetical prote  
hypothetical prote  
proteoglycan link  
brevican precursor  
proteoglycan link  
neurocan - mouse  
chondroitin sulfat  
versican - pig-tai  
proteoglycan link  
proteoglycan link  
hypothetical prote  
hypothetical prote  
hypothetical prote  
brevican precursor  
neural cell adhesi  
zonadhesin - mouse  
hypothetical prote  
LDL receptor 1 pre  
hypothetical prote  
chitinase (EC 3.2.  
hypothetical prote  
hypothetical prote  
neural cell adhesi  
neurexin III-alpha  
hypothetical prote  
neurofascin - chic  
hypothetical prote  
period clock prote  
mucin 5AC (clone J  
hypothetical prote  
hypothetical prote  
BUD3 protein - yea  
hypothetical prote  
CYC8 protein - yea  
acta protein precu  
actin-assembly ind  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
chaperonin 60 - cu  
E2 protein - human  
glucan 1,4-alpha-g  
96K lysosomal memb  
hypothetical prote  
protein-tyrosine k  
salivary glue prot  
lysosome-associate  
endo-1,4-beta-xyla  
probable zinc meta  
hypothetical prote  
hypothetical prote  
MID2 protein - yea  
hypothetical prote  
hypothetical prote  
endoglucanase C (E  
hypothetical prote  
hypothetical prote  
hypothetical prote  
major merozoite su

103	88	5.6	3507	2	T34513	hypotheical prote	176	82.5	5.2	569	2	B84470	Mutator-like trans
104	88	5.6	3570	2	T45025	mucin MUC5B, trach	177	82.5	5.2	726	2	S67044	Nfil protein - yea
105	87.5	5.6	825	2	T48431	hypotheical prote	178	82.5	5.2	825	2	S62042	probable membrane
106	87.5	5.6	1085	2	T40476	Ca(2+)-sensing rec	179	82.5	5.2	871	2	T43427	pob1 protein - fis
107	87.5	5.6	1091	1	IJCHNL	neural cell adhesi	180	82.5	5.2	1206	2	S24407	formin isoform IV
108	87.5	5.6	1802	2	S69703	HK1 protein precu	181	82.5	5.2	1407	2	T18381	latrophilin-2 (spl
109	87	5.5	235	2	PC2022	mucin like protein	182	82.5	5.2	1420	2	T18385	latrophilin-2 (spl
110	87	5.5	752	2	E72616	hypotheical prote	183	82.5	5.2	1422	2	T18383	latrophilin-2, spl
111	87	5.5	1016	2	H71460	probable outer mem	184	82.5	5.2	1435	2	T18387	latrophilin-2 (spl
112	87	5.5	1506	2	T30886	integumentary muc	185	82.5	5.2	1450	2	T18382	latrophilin-2 (spl
113	87	5.5	1537	2	S53465	floculation prote	186	82.5	5.2	1460	2	D81675	polymorphic membra
114	86.5	5.5	400	1	A28172	spasmolysin precu	187	82.5	5.2	1463	2	T18386	latrophilin-2 (spl
115	86.5	5.5	461	2	T22946	hypotheical prote	188	82.5	5.2	1465	2	T18384	latrophilin-2 (spl
116	86.5	5.5	503	2	S63257	probable membrane	189	82.5	5.2	1468	2	SI1515	formin - mouse
117	86.5	5.5	550	2	T29919	hypotheical prote	190	82.5	5.2	1478	2	T18388	latrophilin-2 (spl
118	86.5	5.5	681	2	S33316	structural protein	191	82.5	5.2	2311	1	TVCHSR	kinase-related pro
119	86.5	5.5	740	1	FOLJHD	gag polyprotein -	192	82	5.2	389	2	T33340	hypotheical prote
120	86.5	5.5	768	2	T00073	hypotheical prote	193	82	5.2	476	2	A46118	myosin-binding pro
121	86.5	5.5	1777	2	T34369	hypotheical prote	194	82	5.2	544	2	T15175	hypotheical prote
122	86.5	5.5	2616	2	A37096	nudel protein prec	195	82	5.2	577	2	G89430	protein K02E2.3 [i
123	86	5.5	1785	2	A45546	major merzoite su	196	82	5.2	584	2	T19061	hypotheical prote
124	85.5	5.4	549	2	S29316	chaperonin 60 - cu	197	82	5.2	693	2	T19551	mucin-like protein
125	85.5	5.4	649	2	T04606	protein kinase hom	198	82	5.2	720	2	S51340	nuclcoporin NUP2 -
126	85.5	5.4	786	2	T16509	hypotheical prote	199	82	5.2	894	2	B96557	probable receptor
127	85.5	5.4	895	2	T02597	Mutator-like trans	200	82	5.2	911	2	E86438	hypotheical prote
128	85	5.4	265	2	T33695	hypotheical prote	201	82	5.2	926	2	T38198	COP11 coated vesic
129	85	5.4	576	2	S59829	hypotheical prote	202	82	5.2	973	2	A97522	ribonuclease E, RN
130	85	5.4	627	2	G86860	serine/threonine p	203	82	5.2	977	2	AC2741	major acidic nucle
131	85	5.4	761	2	T00940	hypotheical prote	204	82	5.2	1023	2	JC4013	hypothetical prote
132	85	5.4	989	2	T47503	hypotheical prote	205	82	5.2	1083	2	S59780	hypotheical prote
133	85	5.4	990	2	I51618	nucleolar phosphop	206	82	5.2	1127	2	T25804	hypotheical prote
134	85	5.4	1162	2	T15557	hypotheical prote	207	82	5.2	1672	2	C81675	polymorphic membra
135	85	5.4	1779	2	T31085	xy lanase - Caldice	208	82	5.2	2738	2	E88320	protein P07A11.6 [
136	84.5	5.4	463	2	B82001	probable amino-aci	209	82	5.2	26926	1	I38344	titin, cardiac mus
137	84.5	5.4	493	2	JC5486	membrane glycoprot	210	81.5	5.2	235	2	T47379	hypotheical prote
138	84.5	5.4	562	2	A57088	nuclcoporin-like p	211	81.5	5.2	386	2	B97212	protein containing
139	84.5	5.4	658	2	T39500	serine/threonine-s	212	81.5	5.2	463	2	B81228	sodium/alanine sym
140	84.5	5.4	658	2	S60170	protein kinase pak	213	81.5	5.2	636	2	S63131	probable membrane
141	84.5	5.4	709	2	T28712	hypotheical prote	214	81.5	5.2	687	2	A40711	RNA polymerase II
142	84.5	5.4	1102	2	S65235	probable membrane	215	81.5	5.2	860	2	AG1612	RNA mismatch repai
143	84.5	5.4	1161	2	S57180	probable membrane	216	81.5	5.2	869	2	T22422	hypothetical prote
144	84.5	5.4	2481	2	D90011	FatB protein [lipo	217	81.5	5.2	1151	2	T18297	zinc-finger protei
145	84	5.3	262	2	S76772	hypotheical prote	218	81.5	5.2	1212	2	T13804	shs protein - frui
146	84	5.3	335	2	A36667	AP2-containing DNA	219	81.5	5.2	1216	2	F88473	protein F40H6.5 [i
147	84	5.3	420	2	A82426	hypotheical prote	220	81.5	5.2	1445	1	A48148	protein-tyrosine-p
148	84	5.3	426	2	B53580	neurexin III beta	221	81.5	5.2	1513	2	T23681	hypothetical prote
149	84	5.3	543	2	S35047	mucin JUL7 - human	222	81.5	5.2	2282	2	T42717	DNA-binding protei
150	84	5.3	636	1	VCVWF5	env polyprotein -	223	81.5	5.2	3175	1	RRWVEV	genome polyprotein
151	84	5.3	662	2	A45155	mucin FIM-C.1 - Af	224	81	5.1	339	2	T25562	hypotheical prote
152	84	5.3	793	2	AH1094	probable peptidogl	225	81	5.1	369	2	T01196	transcription fact
153	84	5.3	996	2	J50237	apolipoprotein E r	226	81	5.1	422	1	BMRT2Y	synaptotagmin II -
154	84	5.3	1075	2	S48992	floculation prote	227	81	5.1	683	2	T10720	NADPH-ferrihemopro
155	84	5.3	1331	2	A48954	mannan endo-1,4-be	228	81	5.1	683	2	E86358	Fl2K8.13 protein -
156	84	5.3	1362	2	A75207	amylopullulanase p	229	81	5.1	911	2	S46497	aspartate kinase (
157	84	5.3	1832	2	T31113	mucin-like glycopr	230	81	5.1	967	2	S66852	hypothetical prote
158	84	5.3	3020	2	A3932	mucin 2 precursor,	231	81	5.1	1047	2	A55617	masquerade precurs
159	83.5	5.3	216	2	I51920	mucin - rhesus mac	232	81	5.1	1128	2	A49960	bud emergence prot
160	83.5	5.3	279	2	S53363	mucin 5AC (clone J	233	81	5.1	1169	2	S38181	floculation prote
161	83.5	5.3	446	2	T45525	WSC4 homolog [lipo	234	81	5.1	1367	2	S51959	hypothetical prote
162	83.5	5.3	1043	2	F97302	hypotheical prote	235	81	5.1	1609	2	S25345	probable membrane
163	83.5	5.3	1286	2	A88396	protein M01E10.2 [	236	81	5.1	1726	2	A39401	merozoite surface
164	83	5.3	221	2	S33649	ribosomal protein	237	81	5.1	6642	2	T29757	protein UNC-89 - C
165	83	5.3	409	2	S44346	RAD23 protein homo	238	80.5	5.1	148	1	S07723	immediate-early se
166	83	5.3	463	2	T38444	hypotheical prote	239	80.5	5.1	391	1	SI15617	E2 protein - human
167	83	5.3	605	2	S48940	hypotheical prote	240	80.5	5.1	441	2	T31482	hypothetical prote
168	83	5.3	737	1	S64767	probable serine/th	241	80.5	5.1	543	2	T22585	hypothetical prote
169	83	5.3	797	1	VBEX1	Glycoprotein X pre	242	80.5	5.1	552	2	T34446	hypothetical prote
170	83	5.3	866	2	T45462	membrane glycoprot	243	80.5	5.1	595	2	A42086	CD30 antigen precu
171	83	5.3	867	2	T45463	membrane glycoprot	244	80.5	5.1	742	2	T33514	hypothetical prote
172	83	5.3	977	2	T16232	hypotheical prote	245	80.5	5.1	798	2	T34248	hypothetical prote
173	82.5	5.2	383	1	SI5624	E2 protein - human	246	80.5	5.1	1159	1	A44280	inner layer protei
174	82.5	5.2	416	2	B84030	stage VI sporulati	247	80.5	5.1	2225	2	T26063	hypothetical prote
175	82.5	5.2	456	1	H64099	probable amino aci	248	80	5.1	1133	2	S67294	hypothetical prote

249	80	5.1	177	1	RGBYGI	regulatory protein	322	78.5	5.0	1467	2	T17160
250	80	5.1	345	2	A21776	hypothetical prote	323	78.5	5.0	1478	2	T17185
251	80	5.1	415	2	AE2237	hypothetical prote	324	78.5	5.0	1487	2	T14324
252	80	5.1	451	2	S71754	cellular hepatitis	325	78.5	5.0	1876	2	E97944
253	80	5.1	468	2	A55116	vacuolar Arpase (E	326	78	5.0	253	2	S67719
254	80	5.1	650	2	T41681	probable serine/th	327	78	5.0	260	2	AG2238
255	80	5.1	667	2	A40713	cylicin I - bovine	328	78	5.0	266	2	T30919
256	80	5.1	688	2	T18263	S-layer protein -	329	78	5.0	287	2	T12471
257	80	5.1	702	2	T34313	hypothetical prote	330	78	5.0	293	2	G87018
258	80	5.1	725	2	A41258	a-agglutinin core	331	78	5.0	372	2	T48660
259	80	5.1	738	2	T44194	hypothetical prote	332	78	5.0	373	2	F81333
260	80	5.1	881	2	S56032	probable membrane	333	78	5.0	425	2	T48724
261	80	5.1	1013	1	S04200	NAD ADP-ribosyltra	334	78	5.0	434	2	B84684
262	80	5.1	1348	2	S27812	probable epidermal	335	78	5.0	521	2	S69559
263	79.5	5.0	152	2	T15170	hypothetical prote	336	78	5.0	530	2	A45690
264	79.5	5.0	165	2	A27195	histone H1 - Tetra	337	78	5.0	627	1	VCVM2
265	79.5	5.0	194	2	F72525	hypothetical prote	338	78	5.0	655	2	T30044
266	79.5	5.0	354	2	T46740	microfilarial shea	339	78	5.0	786	1	A47547
267	79.5	5.0	461	1	A35356	tumor necrosis fac	340	78	5.0	1050	2	T31853
268	79.5	5.0	510	2	B72007	conserved hypotet	341	78	5.0	1337	2	T30291
269	79.5	5.0	510	2	A86618	CT861 hypothetical	342	78	5.0	1360	2	T33922
270	79.5	5.0	534	2	G84713	hypothetical prote	343	78	5.0	1442	1	B48148
271	79.5	5.0	554	2	JW0094	neurofilament prot	344	78	5.0	1634	2	T26517
272	79.5	5.0	580	2	T20716	hypothetical prote	345	78	5.0	1723	2	H86557
273	79.5	5.0	693	2	T25878	hypothetical prote	346	78	5.0	1723	2	E72067
274	79.5	5.0	827	2	T04789	hypothetical prote	347	78	5.0	1732	2	C81601
275	79.5	5.0	860	2	AC1250	DNA mismatch repa	348	78	5.0	1955	1	AGCH
276	79.5	5.0	998	2	S31735	NAD ADP-ribosyltra	349	78	5.0	1995	2	T08166
277	79.5	5.0	1011	2	T20785	hypothetical prote	350	78	5.0	527	2	T13564
278	79.5	5.0	1021	2	S64506	protein kinase BUB	351	77.5	4.9	396	2	F81330
279	79.5	5.0	1280	2	E95031	alkaline amylopull	352	77.5	4.9	401	2	AG3552
280	79.5	5.0	1365	2	S14871	suppressor two of	353	77.5	4.9	474	1	BMFESY
281	79.5	5.0	2817	2	B97033	uncharacterized pr	354	77.5	4.9	514	2	JQ1317
282	79	5.0	215	2	S26363	histone H1.1 - hum	355	77.5	4.9	519	2	T45764
283	79	5.0	249	2	G84781	hypothetical prote	356	77.5	4.9	526	2	A56573
284	79	5.0	352	2	T51659	myb-related transc	357	77.5	4.9	607	2	S01939
285	79	5.0	359	2	T13478	hypothetical prote	358	77.5	4.9	623	2	T18892
286	79	5.0	410	1	B31959	lysosome-associate	359	77.5	4.9	816	2	S64439
287	79	5.0	410	1	JC4317	lysosome-associate	360	77.5	4.9	860	2	JC4566
288	79	5.0	534	2	T39903	serine-rich protel	361	77.5	4.9	906	2	G90281
289	79	5.0	575	2	T21775	hypothetical prote	362	77.5	4.9	938	2	A56731
290	79	5.0	611	2	AB1497	internalin protein	363	77.5	4.9	975	2	T08606
291	79	5.0	710	2	S67098	probable membrane	364	77.5	4.9	1127	2	E86386
292	79	5.0	739	2	T49456	hypothetical prote	365	77.5	4.9	1156	2	T23748
293	79	5.0	761	2	A96810	probable Mutator-1	366	77.5	4.9	1312	2	A97879
294	79	5.0	822	2	JC4076	dextranase (EC 3.2	367	77.5	4.9	1475	2	S42718
295	79	5.0	836	2	S49940	cell division cont	368	77.5	4.9	2761	2	T21064
296	79	5.0	1098	2	T08599	probable transcrip	369	77.5	4.9	3968	2	A44265
297	79	5.0	1849	2	C41859	IgA-specific metal	370	77	4.9	350	2	E75341
298	79	5.0	1904	2	T13256	tail-host specific	371	77	4.9	353	2	S22805
299	78.5	5.0	152	2	T28759	hypothetical prote	372	77	4.9	453	2	F75206
300	78.5	5.0	164	2	I53641	mucin SAC - human	373	77	4.9	553	2	T13894
301	78.5	5.0	232	2	A60095	larval glue protel	374	77	4.9	598	2	T22610
302	78.5	5.0	294	2	A37232	mucin, tracheal (A	375	77	4.9	623	2	A48123
303	78.5	5.0	314	1	HNZVW	hemagglutinin prec	376	77	4.9	639	2	T33166
304	78.5	5.0	314	1	JQ1793	hemagglutinin prec	377	77	4.9	669	1	VCWEK
305	78.5	5.0	322	2	A53715	apomucin precursor	378	77	4.9	734	2	B42680
306	78.5	5.0	387	2	A53586	albumin-binding pr	379	77	4.9	750	2	T42614
307	78.5	5.0	413	2	S55890	plasma protein rec	380	77	4.9	771	2	JC7388
308	78.5	5.0	423	2	S69583	hypothetical prote	381	77	4.9	861	2	T23810
309	78.5	5.0	542	2	S64030	probable membrane	382	77	4.9	892	2	T09193
310	78.5	5.0	591	1	WMBPQ2	gene P2 protein -	383	77	4.9	897	2	S50550
311	78.5	5.0	599	2	S46630	hypothetical prote	384	77	4.9	977	2	S49004
312	78.5	5.0	688	2	B42161	GMP-gated cation	385	77	4.9	1237	2	T14633
313	78.5	5.0	815	2	JG0197	myosin-light-chain	386	77	4.9	1401	2	T30247
314	78.5	5.0	825	2	T29634	hypothetical prote	387	77	4.9	1513	2	A54895
315	78.5	5.0	919	1	PKZP1P	H+-exporting ATPas	388	77	4.9	2187	2	T30826
316	78.5	5.0	1011	1	JH0581	NAD ADP-ribosyltra	389	76.5	4.9	284	2	T42367
317	78.5	5.0	1356	2	T16754	hypothetical prote	390	76.5	4.9	349	2	T43457
318	78.5	5.0	1420	2	T17158	CL2AB protein - ra	391	76.5	4.9	382	2	S27388
319	78.5	5.0	1435	2	T46611	CL2BB protein - ra	392	76.5	4.9	391	2	C69673
320	78.5	5.0	1452	2	T17157	CL2AA protein - ra	393	76.5	4.9	421	2	A60058
321	78.5	5.0	1463	2	T17159	CL2AC protein - ra	394	76.5	4.9	433	2	H84120
						CL2BA protein - ra						
						CL2BC protein - ra						
						alpha-latrotoxin r						
						zinc metalloprotei						
						hypothetical prote						
						hypothetical prote						
						hypothetical prote						
						hypothetical prote						
						probable membrane						
						heat shock protein						
						Chaperone DnaJ Cj1						
						hypothetical prote						
						hypothetical prote						
						hypothetical prote						
						transactivator EBN						
						env polyprotein -						
						hypothetical prote						
						serine proteinase						
						hypothetical prote						
						dextranase - Strep						
						hypothetical prote						
						protein-tyrosine-p						
						hypothetical prote						
						polymorphic membra						
						polymorphic membra						
						agrin precursor -						
						probable membrane						
						microtubule-associ						
						probable MFS trans						
						branched-chain ami						
						synaptotagmin - fr						
						activin receptor p						
						hypothetical prote						
						nuclear pore compl						
						hypothetical prote						
						hypothetical prote						
						hypothetical prote						
						chitinase (EC 3.2.						
						conserved hypotet						
						chromatin assembly						
						protein phosphatas						
						probable mutator-1						
						hypothetical prote						
						beta-N-acetylhexos						
						nuclear pore compl						
						hypothetical prote						
						trithorax homolog						
						peptidyl-prolyl ci						
						env polyprotein -						
						maltose-binding pe						
						hypothetical prote						
						hypothetical prote						
						cell cycle regulat						
						hypothetical prote						
						env polyprotein -						
						nucleolus-cytoplas						
						probable envelope						
						M83 protein - huma						
						hypothetical prote						
						ataxin 7 - human						
						SINI-associated pr						
						tyrosine kinase Mp						
						hypothetical prote						
						Werner syndrome pr						
						mucin 2, intestina						
						nascent polypeptid						



395	76.5	4.9	505	2	B46629	mucin 6, gastric (	468	75.5	4.8	482	2	AG1147	P60 extracellular
396	76.5	4.9	518	2	G98961	protein F59A7.8 [i	469	75.5	4.8	484	2	A41487	protein P60 precur
397	76.5	4.9	542	2	I39540	chitinase (EC 3.2.	470	75.5	4.8	496	2	B41322	N-acetylmuramoyl-l
398	76.5	4.9	549	2	S04840	lg heavy chain pre	471	75.5	4.8	511	1	VGB8F4	glycoprotein C - h
399	76.5	4.9	640	1	VCVMM1	env polyprotein -	472	75.5	4.8	609	2	G87496	peptidase, M23/M37
400	76.5	4.9	651	2	CS6653	membrane glycoprot	473	75.5	4.8	639	2	T13151	adaptor protein CM
401	76.5	4.9	718	2	T29708	hypothetical prote	474	75.5	4.8	665	2	G97213	probable membrane-
402	76.5	4.9	727	2	A88131	protein F10G7.9 [i	475	75.5	4.8	709	2	T32089	hypothetical prote
403	76.5	4.9	749	2	B86403	probable mutator-1	476	75.5	4.8	778	2	T43223	hypothetical prote
404	76.5	4.9	803	2	T00502	probable receptor-	477	75.5	4.8	780	2	A48143	HF-1 regulatory el
405	76.5	4.9	806	2	E69424	hypothetical prote	478	75.5	4.8	963	2	T40290	hypothetical prote
406	76.5	4.9	990	2	T16554	hypothetical prote	479	75.5	4.8	1131	2	T41144	hypothetical serin
407	76.5	4.9	1154	1	VGIIIB	E2 glycoprotein pr	480	75.5	4.8	1166	2	S37592	probable tumor sup
408	76.5	4.9	1379	2	T45119	F1M protein [impor	481	75.5	4.8	1235	2	T13710	protein-tyrosine k
409	76.5	4.9	1946	2	J06032	lactocepin (EC 3.4	482	75.5	4.8	1237	2	E86457	probable RNA helic
410	76.5	4.9	3869	2	A48205	All-1 protein +GTE	483	75.5	4.8	1473	2	T31422	C-terminal domain-
411	76.5	4.9	5037	2	B35041	ryanodine receptor	484	75.5	4.8	1655	2	T32633	hypothetical prote
412	76	4.8	167	2	A33532	mucin SMUC-40 - hu	485	75.5	4.8	1737	2	A59235	unconventional myo
413	76	4.8	172	2	T21753	hypothetical prote	486	75.5	4.8	1881	2	H95076	zinc metalloprotei
414	76	4.8	243	2	B41710	promastigote surfa	487	75.5	4.8	2526	2	T20531	hypothetical prote
415	76	4.8	340	2	AH0940	probable ABC trans	488	75.5	4.8	3176	2	CGHU3A	collagen alpha 3 (V
416	76	4.8	356	2	D88979	protein F37B4.9 [i	489	75	4.8	94	2	S53365	mucin 5AC (clone C
417	76	4.8	368	2	S36564	E2 protein - human	490	75	4.8	128	2	T05035	hypothetical prote
418	76	4.8	378	2	A12180	hypothetical prote	491	75	4.8	205	2	S55670	hypothetical prote
419	76	4.8	382	2	B88561	protein F58A4.7b [i	492	75	4.8	248	2	AF1914	carbon dioxide con
420	76	4.8	384	2	A41710	promastigote surfa	493	75	4.8	256	2	T09034	hypothetical prote
421	76	4.8	389	2	E97305	NADH-dependent but	494	75	4.8	310	1	H71054	hypothetical prote
422	76	4.8	389	2	A47013	butanol dehydrogen	495	75	4.8	313	2	AH0734	probable bacteriop
423	76	4.8	499	2	T47722	probable protein k	496	75	4.8	388	2	T16861	hypothetical prote
424	76	4.8	515	2	AD1162	flagellar motor sw	497	75	4.8	390	2	A72108	hypothetical prote
425	76	4.8	532	2	T28784	hypothetical prote	498	75	4.8	390	2	E86514	hypothetical prote
426	76	4.8	536	2	T37544	hypothetical serin	499	75	4.8	418	2	T16713	hypothetical prote
427	76	4.8	539	2	T02512	hypothetical prote	500	75	4.8	425	1	A26431	nerve growth facto
428	76	4.8	549	2	T49298	hypothetical prote	501	75	4.8	453	2	C40511	hypothetical prote
429	76	4.8	592	2	T16725	hypothetical prote	502	75	4.8	475	2	E84745	probable splicing
430	76	4.8	615	2	T47395	hypothetical prote	503	75	4.8	477	2	T32938	hypothetical prote
431	76	4.8	699	2	I38073	nucleolar phosphop	504	75	4.8	481	2	T38149	pre-mrna splicing
432	76	4.8	700	2	A54641	interspersed repea	505	75	4.8	528	2	S69589	hypothetical prote
433	76	4.8	738	2	T44007	hypothetical prote	506	75	4.8	554	2	A56596	chitinase (EC 3.2.
434	76	4.8	763	2	T08929	hypothetical prote	507	75	4.8	604	2	T37994	probable splicing
435	76	4.8	766	2	B85440	receptor kinase-li	508	75	4.8	607	2	S63395	probable membrane
436	76	4.8	824	2	T33923	hypothetical prote	509	75	4.8	651	2	T16450	hypothetical prote
437	76	4.8	929	2	G72677	hypothetical prote	510	75	4.8	679	2	T19703	hypothetical prote
438	76	4.8	940	2	AD1374	internalin protein	511	75	4.8	739	2	I56187	transcription fact
439	76	4.8	960	1	JN0677	protein-tyrosine k	512	75	4.8	778	2	T45221	DNA damage checkpo
440	76	4.8	967	2	G86229	hypothetical prote	513	75	4.8	796	2	E96654	hypothetical prote
441	76	4.8	994	1	MNWVM	nonstructural prot	514	75	4.8	858	1	IJRTNC	neural cell adhesi
442	76	4.8	1014	1	A29725	NAD ADP-ribosyltra	515	75	4.8	904	2	T03806	hypothetical prote
443	76	4.8	1041	2	H71617	SERA antigen/papai	516	75	4.8	916	2	T20909	hypothetical prote
444	76	4.8	1046	2	T29776	hypothetical prote	517	75	4.8	940	2	D89723	protein F39B8.1b [
445	76	4.8	1263	2	AH2011	heterocyst glycoli	518	75	4.8	945	2	T21998	hypothetical prote
446	76	4.8	1348	2	A43917	probable epidermal	519	75	4.8	993	2	F97717	hypothetical prote
447	76	4.8	1401	2	T17452	Werner syndrome pr	520	75	4.8	1048	1	S61388	dotA protein - Leg
448	76	4.8	1422	2	T42636	protein-tyrosine-p	521	75	4.8	1118	2	A48292	mutin, tracheobron
449	76	4.8	1438	2	B71610	Wp40 WEB-1 homolo	522	75	4.8	1253	2	T18528	probable pyruvate
450	76	4.8	1489	2	G71406	probable retroviri	523	75	4.8	1419	2	T30531	agglutinin-like ad
451	76	4.8	1513	2	T44045	hypothetical prote	524	75	4.8	1741	2	T13610	parallel sister ch
452	76	4.8	1890	2	T04556	hypothetical prote	525	75	4.8	1768	2	T13349	collagen alpha 1(V
453	76	4.8	2570	2	T17451	fimbriae-associate	526	75	4.8	1838	1	CGHUIV	hypothetical prote
454	75.5	4.8	260	1	G59223	molybdate-binding	527	75	4.8	1979	2	C71622	hypothetical prote
455	75.5	4.8	261	2	T30170	hypothetical prote	528	75	4.8	3375	2	T19821	hypothetical prote
456	75.5	4.8	273	2	T44657	protein GP80 [impo	529	74.5	4.7	148	2	S50653	hypothetical prote
457	75.5	4.8	319	1	A35163	carbonate dehydrat	530	74.5	4.7	211	2	D28046	TUB8 protein - pot
458	75.5	4.8	321	2	T26152	hypothetical prote	531	74.5	4.7	254	2	D88560	protein F58A4.1 [i
459	75.5	4.8	343	2	T40306	hypothetical prote	532	74.5	4.7	262	2	T33597	myb-related trans
460	75.5	4.8	348	1	B46216	transcription fact	533	74.5	4.7	276	2	T51685	hypb-related trans
461	75.5	4.8	387	2	A86302	hypothetical prote	534	74.5	4.7	281	2	T49537	hypothetical prote
462	75.5	4.8	412	2	E97279	TFR-repeat-contain	535	74.5	4.7	294	2	AI2016	hypothetical prote
463	75.5	4.8	430	1	A46216	transcription fact	536	74.5	4.7	310	1	IAZQ31	300K antigen Ag231
464	75.5	4.8	435	2	S40993	hypothetical prote	537	74.5	4.7	321	2	T50966	hypothetical prote
465	75.5	4.8	443	2	D72393	NADH oxidase - The	538	74.5	4.7	382	2	T25280	hypothetical prote
466	75.5	4.8	445	2	I38521	inwardly rectifyin	539	74.5	4.7	396	2	T50229	probable transmem
467	75.5	4.8	448	2	S17370	DNA-binding protei	540	74.5	4.7	407	2	T26938	hypothetical prote

541	74.5	4.7	429	2	S29044	endoglucanase A pr	614	73.5	4.7	345	2	D91201	type III secretion
542	74.5	4.7	432	2	T08771	hypothetical prote	615	73.5	4.7	345	2	H86047	escU (imported) -
543	74.5	4.7	478	2	A32555	major merozoite su	616	73.5	4.7	358	2	AD2378	hypothetical prote
544	74.5	4.7	482	2	T22754	hypothetical prote	617	73.5	4.7	371	2	S20075	promastigote surfa
545	74.5	4.7	520	2	S14598	E2 glycoprotein -	618	73.5	4.7	376	2	T48245	hypothetical prote
546	74.5	4.7	531	2	S09859	hypothetical prote	619	73.5	4.7	381	2	E69862	hypothetical prote
547	74.5	4.7	551	2	S52287	urbain - silkworm	620	73.5	4.7	397	2	G69287	p2B/LAMP-1 precurs
548	74.5	4.7	636	2	T23232	hypothetical prote	621	73.5	4.7	405	2	A60534	P2B/LAMP-1 precurs
549	74.5	4.7	713	2	J80230	NADPH-cytochrome p	622	73.5	4.7	445	2	A54852	potassium rectifie
550	74.5	4.7	802	2	T21315	hypothetical prote	623	73.5	4.7	447	2	A39321	mucin - rat (fragm
551	74.5	4.7	808	2	T23129	hypothetical prote	624	73.5	4.7	457	2	T20884	hypothetical prote
552	74.5	4.7	862	2	B36786	hypothetical prote	625	73.5	4.7	458	2	T31631	hypothetical prote
553	74.5	4.7	884	2	AB3166	ATP-dependent DNA	626	73.5	4.7	459	2	I48854	gene murine tumour
554	74.5	4.7	998	2	S37627	protein-tyrosine k	627	73.5	4.7	484	1	A24994	cellulose 1,4-beta
555	74.5	4.7	1388	2	A53317	collagen alpha 1(X)	628	73.5	4.7	511	1	VG8E1K	glycoprotein C - h
556	74.5	4.7	1595	2	T31082	endo-1,4-beta-xyla	629	73.5	4.7	542	2	T19952	hypothetical prote
557	74.5	4.7	1630	2	A53577	ascites siialoglyco	630	73.5	4.7	550	1	VG1HD6	E2 glycoprotein pr
558	74.5	4.7	1902	2	C97702	cell surface anti	631	73.5	4.7	555	2	T26413	hypothetical prote
559	74.5	4.7	1965	2	T33216	hypothetical prote	632	73.5	4.7	569	2	A46462	T cell activation
560	74.5	4.7	2688	2	I49477	alpha-A-crystallin	633	73.5	4.7	601	2	H90270	hypothetical prote
561	74.5	4.7	3828	2	T13857	trithorax protein	634	73.5	4.7	603	2	T39866	hypothetical prote
562	74.5	4.7	3944	2	T19997	hypothetical prote	635	73.5	4.7	626	2	AB1328	probable peptidogl
563	74	4.7	147	2	S09762	hypothetical prote	636	73.5	4.7	654	2	T33044	hypothetical prote
564	74	4.7	223	2	T21930	hypothetical prote	637	73.5	4.7	696	2	G81262	probable integral
565	74	4.7	257	1	MGN2BR	major surface glyc	638	73.5	4.7	708	2	F87245	penicillin-binding
566	74	4.7	264	2	A49149	mesoderm developme	639	73.5	4.7	713	2	T44447	neuregulin-3 limpo
567	74	4.7	286	2	S44835	F54H12.3 protein -	640	73.5	4.7	756	2	JC5886	signaling mediator
568	74	4.7	317	2	C85432	hypothetical prote	641	73.5	4.7	819	2	B95136	conserved domain p
569	74	4.7	332	2	T31928	hypothetical prote	642	73.5	4.7	901	2	A44825	phosphoprotein, sy
570	74	4.7	339	1	JT0756	group-V allergen i	643	73.5	4.7	905	2	T02205	Lu-ECAM-1 protein
571	74	4.7	339	2	A56274	sulfur-regulated 3	644	73.5	4.7	976	2	H87576	peptidase, M16 fam
572	74	4.7	384	2	T21929	hypothetical prote	645	73.5	4.7	990	2	H88733	protein F3E10.3 (
573	74	4.7	390	2	C97889	UDPglucose 6-dehyd	646	73.5	4.7	1004	2	T38074	hypothetical prote
574	74	4.7	397	2	E97176	N-terminal domain	647	73.5	4.7	1016	2	T19006	ankyrin related pr
575	74	4.7	412	1	AJBORS	argininosuccinate	648	73.5	4.7	1139	1	E64234	hypothetical prote
576	74	4.7	413	2	S28066	sexual differentiation	649	73.5	4.7	1291	2	T22382	cytadherence-acces
577	74	4.7	417	2	T20327	hypothetical prote	650	73.5	4.7	2232	2	T34434	hypothetical prote
578	74	4.7	435	2	AG1028	prepilin (imported	651	73	4.6	188	2	C96593	unknown protein, 9
579	74	4.7	454	2	T02100	hypothetical prote	652	73	4.6	198	2	E71837	protein-export mem
580	74	4.7	540	1	FOVWHL	gag polyprotein -	653	73	4.6	213	2	S43949	histone H1 - mouse
581	74	4.7	575	2	S3484	DNA-binding protei	654	73	4.6	260	2	I50109	gasstrulation prote
582	74	4.7	586	2	S66697	probable membrane	655	73	4.6	288	2	JQ2365	polyprotein - Bean
583	74	4.7	600	2	T06292	hypothetical prote	656	73	4.6	315	1	HNVZVW	hemagglutinin prec
584	74	4.7	621	2	T20307	hypothetical prote	657	73	4.6	316	2	G86333	hypothetical prote
585	74	4.7	665	1	VCWVKA	env polyprotein pr	658	73	4.6	327	2	S20074	hypothetical prote
586	74	4.7	672	2	T20310	hypothetical prote	659	73	4.6	359	2	S42787	promastigote surfa
587	74	4.7	689	2	B43491	env polyprotein -	660	73	4.6	369	2	E84291	serine/threonine-I
588	74	4.7	731	2	T04455	hypothetical prote	661	73	4.6	422	2	A55417	iron (III) ABC tra
589	74	4.7	739	1	A34873	transcription fact	662	73	4.6	428	1	Q4ECAD	synaptotagmin II -
590	74	4.7	775	2	A32494	transposable eleme	663	73	4.6	441	2	A43555	GAP-43-related pro
591	74	4.7	823	2	G90848	probable exonuclea	664	73	4.6	461	2	T51044	related to spore c
592	74	4.7	852	2	B85706	probable exonuclea	665	73	4.6	469	2	E64456	hypothetical prote
593	74	4.7	852	2	T06310	hypothetical prote	666	73	4.6	486	2	S66097	cell-cycle protein
594	74	4.7	903	2	T00705	N-chimerin homolog	667	73	4.6	486	2	A89927	elastin binding pr
595	74	4.7	1018	2	T40253	hypothetical prote	668	73	4.6	492	1	CHBOA3	gamma-aminobutyric
596	74	4.7	1099	2	G90546	conserved hypotet	669	73	4.6	496	2	E90181	hypothetical prote
597	74	4.7	1104	2	S59310	probable membrane	670	73	4.6	550	2	C75557	hypothetical prote
598	74	4.7	1110	2	I51116	NF-180 - sea lamp	671	73	4.6	558	2	A98199	translocated intlm
599	74	4.7	1115	1	IJMSNL	neural cell adhesi	672	73	4.6	558	2	E86045	probable transloca
600	74	4.7	1159	2	S62562	probable nuclear p	673	73	4.6	600	2	E72027	phosphoenolpyruvat
601	74	4.7	1216	2	B90580	hypothetical prote	674	73	4.6	600	2	A86597	phosphoenolpyruvat
602	74	4.7	1390	2	T14004	trfa protein - eli	675	73	4.6	669	2	A45511	phosphoenolpyruvat
603	74	4.7	1694	2	H64106	IgA-specific metal	676	73	4.6	688	2	A43491	envelope protein -
604	74	4.7	1828	2	A40115	microtubule-associ	677	73	4.6	720	2	T51007	env polyprotein -
605	74	4.7	1938	1	MWKV1	myosin heavy chain	678	73	4.6	728	2	T20561	hypothetical prote
606	74	4.7	2414	2	A54277	transcription adap	679	73	4.6	771	2	T34376	hypothetical prote
607	74	4.7	3224	1	S58884	Ran-binding protei	680	73	4.6	781	2	T49472	hormone-sensitive
608	73.5	4.7	168	2	A31196	prespore-specific	681	73	4.6	814	2	T33140	hypothetical prote
609	73.5	4.7	182	2	T30078	hypothetical prote	682	73	4.6	918	2	A36337	membrane glycoprot
610	73.5	4.7	253	2	T32879	hypothetical prote	683	73	4.6	932	1	VG8EBC	glycoprotein gi pr
611	73.5	4.7	263	2	T38003	hypothetical ser-t	684	73	4.6	958	2	T10679	hypothetical prote
612	73.5	4.7	290	2	S66355	lectin-related sto	685	73	4.6	1016	2	T41720	hypothetical prote
613	73.5	4.7	292	2	S24169	mucin - rat	686	73	4.6	1055	2	H90023	hypothetical prote

687 73 4.6 1071 2 T23237  
688 73 4.6 1256 1 A43829  
689 73 4.6 1320 2 JCS630  
690 73 4.6 1345 2 S46817  
691 73 4.6 1702 2 A41859  
692 73 4.6 1993 2 A41450  
693 73 4.6 2179 1 GNNYH4  
694 73 4.6 2285 2 T12796  
695 73 4.6 2416 2 T13825  
696 73 4.6 2468 2 A83412  
697 73 4.6 2722 2 T20532  
698 72.5 4.6 263 2 I51225  
699 72.5 4.6 314 2 B95034  
700 72.5 4.6 321 2 T26153  
701 72.5 4.6 328 2 S35336  
702 72.5 4.6 382 2 T27058  
703 72.5 4.6 391 2 T32934  
704 72.5 4.6 406 2 T33934  
705 72.5 4.6 415 2 T32490  
706 72.5 4.6 463 1 A36479  
707 72.5 4.6 487 2 S40820  
708 72.5 4.6 498 1 V0XPLM  
709 72.5 4.6 499 2 A12449  
710 72.5 4.6 507 2 S05542  
711 72.5 4.6 511 2 T35194  
712 72.5 4.6 560 2 T32661  
713 72.5 4.6 580 2 B38418  
714 72.5 4.6 610 2 S35049  
715 72.5 4.6 642 2 T39607  
716 72.5 4.6 648 2 PC4395  
717 72.5 4.6 657 2 A82415  
718 72.5 4.6 663 2 T18631  
719 72.5 4.6 687 2 A49636  
720 72.5 4.6 710 2 A39486  
721 72.5 4.6 728 2 F72693  
722 72.5 4.6 729 2 G96559  
723 72.5 4.6 743 2 D86888  
724 72.5 4.6 765 1 T44946  
725 72.5 4.6 896 2 S36326  
726 72.5 4.6 907 1 Q0BE21  
727 72.5 4.6 915 2 S36327  
728 72.5 4.6 944 2 C70839  
729 72.5 4.6 982 2 A53253  
730 72.5 4.6 1016 1 J50428  
731 72.5 4.6 1036 2 S73601  
732 72.5 4.6 1148 2 T09073  
733 72.5 4.6 1152 2 A33183  
734 72.5 4.6 1180 2 E86719  
735 72.5 4.6 1199 2 A40670  
736 72.5 4.6 1219 2 T14578  
737 72.5 4.6 1222 2 T22490  
738 72.5 4.6 1309 1 BVBYP9  
739 72.5 4.6 1312 2 E95006  
740 72.5 4.6 1338 2 S09982  
741 72.5 4.6 1555 2 T18688  
742 72.5 4.6 1635 2 T14075  
743 72.5 4.6 1736 2 F86178  
744 72.5 4.6 1847 2 T18308  
745 72.5 4.6 1973 2 G89608  
746 72.5 4.6 1973 2 T18686  
747 72.5 4.6 2305 2 B96608  
748 72.5 4.6 2305 2 T15571  
749 72.5 4.6 2314 1 A46151  
750 72.5 4.6 2897 2 B48666  
751 72.5 4.6 3069 2 H70656  
752 72.5 4.6 3256 2 A48666  
753 72 4.6 139 2 G98226  
754 72 4.6 139 2 A13059  
755 72 4.6 159 2 F72758  
756 72 4.6 197 2 T33525  
757 72 4.6 199 2 J80351  
758 72 4.6 236 2 T03041  
759 72 4.6 246 2 PC4397

hypothetical prote  
muramidase-release  
TCOF1 protein - mo  
hypothetical prote  
IGA-specific metal  
probable peptidogl  
genome polyprotein  
probable transglyc  
adenomatous polyo  
hypothetical prote  
hypothetical prote  
snail1 protein - z  
dihydroperoxide sy  
hypothetical prote  
transcription fact  
hypothetical prote  
probable integral  
hypothetical prote  
hypothetical prote  
milk fat globule m  
probable permease  
surface glycoprote  
hypothetical prote  
hypothetical prote  
transcriptional in  
hypothetical prote  
jockey protein 1 -  
mucin JER57 - huma  
mucin 3 - human (f  
conserved hypothet  
hypothetical prote  
soluble vascular e  
ABC transporter, b  
probable phosphoe  
hypothetical prote  
penicillin-binding  
transducer protein  
clathrin assembly  
membrane antigen g  
clathrin assembly  
probable mmp13 pro  
microtubule-associ  
NAD ADP-ribosyltra  
protein F200 - Mgc  
splicing factor Si  
microtubule-associ  
hypothetical prote  
nuclear envelope p  
nucleoporin Nup153  
hypothetical prote  
RAD9 protein - yea  
beta-N-acetylhexos  
protein-tyrosine k  
hypothetical prote  
chitinase (EC 3.2.2.  
hypothetical prote  
probable vitelloge  
protein B0272.5 [i  
hypothetical prote  
protein C23F12.1 [i  
hypothetical prote  
protein-tyrosine-p  
cell proliferation  
fatty-acid synthas  
cell proliferation  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
OX40 ligand protei  
hypothetical prote  
mucin 3 T10 - huma

760 72 4.6 282 2 B37994  
761 72 4.6 303 2 S40973  
762 72 4.6 317 1 GEHUS  
763 72 4.6 322 2 G69946  
764 72 4.6 324 2 S36646  
765 72 4.6 330 2 T49644  
766 72 4.6 334 2 T19637  
767 72 4.6 411 2 T03154  
768 72 4.6 428 2 D86003  
769 72 4.6 428 2 F91157  
770 72 4.6 460 2 A84154  
771 72 4.6 468 2 S70297  
772 72 4.6 482 2 A44987  
773 72 4.6 508 2 A33378  
774 72 4.6 509 2 A96563  
775 72 4.6 544 2 S07144  
776 72 4.6 548 1 QPFG  
777 72 4.6 576 2 T38293  
778 72 4.6 587 2 S38634  
779 72 4.6 592 2 D70863  
780 72 4.6 622 2 A90570  
781 72 4.6 674 2 S74506  
782 72 4.6 677 2 T00369  
783 72 4.6 679 2 S64258  
784 72 4.6 736 2 T41259  
785 72 4.6 770 1 S30293  
786 72 4.6 855 2 D98004  
787 72 4.6 876 2 T49801  
788 72 4.6 884 2 T20405  
789 72 4.6 958 2 T26258  
790 72 4.6 993 1 P1VXTA  
791 72 4.6 1034 2 S49947  
792 72 4.6 1038 2 A92187  
793 72 4.6 1146 2 S46837  
794 72 4.6 1176 2 T49482  
795 72 4.6 1196 2 H85061  
796 72 4.6 1203 2 T17415  
797 72 4.6 1388 2 A57655  
798 72 4.6 1489 2 T31108  
799 72 4.6 1547 2 T28657  
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801 72 4.6 1778 2 T50074  
802 72 4.6 1829 2 T24583  
803 72 4.6 2441 2 S39161  
804 72 4.6 2578 2 A56922  
805 72 4.6 2971 2 T08026  
806 71.5 4.5 141 2 A38196  
807 71.5 4.5 146 2 S52800  
808 71.5 4.5 162 2 C84948  
809 71.5 4.5 164 2 A26490  
810 71.5 4.5 178 2 JQ1547  
811 71.5 4.5 231 2 F84311  
812 71.5 4.5 263 2 S01360  
813 71.5 4.5 305 2 AB2149  
814 71.5 4.5 313 2 JQ1862  
815 71.5 4.5 313 2 T28598  
816 71.5 4.5 363 2 T25278  
817 71.5 4.5 372 2 F43674  
818 71.5 4.5 373 2 S43455  
819 71.5 4.5 381 2 S65212  
820 71.5 4.5 385 2 T38113  
821 71.5 4.5 392 2 T49471  
822 71.5 4.5 393 2 T49578  
823 71.5 4.5 395 2 I52842  
824 71.5 4.5 395 2 A43545  
825 71.5 4.5 408 2 A46712  
826 71.5 4.5 414 2 B84600  
827 71.5 4.5 442 1 S11712  
828 71.5 4.5 443 1 D64584  
829 71.5 4.5 466 2 A10957  
830 71.5 4.5 503 2 G75262  
831 71.5 4.5 507 2 T50398  
832 71.5 4.5 540 1 A55145

RP2 protein - saim  
hypothetical prote  
bone sialoprotein  
phage-related prot  
integrin-associate  
hypothetical prote  
hypothetical prote  
DNA polymerase pro  
hypothetical prote  
probable membrane  
amino acid transpo  
SPS2 protein homol  
fasciclin III prec  
probable protein k  
neurofilament trip  
neurofilament trip  
hypothetical serin  
chaperonin, mitoch  
hypothetical prote  
lipoprotein [impor  
ribonuclease E - S  
hypothetical prote  
hypothetical prote  
transcription fact  
histidine Motif-Co  
hypothetical prote  
hypothetical prote  
hypothetical prote  
RNA 1 protein - to  
SWT4 protein - yea  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
mycelial surface a  
tim (timeless) pro  
cyst germination s  
blackjack protein,  
1-phosphatidylinos  
probable nucleopor  
hypothetical prote  
CREB-binding prote  
transcription fact  
hypothetical prote  
non-structural hyp  
hypothetical prote  
NADH2 dehydrogenas  
histone H1, macron  
stripe disease-spe  
hypothetical prote  
salivary glue prot  
hypothetical prote  
31R protein - vari  
hypothetical prote  
hypothetical prote  
US7 protein - huma  
hypothetical prote  
hypothetical prote  
mucin (muc3) relat  
CD43 lp-3 antigen  
leukosialin CD43 p  
glycoprotein Iia -  
hypothetical prote  
transcription init  
heat shock protein  
chromosomal replic  
hypothetical prote  
hypothetical serin  
thiamine-phosphate

833	71.5	4.5	540	2	H98086	chaperonin GroEL [	906	71	4.5	1326	2	H89134	protein F2566.9 [
834	71.5	4.5	540	2	G95222	chaperonin, 60 kDa	907	71	4.5	1367	2	T33819	hypothetical prote
835	71.5	4.5	584	2	T19565	hypothetical prote	908	71	4.5	1533	2	T00344	hypothetical prote
836	71.5	4.5	631	1	V52257	episialin - mouse	909	71	4.5	1583	2	S59644	sister chromatid c
837	71.5	4.5	661	1	VCWVCB	env polyprotein -	910	71	4.5	1751	2	A45604	major blood-stage
838	71.5	4.5	675	2	T47378	probable transpos	911	71	4.5	1819	2	T32008	hypothetical prote
839	71.5	4.5	681	2	A45705	type I transmembr	912	71	4.5	1819	2	T32008	hypothetical prote
840	71.5	4.5	755	2	T20950	hypothetical prote	913	71	4.5	1842	2	T43409	probable fatty-aci
841	71.5	4.5	760	1	S07896	transcription fact	914	71	4.5	1842	2	T38781	fatty acid synthas
842	71.5	4.5	882	2	T01168	hypothetical prote	915	71	4.5	2035	2	A40718	host cell factor C
843	71.5	4.5	918	2	I58178	glutamate receptor	916	71	4.5	2090	2	S26058	hypothetical prote
844	71.5	4.5	1042	2	T48801	hypothetical prote	917	71	4.5	2488	2	T32550	hypothetical prote
845	71.5	4.5	1043	2	T23875	hypothetical prote	918	71	4.5	2557	2	T33152	hypothetical prote
846	71.5	4.5	1121	2	T02764	myosin-I binding p	919	70.5	4.5	5035	1	I46646	ryanodine receptor
847	71.5	4.5	1156	2	T43326	germline RNA helic	920	70.5	4.5	118	2	S49913	cryptogin - Phyto
848	71.5	4.5	1172	2	T32759	hypothetical prote	921	70.5	4.5	128	2	A35690	mucin 3 (clone SIB
849	71.5	4.5	1234	2	T31623	hypothetical prote	922	70.5	4.5	146	1	ERAD32	early E3 16K glyco
850	71.5	4.5	1260	2	A87046	hypothetical prote	923	70.5	4.5	172	2	F49247	merozoite surface
851	71.5	4.5	1297	2	T30274	proteolisin - se	924	70.5	4.5	174	2	E49247	merozoite surface
852	71.5	4.5	1459	2	T32271	hypothetical prote	925	70.5	4.5	193	2	G90125	hypothetical prote
853	71.5	4.5	1557	2	D41214	protein-tyrosine-p	926	70.5	4.5	204	2	S67295	probable membrane
854	71.5	4.5	1566	2	T20058	hypothetical prote	927	70.5	4.5	209	2	C89850	conserved endothe
855	71.5	4.5	1630	2	C41214	protein-tyrosine-p	928	70.5	4.5	211	2	C71482	probable endonucle
856	71	4.5	98	2	S53367	mucin 5AC (clone M	929	70.5	4.5	212	2	F86545	hypothetical prote
857	71	4.5	135	2	T49996	AtAGP4 - Arabidops	930	70.5	4.5	212	2	F72077	hypothetical prote
858	71	4.5	168	2	JN0073	glycophorin A - mo	931	70.5	4.5	236	2	PC4396	mucin 3 T9 - human
859	71	4.5	177	2	G75285	hypothetical prote	932	70.5	4.5	255	2	I46606	MHC SLA-DQ alpha c
860	71	4.5	213	2	A86228	hypothetical prote	933	70.5	4.5	264	2	T09377	hypothetical prote
861	71	4.5	240	2	T33698	hypothetical prote	934	70.5	4.5	275	2	T21933	hypothetical prote
862	71	4.5	242	2	T27226	hypothetical prote	935	70.5	4.5	284	2	T28018	hypothetical prote
863	71	4.5	304	2	T15922	hypothetical prote	936	70.5	4.5	288	2	T41112	hypothetical prote
864	71	4.5	310	2	T20535	hypothetical prote	937	70.5	4.5	308	2	T29756	hypothetical prote
865	71	4.5	329	2	T43012	conserved hypotet	938	70.5	4.5	312	2	T25994	hypothetical prote
866	71	4.5	343	2	S75435	hypothetical prote	939	70.5	4.5	314	2	B97905</	

979	70.5	4.5	1131	2	TJ15787	1052	70	4.4	971	2	T19431	hypothetical prote
980	70.5	4.5	1204	2	C75015	1053	70	4.4	971	2	F88448	protein C4589.10 [
981	70.5	4.5	1221	2	A10193	1054	70	4.4	1004	2	A55142	myosin-light-chain
982	70.5	4.5	1520	2	T44231	1055	70	4.4	1186	2	T19050	hypothetical prote
983	70.5	4.5	1603	2	S17933	1056	70	4.4	1213	2	A41724	limb deformity (ld
984	70.5	4.5	1742	2	T17120	1057	70	4.4	1274	2	JN0015	trp protein - frui
985	70.5	4.5	1872	2	T00339	1058	70	4.4	1275	2	JU0092	trp protein - frui
986	70.5	4.5	2717	2	A34203	1059	70	4.4	1415	2	T08945	hypothetical prote
987	70.5	4.5	3054	1	GMBVEV	1060	70	4.4	1420	1	A44361	amiloride-sensitiv
988	70	4.4	147	2	JC7938	1061	70	4.4	1589	2	C44766	defective chorion-
989	70	4.4	148	2	T32622	1062	70	4.4	1868	2	S48938	hypothetical prote
990	70	4.4	150	2	T52587	1063	70	4.4	2440	2	S39162	transcription coac
991	70	4.4	150	2	T48611	1064	70	4.4	3163	1	JQ1895	genome polyprotein
992	70	4.4	202	2	A82218	1065	69.5	4.4	120	1	W4WL42	E4 protein - human
993	70	4.4	210	2	JC7830	1066	69.5	4.4	124	2	E84613	hypothetical prote
994	70	4.4	214	2	A46629	1067	69.5	4.4	146	2	S52810	hypothetical prote
995	70	4.4	221	2	T47592	1068	69.5	4.4	202	2	AB2378	hypothetical prote
996	70	4.4	234	2	G64858	1069	69.5	4.4	217	2	S01358	salivary glue prot
997	70	4.4	239	2	B83709	1070	69.5	4.4	219	2	B72291	hypothetical prote
998	70	4.4	298	2	C55223	1071	69.5	4.4	266	2	H55590	hypothetical prote
999	70	4.4	310	2	T26267	1072	69.5	4.4	271	2	B96773	hypothetical prote
1000	70	4.4	311	2	H96002	1073	69.5	4.4	299	2	G70784	probable mmpS3 pro
1001	70	4.4	321	2	T42750	1074	69.5	4.4	313	2	H36854	hemagglutinin - va
1002	70	4.4	329	2	S38082	1075	69.5	4.4	316	2	S58719	probable membrane
1003	70	4.4	333	2	G38227	1076	69.5	4.4	326	2	I48351	fos-related anige
1004	70	4.4	333	2	AH2985	1077	69.5	4.4	338	2	S28004	probable cell surf
1005	70	4.4	340	2	C90894	1078	69.5	4.4	364	2	T32589	hypothetical prote
1006	70	4.4	342	2	F85723	1079	69.5	4.4	372	1	QQB888	glycoprotein I pre
1007	70	4.4	340	2	G64905	1080	69.5	4.4	400	2	T32705	hypothetical prote
1008	70	4.4	350	2	S22456	1081	69.5	4.4	417	2	AD0200	isocitrate dehydro
1009	70	4.4	350	2	AH3043	1082	69.5	4.4	423	2	T24383	hypothetical prote
1010	70	4.4	350	2	D98242	1083	69.5	4.4	425	1	FOMVGC	gag polyprotein -
1011	70	4.4	355	2	B36883	1084	69.5	4.4	425	2	T24111	hypothetical prote
1012	70	4.4	357	2	E72245	1085	69.5	4.4	427	2	T38526	ubiquitin regulato
1013	70	4.4	358	2	A80802	1086	69.5	4.4	441	2	C75076	heme biosynthesis
1014	70	4.4	360	2	T33835	1087	69.5	4.4	450	2	C90608	hypothetical prote
1015	70	4.4	360	2	T08673	1088	69.5	4.4	458	2	F86433	protein T17H7.5 [i
1016	70	4.4	409	2	T18726	1089	69.5	4.4	514	2	A44100	cell adhesion mole
1017	70	4.4	424	2	I51210	1090	69.5	4.4	514	2	A31643	cell adhesion 80K
1018	70	4.4	425	2	T18723	1091	69.5	4.4	519	2	S69989	unspecific monooxy
1019	70	4.4	426	2	T04995	1092	69.5	4.4	520	2	S14600	E2 glycoprotein pr
1020	70	4.4	433	2	S19996	1093	69.5	4.4	538	2	AG2902	conserved hypochet
1021	70	4.4	445	2	S45713	1094	69.5	4.4	550	2	H97677	hypothetical prote
1022	70	4.4	446	2	S66268	1095	69.5	4.4	551	2	G95176	conserved hypochet
1023	70	4.4	456	2	T38221	1096	69.5	4.4	552	2	T25593	hypothetical prote
1024	70	4.4	458	2	T26630	1097	69.5	4.4	568	2	A34891	Ig heavy chain pre
1025	70	4.4	461	2	T38698	1098	69.5	4.4	593	2	S55189	hypothetical prote
1026	70	4.4	462	2	T19830	1099	69.5	4.4	610	2	S59394	protein kinase RCK
1027	70	4.4	487	2	A11505	1100	69.5	4.4	611	2	A54086	calnexin-t - mouse
1028	70	4.4	497	2	T51195	1101	69.5	4.4	629	2	S20516	dnak-type molecula
1029	70	4.4	529	2	S18453	1102	69.5	4.4	640	2	T25367	hypothetical prote
1030	70	4.4	542	2	B47022	1103	69.5	4.4	645	2	S41372	dnak-type molecula
1031	70	4.4	589	2	A10684	1104	69.5	4.4	646	2	T19206	hypothetical prote
1032	70	4.4	599	2	G71481	1105	69.5	4.4	658	2	JC8011	G protein-coupled
1033	70	4.4	611	2	T22456	1106	69.5	4.4	675	2	T03744	myoD protein inhib
1034	70	4.4	613	2	B90294	1107	69.5	4.4	736	2	T19366	hypothetical prote
1035	70	4.4	617	2	T15408	1108	69.5	4.4	782	2	A82940	hypothetical prote
1036	70	4.4	622	2	AC1236	1109	69.5	4.4	833	2	AF2089	hypothetical prote
1037	70	4.4	625	2	S34035	1110	69.5	4.4	844	2	B64678	NADH2 dehydrogenas
1038	70	4.4	651	2	S18874	1111	69.5	4.4	850	1	MMHUE4	erythrocyte membra
1039	70	4.4	653	2	E86787	1112	69.5	4.4	852	2	T46091	hypothetical prote
1040	70	4.4	662	2	T50464	1113	69.5	4.4	862	2	T46289	hypothetical prote
1041	70	4.4	697	2	E36752	1114	69.5	4.4	871	2	S47518	cadherin - African
1042	70	4.4	706	2	S33761	1115	69.5	4.4	942	2	T19553	hypothetical prote
1043	70	4.4	714	2	T22454	1116	69.5	4.4	993	2	AE1905	outer membrane sec
1044	70	4.4	753	2	T24869	1117	69.5	4.4	1051	2	JC4091	glycoprotein A - p
1045	70	4.4	768	2	E86417	1118	69.5	4.4	1087	1	QFMSH	neurofilament trip
1046	70	4.4	770	2	T51024	1119	69.5	4.4	1132	2	T43483	translation initia
1047	70	4.4	822	2	T51049	1120	69.5	4.4	1460	2	S48457	nucleoporin RAV7 -
1048	70	4.4	823	2	F90914	1121	69.5	4.4	1502	2	S45429	probable purine nu
1049	70	4.4	835	2	JC6140	1122	69.5	4.4	1522	2	S48904	cell surface-assoc
1050	70	4.4	937	2	A56517	1123	69.5	4.4	1870	2	D88486	nucleoporin Nup98
1051	70	4.4	949	2	S19808	1124	69.5	4.4	1875	2	S38173	glutamate receptor

1125	69.5	4.4	1957	2	A45627	myosin heavy chain	1198	69	4.4	2329	2	S44625	C50C3.6 protein -
1126	69.5	4.4	2271	2	F90073	hypothetical prote	1199	69	4.4	2361	2	T25752	hypothetical prote
1127	69.5	4.4	2894	2	C64474	hypothetical prote	1200	69	4.4	2464	1	QRWSP1	microtubule-associ
1128	69.5	4.4	4199	2	S76412	hypothetical prote	1201	69	4.4	3122	2	T17202	DNA-directed DNA p
1129	69	4.4	171	2	T31478	hypothetical prote	1202	68.5	4.3	168	2	S52994	arabinogalactan-li
1130	69	4.4	234	2	T35448	hypothetical prote	1203	68.5	4.3	189	1	ERAD75	early E3 20.6K gly
1131	69	4.4	255	2	T22429	hypothetical prote	1204	68.5	4.3	189	2	JX0235	core protein MGC-2
1132	69	4.4	258	2	S23106	priA protein - shi	1205	68.5	4.3	204	2	S51232	giberellin-reapon
1133	69	4.4	284	2	T06241	histone H1 (clone	1206	68.5	4.3	218	2	AH1837	hypothetical prote
1134	69	4.4	299	2	S44554	citrate transport	1207	68.5	4.3	246	2	S47805	hypothetical prote
1135	69	4.4	303	2	S29185	sodium channel pro	1208	68.5	4.3	246	2	D91186	probable outer mem
1136	69	4.4	338	2	F69437	hypothetical prote	1209	68.5	4.3	246	2	C86033	probable outer mem
1137	69	4.4	339	2	S08981	malate dehydrogena	1210	68.5	4.3	257	2	C84890	hypothetical prote
1138	69	4.4	344	1	RWRTC2	T-cell surface gly	1211	68.5	4.3	261	2	T42965	hypothetical prote
1139	69	4.4	344	2	T13975	NADH2 dehydrogenas	1212	68.5	4.3	280	2	AE2031	gamma-tocopherol m
1140	69	4.4	356	2	S73315	protoporphyrin IX	1213	68.5	4.3	287	2	S45662	histone H1 - tomat
1141	69	4.4	382	2	S71669	finger protein MIG	1214	68.5	4.3	288	2	T22846	hypothetical prote
1142	69	4.4	396	2	T26987	hypothetical prote	1215	68.5	4.3	318	2	T20063	hypothetical prote
1143	69	4.4	400	1	A39822	leukosialin precu	1216	68.5	4.3	359	2	G70814	glycoprotein - ate
1144	69	4.4	416	2	T34279	hypothetical prote	1217	68.5	4.3	359	2	T35403	probable far prote
1145	69	4.4	423	2	T44258	transducer protein	1218	68.5	4.3	378	2	H97239	probable polypreny
1146	69	4.4	431	2	G86277	F14L17.11 protein	1219	68.5	4.3	385	2	JC7783	polyferredoxin [im
1147	69	4.4	443	2	T14516	mitosis-specific c	1220	68.5	4.3	385	2	G84206	RAD 23B protein -
1148	69	4.4	467	2	T26195	hypothetical prote	1221	68.5	4.3	394	2	AJMSRS	argininosuccinate
1149	69	4.4	482	2	T48397	S-receptor kinase-	1222	68.5	4.3	412	1	AJMSRS	argininosuccinate
1150	69	4.4	483	2	G86902	dextranucrase (EC	1223	68.5	4.3	412	1	AJMSRS	hypothetical prote
1151	69	4.4	486	2	D64474	hypothetical prote	1224	68.5	4.3	413	2	T04520	hypothetical prote
1152	69	4.4	490	1	C57150	NADP-reducing hydr	1225	68.5	4.3	414	2	G64091	cell division prot
1153	69	4.4	495	2	T38959	hypothetical prote	1226	68.5	4.3	420	2	A88962	protein F59A7.1 [i
1154	69	4.4	511	2	T50114	early growth respo	1227	68.5	4.3	421	2	S09595	synaptotagmin P65
1155	69	4.4	513	2	S50915	SIN3 protein-bindi	1228	68.5	4.3	426	2	A35641	5-aminimidazole r
1156	69	4.4	525	2	A35596	nuclear pore glyco	1229	68.5	4.3	435	2	C86340	protein F2D10.28 [
1157	69	4.4	555	2	B41492	58K antigen - Rick	1230	68.5	4.3	435	2	T25350	hypothetical prote
1158	69	4.4	556	2	S06838	gamma-aminobutyric	1231	68.5	4.3	443	2	F71929	heat shock protein
1159	69	4.4	556	2	S51892	probable membrane	1232	68.5	4.3	458	2	AC0121	probable exported
1160	69	4.4	583	2	T18999	hypothetical prote	1233	68.5	4.3	498	1	SGXPLA	surface glycoprote
1161	69	4.4	609	2	S62518	hypothetical prote	1234	68.5	4.3	500	1	S60929	probable aldehyde
1162	69	4.4	610	1	I46001	C4b-binding protei	1235	68.5	4.3	509	2	T48459	cytochrome P450-11
1163	69	4.4	611	2	A53418	calnegin precursor	1236	68.5	4.3	514	1	A47692	cytochrome P450-11
1164	69	4.4	611	2	A53418	204 protein - mous	1237	68.5	4.3	527	2	T26732	fumarate hydratase
1165	69	4.4	647	2	B34457	alpha-agglutinin -	1238	68.5	4.3	535	2	B84443	hypothetical prote
1166	69	4.4	650	2	S22835	hypothetical prote	1239	68.5	4.3	535	2	AG1482	hypothetical prote
1167	69	4.4	651	2	T21175	surface layer prot	1240	68.5	4.3	553	2	A49364	59 protein, brain
1168	69	4.4	652	2	S50210	hypothetical threo	1241	68.5	4.3	573	2	H96744	probable cytosolic
1169	69	4.4	658	2	T41309	hypothetical prote	1242	68.5	4.3	588	2	JC8021	chitinase [EC 3.2.
1170	69	4.4	670	2	F84540	hypothetical prote	1243	68.5	4.3	592	2	T32402	hypothetical prote
1171	69	4.4	677	2	S54561	RNAI4 protein - ye	1244	68.5	4.3	594	2	S51412	hypothetical prote
1172	69	4.4	739	2	H72364	aspartokinase II -	1245	68.5	4.3	630	2	A39344	tumor-associated m
1173	69	4.4	790	2	T34293	hypothetical prote	1246	68.5	4.3	637	2	T20981	hypothetical prote
1174	69	4.4	793	1	KKRTF	furin (SC 3.4.21.7	1247	68.5	4.3	647	2	S26386	transcription fact
1175	69	4.4	814	2	T49207	receptor kinase-li	1248	68.5	4.3	659	2	T40383	hypothetical prote
1176	69	4.4	825	2	S26706	transcription fact	1249	68.5	4.3	670	2	S22293	hypothetical prote
1177	69	4.4	836	2	T21631	hypothetical prote	1250	68.5	4.3	696	2	G71829	probable outer mem
1178	69	4.4	854	1	QRHYLD	LDL receptor precu	1251	68.5	4.3	697	2	A86402	protein T22C5.17 [
1179	69	4.4	871	2	T28706	hypothetical prote	1252	68.5	4.3	699	2	T09483	Cys-rich protein R
1180	69	4.4	879	1	QRRTLD	LDL receptor precu	1253	68.5	4.3	721	2	E70766	hypothetical prote
1181	69	4.4	903	1	VBEBK1	glycoprotein B pre	1254	68.5	4.3	725	2	T01268	leucine-rich repea
1182	69	4.4	942	2	S53963	MCS1 protein - yea	1255	68.5	4.3	737	2	AG2156	hypothetical prote
1183	69	4.4	988	2	A40628	probable transposa	1256	68.5	4.3	751	2	AC2098	hypothetical prote
1184	69	4.4	995	2	T27327	hypothetical prote	1257	68.5	4.3	763	2	S55616	glycoprotein H - e
1185	69	4.4	1007	2	JC8066	138K protein - Tet	1258	68.5	4.3	770	2	G88445	protein C26E6.2 [i
1186	69	4.4	1215	2	S60904	hypothetical prote	1259	68.5	4.3	795	2	T20609	hypothetical prote
1187	69	4.4	1360	2	T34302	cell polarity prot	1260	68.5	4.3	798	2	T50514	hypothetical prote
1188	69	4.4	1385	2	T13415	hypothetical prote	1261	68.5	4.3	825	1	GLHQ	beta-glucosidase (
1189	69	4.4	1455	1	A48925	mannose receptor p	1262	68.5	4.3	839	2	I50590	class I INCENP pro
1190	69	4.4	1624	2	T25592	hypothetical prote	1263	68.5	4.3	846	2	S52418	GRP-binding regula
1191	69	4.4	1633	2	T01879	hypothetical prote	1264	68.5	4.3	865	2	AC1966	hypothetical prote
1192	69	4.4	1680	2	T41628	probable transcrip	1265	68.5	4.3	877	2	I50591	class II INCENP pr
1193	69	4.4	1758	2	S57015	probable purine nu	1266	68.5	4.3	914	2	T25220	hypothetical prote
1194	69	4.4	1804	2	H96597	hypothetical prote	1267	68.5	4.3	952	2	T18837	hypothetical prote
1195	69	4.4	1819	2	D97033	uncharacterized pr	1268	68.5	4.3	1043	2	T13172	gag-like protein p
1196	69	4.4	1963	1	MWK	myosin heavy chain	1269	68.5	4.3	1278	2	A71609	probable secreted
1197	69	4.4	2067	2	A42854	probable spindle p	1270	68.5	4.3	1285	2	H85041	hypothetical prote

1271	68.5	4.3	1311	2	A56390	mannosyl-glycoprote	1344	68	4.3	730	2	A75486	hypothetical prote
1272	68.5	4.3	1435	2	S69632	regulatory protein	1345	68	4.3	733	2	T01875	probable long-chain
1273	68.5	4.3	1438	2	A48216	neurexin III-alpha	1346	68	4.3	752	2	T34355	hypothetical prote
1274	68.5	4.3	1444	1	A30598	140K adhesin precu	1347	68	4.3	761	2	T03719	probable thyroid r
1275	68.5	4.3	1541	2	S46686	hypothetical prote	1348	68	4.3	775	1	WMBE19	ribonucleoside-dip
1276	68.5	4.3	1791	2	T24089	hypothetical prote	1349	68	4.3	784	2	C82679	cell division prot
1277	68.5	4.3	2114	2	E96505	hypothetical prote	1350	68	4.3	785	2	S54016	SOK2 protein - yea
1278	68.5	4.3	2292	1	GNMYEB	genome polyprotein	1351	68	4.3	793	2	S65240	probable membrane
1279	68.5	4.3	2292	1	GNMYEB	genome polyprotein	1352	68	4.3	809	2	T18970	hypothetical prote
1280	68.5	4.3	2292	2	S55401	capsid polyprotein	1353	68	4.3	817	2	T21336	hypothetical prote
1281	68	4.3	62	2	S53366	mucin 5AC (clone M	1354	68	4.3	833	2	G75621	arylesterase/monox
1282	68	4.3	208	1	HSRTJT	histone H1t - rat	1355	68	4.3	859	2	S66827	aluminum resistan
1283	68	4.3	211	2	H72698	hypothetical prote	1356	68	4.3	893	1	GNMYVM	pol polyprotein -
1284	68	4.3	228	2	T33579	hypothetical prote	1357	68	4.3	903	2	T00074	hypothetical prote
1285	68	4.3	245	2	D81977	hypothetical prote	1358	68	4.3	923	2	A86334	T20H2.17 protein -
1286	68	4.3	246	2	H90833	major tail protein	1359	68	4.3	971	2	T10678	hypothetical prote
1287	68	4.3	256	2	B85691	probable tail comp	1360	68	4.3	974	2	S34189	starch phosphoryla
1288	68	4.3	268	2	T32740	hypothetical prote	1361	68	4.3	991	2	S43891	dna exoribonuclea
1289	68	4.3	288	2	T21790	hypothetical prote	1362	68	4.3	1010	2	T16616	hypothetical prote
1290	68	4.3	295	2	S50316	CIN5 protein - yea	1363	68	4.3	1018	2	T18249	conserved hypotet
1291	68	4.3	301	2	H70644	hypothetical prote	1364	68	4.3	1052	2	T14343	zinc finger RNA bi
1292	68	4.3	333	2	T15367	hypothetical prote	1365	68	4.3	1072	2	A37127	microtubule-associ
1293	68	4.3	339	2	AH0050	probable periplasm	1366	68	4.3	1117	2	S63399	probable membrane
1294	68	4.3	360	2	S69063	probable membrane	1367	68	4.3	1173	2	S48877	Ca2+-transporting
1295	68	4.3	372	2	T45628	glycerophosphodies	1368	68	4.3	1196	2	S35594	DNA repair protein
1296	68	4.3	378	2	S61992	Sigl1 protein - yea	1369	68	4.3	1203	2	T51029	related to pathway
1297	68	4.3	380	1	S51826	alcohol dehydrogen	1370	68	4.3	1204	2	F81158	exodeoxyribonuclea
1298	68	4.3	384	2	H64161	hypothetical prote	1371	68	4.3	1230	2	T22458	hypothetical prote
1299	68	4.3	387	2	A56275	1,3-propanediol de	1372	68	4.3	1275	2	T33369	hypothetical prote
1300	68	4.3	388	2	T43019	probable DNA-bindi	1373	68	4.3	1279	2	T13613	hypothetical prote
1301	68	4.3	402	2	T20595	hypothetical prote	1374	68	4.3	1280	2	T00365	hypothetical prote
1302	68	4.3	416	2	T19149	hypothetical prote	1375	68	4.3	1338	2	T40993	protein kinase cek
1303	68	4.3	420	2	T42616	envelope protein -	1376	68	4.3	1371	2	T29019	hypothetical prote
1304	68	4.3	422	1	BMHUIY	synaptotagmin I -	1377	68	4.3	1541	2	A37023	IGa-specific metal
1305	68	4.3	423	2	T14531	S-locus-specific q	1378	68	4.3	1545	2	B41859	neurexin III-alpha
1306	68	4.3	423	2	H84257	Htr13 transducer l	1379	68	4.3	1578	2	I48216	1,4-beta-glucanase
1307	68	4.3	426	2	T48379	gene hb protein -	1380	68	4.3	1711	2	T31337	major merozoite su
1308	68	4.3	427	2	JH0413	synaptotagmin o-p6	1381	68	4.3	1772	2	A45532	myosin heavy chain
1309	68	4.3	452	2	T46147	zinc finger protei	1382	68	4.3	1968	1	S05697	variant-specific s
1310	68	4.3	479	2	A84588	probable tyrosine	1383	68	4.3	2228	2	T14029	hypothetical prote
1311	68	4.3	487	1	S07061	glutamate receptor	1384	68	4.3	2810	2	T22298	hypothetical prote
1312	68	4.3	500	2	AI1913	apolipoprotein N-a	1385	68	4.3	3191	2	T22945	hypothetical prote
1313	68	4.3	502	2	T21935	hypothetical prote	1386	68	4.3	3712	2	S18253	lamin alpha-1 ch
1314	68	4.3	503	2	T51782	hypothetical prote	1387	67.5	4.3	127	2	T30102	hypothetical prote
1315	68	4.3	515	2	B84406	TRK potassium upa	1388	67.5	4.3	137	2	F95239	conserved domain p
1316	68	4.3	516	2	A31270	radial spoke prote	1389	67.5	4.3	137	2	H98103	hypothetical prote
1317	68	4.3	537	1	F0MVW7	gag polyprotein -	1390	67.5	4.3	159	2	T31598	hypothetical prote
1318	68	4.3	543	2	A38093	SAR DNA-binding pr	1391	67.5	4.3	180	2	T31974	hypothetical prote
1319	68	4.3	550	2	T06379	hypothetical prote	1392	67.5	4.3	191	2	S38117	hypothetical prote
1320	68	4.3	573	2	S50661	hypothetical prote	1393	67.5	4.3	210	2	B88082	protein T05A8.6 [i
1321	68	4.3	576	2	S75958	hypothetical prote	1394	67.5	4.3	232	1	WVABC2	early E1A 25k prot
1322	68	4.3	581	2	T22455	hypothetical prote	1395	67.5	4.3	235	2	T02598	probable replicati
1323	68	4.3	590	2	S66956	hypothetical prote	1396	67.5	4.3	238	2	T07921	probable starch sy
1324	68	4.3	599	1	A54906	afamin precursor -	1397	67.5	4.3	240	2	H69932	hypothetical prote
1325	68	4.3	600	2	S56744	mucin (clone pGM7-	1398	67.5	4.3	248	2	PQ0769	glycoprotein G - b
1326	68	4.3	610	2	T22909	hypothetical prote	1399	67.5	4.3	252	2	AG1423	hypothetical prote
1327	68	4.3	621	1	YRNC	monophenol monooxy	1400	67.5	4.3	256	2	H36857	B26R protein - var
1328	68	4.3	630	2	S77346	hypothetical prote	1401	67.5	4.3	297	2	S55063	conserved hypotet
1329	68	4.3	632	2	T48616	hypothetical prote	1402	67.5	4.3	311	2	T40921	hypothetical prote
1330	68	4.3	638	2	S36723	FUN36 protein - ye	1403	67.5	4.3	326	2	S15749	transforming prote
1331	68	4.3	645	2	T16078	hypothetical prote	1404	67.5	4.3	327	2	D90530	hypothetical prote
1332	68	4.3	647	2	T39141	hypothetical prote	1405	67.5	4.3	345	2	E88103	protein W10G11.5 [
1333	68	4.3	648	2	T04837	probable serine/th	1406	67.5	4.3	346	2	T40623	hypothetical prote
1334	68	4.3	655	1	A55726	RNA-binding protei	1407	67.5	4.3	348	2	T46916	probable polyA-bin
1335	68	4.3	659	2	H81431	methyl-accepting c	1408	67.5	4.3	355	2	T15526	hypothetical prote
1336	68	4.3	659	2	A98085	hypothetical prote	1409	67.5	4.3	358	2	T01296	leucine-rich repea
1337	68	4.3	662	2	B81251	probable methyl-ac	1410	67.5	4.3	369	2	AG1950	hypothetical prote
1338	68	4.3	665	2	B81444	probable methyl-ac	1411	67.5	4.3	383	2	E96372	riboflavin biosynt
1339	68	4.3	668	2	B86831	hypothetical prote	1412	67.5	4.3	387	2	T15462	hypothetical prote
1340	68	4.3	669	2	B70186	translational elonga	1413	67.5	4.3	391	2	A44063	paired box transcr
1341	68	4.3	686	2	S66693	hypothetical prote	1414	67.5	4.3	399	2	T42242	hypothetical 44.2K
1342	68	4.3	695	2	T51652	daRNA-binding prot	1415	67.5	4.3	410	2	C84638	probable WRKY-type
1343	68	4.3	709	2	S51793	dibasic processing	1416	67.5	4.3	426	2	AI1920	ABC transporter AT



protein T12M4.6 [i  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
gamma-aminobutyric  
I2 protein - trypa  
hypothetical prote  
hypothetical prote  
probable coA ligas  
related to COP1-in  
chitinase [EC 3.2.  
hypothetical prote  
chaperonin hsp60 p  
neutral proteinase  
probable PPR2 fami  
hypothetical prote  
nucleoporin-like p  
probable molybdopt  
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Bts-related transc  
scaffoldin dockeri  
surface glycoprote  
oligopeptide-bind  
polo-like kinase-1  
RNA-binding protei  
fibroin-3 related  
probable protein k  
NADPH-ferrihemopro  
Maturator-like trans  
heat shock protein  
probable serine/th  
hypothetical prote  
protein-tyrosine-p  
probable zinc-fing  
phospholipase D (E  
aspartate kinase (i  
hypothetical prote  
hypothetical prote  
P95 orf83 - Bombyx  
metabotropic gluta  
hypothetical prote  
glycoprotein 350/2  
hypothetical prote  
hypothetical prote  
glycoprotein gi pr  
transcription acti  
hypothetical prote  
hypothetical prote  
polymorphic outer  
polymorphic outer  
NF-kappa-B p50 sub  
polymorphic membra  
neurofilament trip  
hypothetical prote  
hypothetical prote  
cyclin F - fruit f  
hypothetical prote  
protein F54D8.1 [i  
probable helicase  
period protein PER  
glycoprotein A - m  
aggregation protei  
agrin - electric r  
cell surface prote  
protein C47B8.8 [i  
probable retroelem  
hypothetical prote  
sodium channel pro  
gag-pol polyprotei  
collagen alpha 1(V  
D15R protein - var

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1462 67.5 4.3 915 2 VGB8EG  
1463 67.5 4.3 928 1 VGB8EG  
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1466 67.5 4.3 969 2 T15446  
1467 67.5 4.3 973 2 B86547  
1468 67.5 4.3 973 2 F72076  
1469 67.5 4.3 984 2 A41996  
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1474 67.5 4.3 1097 2 T13033  
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1487 67.5 4.3 1784 2 T10532  
1488 67.5 4.3 1843 2 S18803  
1489 67.5 4.3 1896 2 B72175

hypothetical prote  
hemagglutinin/hemo  
hemagglutinin/hemo  
probable peptidogl  
hypothetical prote  
rhopty protein -  
nuclear receptor c  
probable guanine n  
homeotic protein z  
hypothetical prote  
hypothetical prote

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1492 67.5 4.3 1995 2 G81044  
1493 67.5 4.3 2044 2 AB1180  
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ALIGNMENTS

RESULT 1

A37009  
CD44 homolog membrane glycoprotein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 09-Jul-2004  
C:Accession: A37009  
R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatzke, R.F.; Butcher, E.C.; Goeddel, D.V.  
J. Immunol. 143, 3390-3395, 1989  
A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CA  
A;Reference number: A37009; MUID:90038499; PMID:2681416  
A;Accession: A37009  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-363 <ZHO>  
A;Cross-references: UNIPROT:PI5379; UNIPARC:UPI00002A5F4; GB:M30655; NID:g200332; PIDN  
C;Superfamily: human cell adhesion protein CD44  
C;Keywords: cell adhesion, glycoprotein, membrane protein

Query Match 14.5%; Score 229; DB 2; Length 363;  
Best Local Similarity 24.9%; Pred. No. 6.4e-11;  
Matches 87; Conservative 57; Mismatches 145; Indels 60; Gaps 13;

QY 4 LVQSLRAEELSIOVSCRMGITLYSKKANQQLNFTFEAKCELLGLSLAGKDOVETALK 63  
DB 14 LQLSLAHQOIDLNVTCRYAGVFHVEKNGYSISRTEAADLCOAFNSTLPTMDQMKLALS 73  
QY 64 ASFTCSYGVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCVNSDWTNSC 123  
DB 74 KGEFCRYGFI-EGNVVPIHPNCAANHGVILVTNTSHYTYCFNASAPPEDC 132  
QY 124 IPEIITKDPINFNTQATOTTFIVSDST-YVASPYST----IPAPT----- 166  
DB 133 -----TSVTDLPNSFDGPVTITVNRDGRYSKKGGRYTHQEDIDASNIIDDDVSSGSTI 187  
QY 167 --TTPPA-PASTSIPIPRKKLICVTEVFMTSTMT-ETEPFFVENKAFFK-----NEAAGF 217  
DB 188 EKSTPEGYLHTLYLTPTEQTGDDDSFFIRSTLATRDRSDSKDSRGSSRTVTHGSELGH 247  
QY 218 GG-----VPTALIVLALLFFGAAGLGFVCVKRYKVAFFPTNKNQOK 259  
DB 248 SSANQDSGVTTTSGPMRRPQIPFWLIIILASL-LALALILAVC-----IAVSRRCGQKK 301  
QY 260 EMI---ETKVKVEKANDSNPNESKTKTDKNPEESKSPKSTTVRCLEAE 305  
DB 302 KLIVINGNGTVEDRKPSELN-GEASKSQEMVHLVNKEPSETPDQCMTAD 349

RESULT 2

A30901  
lymphocyte adhesion receptor precursor - baboon  
C:Species: Papio sp. (baboon)  
C>Date: 18-Apr-1989 #sequence\_revision 18-Apr-1989 #text\_change 21-Jul-2000  
C:Accession: A33935; A30901  
R;Idzarda, R.L.; Carter, W.G.; Nottenburg, C.; Wayner, E.A.; Gallatin, W.M.; St. John, I.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4659-4663, 1989  
A;Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion recei  
A;Reference number: A33935; MUID:89282830; PMID:2471974





Db 251 QDSGANTTSPGRKPQIPWLLVLAFL-LALALILAVC-----I AVNSRRRCQKKLVI 304  
QY 264 TKVKEKANDSNENESKTKDNPE-----ESKSPSKTIVRCLEAE 305  
Db 305 NS--GNGKVERKSELNGEASKSQEMVHLVNKEPSTPDQMTAD 348

RESULT 5  
B38745  
cell adhesion molecule CD44 precursor, long form (meta-1) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 09-Jul-2004  
C:Accession: B38745; A38745  
R:Guenther, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; Haubmann, I.; Matzku, S.  
Cell 65, 13-24, 1991  
A:Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcinoma  
A:Reference number: A38745; MUID:91191552; PMID:1707342  
A:Accession: B38745  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-503 <GUE>  
A:CROSS-references: UNIPROT:P26051; UNIPARC:UPI0000012736D; GB:M61874; NID:g576534; PIDN:  
A:Accession: A38745  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-223,386-503 <GU2>  
A:CROSS-references: UNIPARC:UPI00000179A9B; GB:M61875  
C:Keywords: cell adhesion

Query Match 13.8%; Score 217; DB 2; Length 503;  
Best Local Similarity 25.8%; Pred. No. 9e-10;  
Matches 83; Conservative 40; Mismatches 161; Indels 38; Gaps 11;

QY 4 LVQSLRAEELSIVQSCRMGITLVSKKANQQLNFTKEAKRLLGLSLAGKQDVETALK 63  
Db 15 LQLSLAQQIDILNITRYAGVHFVEKNGRYSISRTEAADLCEAFNITLPTMAQMEALR 74

QY 64 ASPTCSYGVWGDGVFVVISRISPNPKCGKNGVGLVWKVPVSRQFAAYCVNSSDTWTNSC 123  
Db 75 KGFETCRYGFI-EGHVVIPRIHPNACAANTGVYLLASNTSHYDTYCFNAPALEEDC 133

QY 124 IPEIITTKDPIFNTQTATOTTEFIVSDST--YSVASPYST-----IPAPT----- 166  
Db 134 -----TSVTDLPNSFDGPVITIVNRDGTYSKKGEVTRHQEIDASNIIDEDVSSGTI 188

QY 167 --TTPPA-PASTSIPRRKLLICVTEVPMTSTWST-ETEPFVNKAFAFNKAAAGFGV-- 220  
Db 189 EKSTPEGYILHLDLPTSQPTGDRDDAFFIGSTILATITTPWSAHTKQOERTQWNPIS 248

QY 221 -PTALLVLALLFFGAAAGLFCVYKRYVK--AFPFTNKQOKEMIETKVVKKEKANDSNP 277  
Db 249 NPEVLQTTTRMTDIDRNSTSAHGENWNTQPPFNNHEVQDBE-ETPHATSTTWDAPNS 307

QY 278 NEESKTKDK-----NPEESKSP 294  
Db 308 TTEEAATQKEWFENWQGNP 329

RESULT 6  
A53286  
cell-surface glycoprotein CD44 precursor - bovine  
N:Alternate names: CD44 protein  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A53286; S22123  
R:Rosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.  
Mol. Immunol. 28, 1131-1135, 1991  
A:Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.  
A:Reference number: A53286; MUID:92017904; PMID:1922105  
A:Accession: A53286  
A:Molecule type: mRNA  
A:Residues: 1-366 <BOS>

A:CROSS-references: UNIPROT:Q29423; UNIPARC:UPI00000127366; EMBL:X62881; NID:g186; PIDN:  
A>Note: sequence extracted from NCBI backbone (NCBI:63418, NCBI:63419)  
C:Superfamily: human cell adhesion protein CD44  
C:Keywords: cell adhesion; glycoprotein; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>  
F:274-294/Domain: transmembrane #status predicted <TM>  
F:25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.2%; Score 208.5; DB 2; Length 366;  
Best Local Similarity 23.8%; Pred. No. 2.9e-09;  
Matches 81; Conservative 44; Mismatches 142; Indels 73; Gaps 11;

QY 4 LVQSLRAEELSIVQSCRMGITLVSKKANQQLNFTKEAKRLLGLSLAGKQDVETALK 63  
Db 14 LVQLSL--AQIDINITRYAGVHFVEKNGRYSISRTEAADLCEAFNITLPTMAQMEALR 71

QY 64 ASPTCSYGVWGDGVFVVISRISPNPKCGKNGVGLVWKVPVSRQFAAYCVNSSDTWTNSC 123  
Db 72 IGFETCRYGFI-EGHVVIPRIHPNACAANTGVYLLTNTS-QYDTICFNASAPPGEDC 129

QY 124 IPEIITTKDPIFNTQTATOTTEFIVSDST--YSVASPYSTIP-----APTTPPAPAS 174  
Db 130 -----TSVTDLPNAFEGPITITIVNRDGTTRYTKGGEYRTNPEDINPSVSPSPDDEMS 184

QY 175 TSIPRRKLLICVTEVP-----METSTMSTETETEPFVNKAAPK 211  
Db 185 SGSPSERSTSGGYSIFHTHLPTVHPSPRRPMSQRANSTSDTRDYGSSHDPSGRSYTHA 244

QY 212 NEAAGFGG-----VPTALLVLALLFFGAAAGLFCVYKRYKRVKAPFT 253  
Db 245 SESAGHSSGSEHGANTTSGPMRKQIPWLLILASL-LALALILAVC-----IAVNSRR 298

QY 254 NKNQOKEMETKVVKKEKANDSNPNEESKTKDNPEESKS 293  
Db 299 RCQKKKLVIN-----NGNGTMEERKPSGLNGEASKS 330

RESULT 7  
JH0417  
cell adhesion molecule CD44 - human  
C:Species: Homo sapiens (man)  
C>Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 31-Dec-2004  
C:Accession: JH0417; A32376; G02251; A32377  
R:Harn, H.J.; Isola, N.; Cooper, D.L.  
Biochem. Biophys. Res. Commun. 178, 1127-1134, 1991  
A:Title: The multispecific cell adhesion molecule CD44 is represented in reticulocyte  
A:Reference number: JH0417; MUID:91337049; PMID:1840487  
A:Accession: JH0417  
A:Molecule type: mRNA  
A:Residues: 1-361 <HAR>  
A:CROSS-references: UNIPROT:Q92493; UNIPARC:UPI000016A68F; GB:M59040; NID:g180129; PIDN:  
A:Experimental source: reticulocyte  
A>Note: The authors translated the codon ATG for residues 63, 66 and 239 as Trp and GGA  
R:Stamenkovic, I.; Amiot, M.; Pesando, J.M.; Seed, B.  
Cell 56, 1057-1062, 1989  
A:Title: A lymphocyte molecule implicated in lymph node homing is a member of the cartil  
A:Reference number: A32376; MUID:89168434; PMID:2466575  
A:Accession: A32376  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-238, 'E', 240-361 <STA>  
A:CROSS-references: UNIPARC:UPI0000143A5B; GB:M24915; NID:g180196; PIDN:AAA35674.1; PID  
R:Bosch, P.P.; Stevens, J.W.; Buckwalter, J.A.; Midura, R.J.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: H00921  
A:Accession: G02251  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-25, 'M', 27-108, 'S', 110-361 <BOS>  
A:CROSS-references: UNIPARC:UPI000016A285; EMBL:U40373; NID:g1101785; PID:g1101786  
R:Goldstein, L.A.; Zhou, D.F.H.; Picker, L.J.; Minty, C.N.; Bargatze, R.F.; Ding, J.F.;  
Cell 56, 1063-1072, 1989

A>Title: A human lymphocyte homing receptor, the hermes antigen, is related to cartilage  
A:Reference number: A32377; MUID:89169435; PMID:2466576  
A:Accession: A32377  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108,'S',110-293,'S' <GOL>  
A:Cross-references: UNIPARC:UPI0000070BED; GB:W25078; NID:ig186660; PIDN:AAA36138.1; PID:  
C:Keywords: alternative splicing; cell adhesion; surface antigen; transmembrane protein  
F:269-285/Domain: transmembrane #status predicted <TMM>

Query Match 13.0%; Score 205; DB 2; Length 361;  
Best Local Similarity 23.2%; Pred. No. 9.3e-09;  
Matches 83; Conservative 46; Mismatches 145; Indels 66; Gaps 14;

Qy 9 LRABELGIQVSCRMIGITLVSKKANQQLNFTEAKACRLGLSLAGKDDQVETALKASFET 68  
Db :  
17 LSLAQIDLNTICRVAGVFHVEKNGRYSISRTAAADLCKAFNSTLPTWAQERALSVCGET 76  
Qy CSYGWVGDFGVVISRI SPNPKCGKGNVGVLWKVPVSQRQAAYCYNSSDTWTNSCIPEII 128  
Db :  
77 CRYGFI-EGHVVI-PRIHPNSICAANTGVILTYNTS-QYDITYCFNASAPPEEDC----- 129  
Qy TTKDPINFQTATOTTFFIVSDST-YSVASPSYTI PA---PTTPPPAPASTSI PRKKLI 184  
Db :  
130 TSVYDLNFAFDGPITITIVNRDGRYYQKG EYRNPNEDI YPSNPDTDDVSSGGSSERSST 189  
Qy 185 CVTEVFVETSTM-----STETSPFVNKA AFK-----NEAAGF---- 217  
Db :  
190 SGGYIFTFSTVHIPIPEDSPWITDSIRI PATRDQOTFHPSGGSHTHSESDGHS HGS 249  
Qy 218 --GG-----VPTALLVALLEFPGAAGLGF CYVKRYKAFPTFNKQKQEMIE 263  
Db || :  
250 QEGGANITSGPI RTPQIP EMLI I LASL-LALALILAVC-----IAVNSRRRCG KKLVI 303  
Qy 264 TK---VVKEEKANDSNPESKTKDK-----NPESKSPSK 296  
Db :  
304 NSGNGAVE DRKPGLN-GEASKSQE MVHLV NKESSETPDQ 342

RESULT 8  
S45305  
CD44 antigen precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C>Date: 20-Oct-1994 #sequence\_revision 21-Jul-1995 #text\_revision 09-Jul-2004  
C:Accession: S45305  
E:Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.  
Biochim. Biophys. Acta 1218, 112-114, 1994  
A>Title: Molecular cloning of the canine CD44 antigen cDNA.  
A:Reference number: S45305; MUID:94250687; PMID:7514890  
A:Accession: S45305  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-351 <MIL>  
A:Cross-references: UNIPROT:Q28284; UNIPARC:UPI0000127367; EMBL:Z27115; NID:9473226; PID:  
C:Superfamily: human cell adhesion protein CD44

Query Match 12.8%; Score 202; DB 2; Length 351;  
Best Local Similarity 23.2%; Pred. No. 9.3e-09;  
Matches 81; Conservative 49; Mismatches 141; Indels 78; Gaps 14;

Qy 9 LRABELGIQVSCRMIGITLVSKKANQQLNFTEAKACRLGLSLAGKDDQVETALKASFET 68  
Db :  
10 LSLAQIDLNTICRVAGVFHVEKNGRYSISRTAAADLCKAFNSTLPTWAQERALSVCGET 69  
Qy CSYGWVGDFGVVISRI SPNPKCGKGNVGVLWKVPVSQRQAAYCYNSSDTWTNSCIPEII 128  
Db :  
70 CRYGFI-EGHVVI-PRIQPNAICAAHTGVVI-LISNTSYDYTCFNASAPPEEDC----- 122  
Qy TTKDPINFQTATOTTFFIVSDST-YSVASPSYTI PA---PTTPPPAPASTSI PRKKLI 184  
Db :  
123 TSVYDLNFAFDGPITITIVNRDGRYYQKG EYRNPNEDI YPSNPDTDDVSSGGSSERSST 182  
Qy 185 CVTEVFV-----METSTMTSTETE-----PFVENKA AFKN EAAGF-- 217

A;Experimental source: lymphocyte, cell line KGla  
R;Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta,  
Biochem. Biophys. Res. Commun. 182, 569-578, 1992  
A;Title: The complex CD44 transcriptional unit: alternative splicing of three internal e  
A;Reference number: PH0859; MUID:92134271; PMID:1734871  
A;Accession: PH0859  
A;Molecule type: DNA  
A;Residues: 223-357 <COO>  
A;Cross-references: UNIPARC:UPI000017951B  
R;Brown, T.A.; Bouchard, T.; St. John, T.; Wayne, E.; Carter, W.G.  
J. Cell Biol. 113, 207-221, 1991  
A;Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfat  
A;Reference number: A39209; MUID:91177958; PMID:2007624  
A;Accession: A39209  
A;Molecule type: mRNA  
A;Residues: 184-376 <BRO>  
A;Cross-references: UNIPARC:UPI000016A690; GB:X55938; NID:G29802; PIDN:CAA39404.1; PID:9  
R;Jackson, D.G.; Buckley, J.; Bell, J.I.  
J. Biol. Chem. 267, 4732-4739, 1992  
A;Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by ind  
A;Reference number: A42402; MUID:92165834; PMID:1537855  
A;Accession: A42402  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 217-223,288-359 <JAC>  
A;Cross-references: UNIPARC:UPI000017951C  
A;Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)  
A;Note: variant B  
A;Accession: C42402  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 217-320 <JA2>  
A;Cross-references: UNIPARC:UPI000017951D  
A;Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)  
A;Note: variant D  
R;Shepley, M.P.; Racantello, V.R.  
J. Virol. 68, 1301-1308, 1994  
A;Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocy  
A;Reference number: A53029; MUID:94149816; PMID:7508992  
A;Accession: A53029  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 67-76,'X',78-89 <SHE>  
A;Cross-references: UNIPARC:UPI000006D03F  
C;Genetics:  
A;Gene: GDB:CD44; MDU2; MDU3; MI  
A;Cross-references: GDB:120739; OMIM:107269  
A;Map position: lppter-11p13  
A;Introns: 35/1; 65/1; 133/1  
C;Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glyco  
F;1-426/Product: lymphocyte homing receptor CD44, splice form CD44R1 #status predicted  
F;1-223,288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status pre  
F;299/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;354/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 12.7%; Score 199.5; DB 2; Length 426;  
Best Local Similarity 22.2%; Pred. No. 1.9e-08;  
Matches 83; Conservative 48; Mismatches 138; Indels 105; Gaps 12;

QY 9 LRAEELSIQVSCRMIGITLVSKKANQNLNFTKAEACRLGLSLAGKQDVETALKASFET 68  
Db 17 LSLAQIDLNITCFAGVFHVEKNGRYSISRTAEADLCKAFNSTLPTMAQEKALSTGFET 76

QY 69 CSYGWVGDFVVISRISPNPKCGKGVLIWKVPVSQFAAYCYNNSDTWTNSCI-----124  
Db 77 CRYGFI-EGHVVIPIHPNSICAAANTGVYILTNTS-QYDTYCFNASAPPEDECTSVTD 134

QY 125 -----PEIITTKDPIFNQTATQTE-----FI 147  
Db 135 LPNAFDGPITITIVNRDGRYVQKGEYRTNPEDIYPSNPTDDVSSGSSERSSTSGGYI 194

QY 148 -----VSDST-----YSVASPYSTIPAPTTTPPAPASTSIPRRKKLIC 185

Db 195 FYTFSTVHPIDEDSPWITDSDRIPATNMDSHSTLTQPTANPTGLVEDLDRGTGLSM 254  
QY 186 VTEVFNETMTSTETETPPFVENK-----AAFKEAEAGFGGVP-----TALLVLALL 230  
Db 255 TTQQ-SNSQSFSTSHGLEEDKDHPTTSTLTSSNRNDVTGRRDPNHSBGSITLL-----308  
QY 231 FFGAAAGLGCYVRYKVPFNTNKKQKEMETKV-----VKEEKANDSNPN-BESKKT 284  
Db 309 -----EGYTSHPHTKESRTFIPVTSKTSFGVTATVGDNSNVNRLSLG 355  
QY 285 DKNPEESKSPSKTT 298  
Db 356 DDTFHPGSGSHTT 369

RESULT 11  
SI3530  
CD44E protein, epithelial - human  
C;Species: Homo sapiens (man)  
C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
C;Accession: SI3530  
R;Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.  
EMBO J. 10, 343-348, 1991  
A;Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with  
A;Reference number: SI3530; MUID:91122041; PMID:1991450  
A;Accession: SI3530  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-493 <STA>  
A;Cross-references: UNIPARC:UPI0000159271; EMBL:X55150; NID:G29800; PIDN:CAA38951.1; PID:  
C;Keywords: transmembrane protein

Query Match 12.7%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 2.3e-08;  
Matches 66; Conservative 39; Mismatches 100; Indels 75; Gaps 8;

QY 9 LRAEELSIQVSCRMIGITLVSKKANQNLNFTKAEACRLGLSLAGKQDVETALKASFET 68  
Db 17 LSLAQIDLNITCFAGVFHVEKNGRYSISRTAEADLCKAFNSTLPTMAQEKALSTGFET 76

QY 69 CSYGWVGDFVVISRISPNPKCGKGVLIWKVPVSQFAAYCYNNSDTWTNSCI-----124  
Db 77 CRYGFI-EGHVVIPIHPNSICAAANTGVYILTNTS-QYDTYCFNASAPPEDECTSVTD 134

QY 125 -----PEIITTKDPIFNQTATQTE-----FI 147  
Db 135 LPNAFDGPITITIVNRDGRYVQKGEYRTNPEDIYPSNPTDDVSSGSSERSSTSGGYI 194

QY 148 -----VSDST-----YSVASPYSTIPAPTTTPPAPASTSIPRRKKLIC 185

Db 195 FYTFSTVHPIDEDSPWITDSDRIPATNMDSHSTLTQPTANPTGLVEDLDRGTGLSM 254

QY 186 VTEVFNETMTSTETETPPFVENK-----AAFKEAEAG 216  
Db 255 TTQQ-SNSQSFSTSHGLEEDKDHPTTSTLTSSNRNDVTG 293

RESULT 12  
I77371

CD44R5 - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jul-2000  
C;Accession: I77371  
R;Tanabe, K.K.; Nishi, T.; Saya, H.  
Mol. Carcinog. 7, 212-220, 1993  
A;Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44  
A;Reference number: I57483; MUID:93356912; PMID:8352881  
A;Accession: I77371  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-395 <RES>  
A;Cross-references: UNIPARC:UPI000016B3F6; GB:S66400; NID:G435697; PIDN:AAB27919.1; PID:  
C;Genetics:

A; Gene: GDB:CD44  
A; Cross-references: GDB:120739; OMIM:107269  
A; Map position: 11pter-11p13  
A; Introns: 257/1  
C; Superfamily: human cell adhesion protein

Query Match	12.6%;	Score 198;	DB 2;	Length 395;
Best Local Similarity	23.0%;	Pred. No. 2.3e-08;		
Matches	85;	Conservative 49;	Mismatches 145;	Indels 90; Gaps 14
Qy	9	LRAELSTFOVSCRIMGITLVSKKANQQLNFTFEAKELGLSLAGKQDVETALKASPET	68	
Db	17	LSLAQIDLNIITCRFAGVHVFKNGRYSISRTAEADLCRAFNSILFTMAQMEKALSIGPET	76	
Qy	69	CSYGWVGDFGVVISRISPNPCGKNGVGLWKVPVSQFAAYCNSSDTWTNSCI----	124	
Db	77	CRYGFI-EGHVVIPIRIHENSICAAANTGVYILTSNTS-QYDYTCFNASAPPEEDCTSVTD	134	
Qy	125	-----PEILTKDPIENTQTATQTTTFEIVSDS----	151	
Db	135	LPNAPDGIITIVNRDGRYVQGEYTNPDYPSNPTDDVSSGSSRSSTSGGYI	194	
Qy	152	---TYSVASPY-----STIPATPTTPAPASTSI-PRKKLICVTEVFMEFTSTWST	198	
Db	195	FYTETVHPIPDSDSPWITDSTRIPATNMDSHSTTLOPTANPNMTGLVEDLDRGPIISM	254	
Qy	199	ET-----EPFVENKAAFNRBAAGF-----GG-----VPTALLVLIALLFPGA	234	
Db	255	TTRDQDTFHPGGSHHTTHGSESDGHSGSQEGGANTTSGPIRTPOIPEWLIIASL-LAL	313	
Qy	235	AAGLGFCYVKRYVKAFFPTNKNOQKEMLETK--VVEEKANDSNPNESKTKDK----	287	
Db	314	ALIILAVC-----IAVNSRRRCGOKKXVLVNSNGAVEDRKPSGLN-GEASKSQEWMHLVN	367	
Qy	288	PEESKPSPK	296	
Db	368	KESSETPDO	376	

RESULT 13  
I37369  
epican - human  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 03-Aug-2001  
C:Accession: I37369; S24631  
R:Kugelman, L.C.; Ganguly, S.; Haggerty, J.G.; Weissman, S.M.; Milstone, L.M.  
J. Invest. Dermatol. 99, 866-891, 1992  
A:Title: The core protein of epican, a heparan sulfate proteoglycan on keratinocytes, is  
A:Reference number: I37369; PMID:1281868  
A:Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992  
A:Accession: I37369  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-699 <RSS>  
A:Cross-references: UNIPARC:UPI000016A89D; EMBL:X66733; NID:g311190; PID:g31191

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Qy	9	LRAELSIGQVSCRMGITLTKSKANQOLNFTPEAKERLLGLSLAGKQDVETALKASPET	68	
Db	17	LSLAQIDLNITCRFAGVHFVEKGRYGISRTEAADLCKAFNSTIPTTWAQMEKALUSIGFET	76	
Qy	69	CSYGWVGDGFFVIGRIISPNPKCGNGVGLIWKVFSRQFAAYCYNSSSDTWTNSCI----	124	
Db	77	CRYGFI-EGHVVIPIRIHENSICAAANTGVYILTNTS-QYDITYCFNASAPPEEDCTSVTD	134	
Qy	125	-----PEITTKDPINQATQTATQTTTFEIVSDSTYS	154	
Db	135	LPNAFDGPITITIVNRDTRFYVKGERYTNPEDYPSNPTDDDDVSSGSSRSSTSGGY-	193	
Qy	155	VASPSYTI-PAPTTTTP--APASTSIPIRRKKLICVTEVFMEITSMSTETETPFPVFNK	207	

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Db      194 IFYFTSVHPIDEDSPWITDTRIPATS-:::|||::|||:
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RESULT 14
S24240 lymphocyte surface antigen CD44 precursor - horse
C/Species: Equus caballus (domestic horse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2000
C/Accession: I46245; S24240
R/Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; D
Immunogenetics 37, 474-477, 1993
A/Title: Molecular cloning of equine CD44 cDNA by a COS cell expression sy
A/Reference number: I46245; MUID: 93170897; PMID: 8436424
A/Accession: I46245
B/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-359 <YA2>
A/Cross-references: UNIPROT:Q05078; UNIPARC:UPI0000127369; EMBL:X66862; NI
C/Superfamily: human cell adhesion protein CD44
C/Keywords: surface antigen; transmembrane protein

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Qy	69	CSYGWVGDGFWFVISRISPNPKCGKNGVGVLTKWVPVSRQFAAYCVNSSDWTNNSCI----	124				
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Qy	125	-----PEIIT-----TKDPIENTOTATOTTFFIVSDSYSVASVPYST	161				
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Qy	208	AAFKNEAAGFGGVPALTLLVLLALFPFGAAAGLFCVVKRYKAFPTNKNQOKEMTIETK--	265				
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RESULT 15  
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N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein  
C;Species: Gallus gallus (Chicken)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072  
R;Li, H.; Schwartz, N.B.; Vertel, B.M.  
J. Biol. Chem. 268, 23504-23511, 1993  
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and  
A;Reference number: A48884; MUID: 94043149; PMID: 8226878  
A;Accession: I50421  
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A;Residues: 1-2109 <IIX>  
A;Cross-references: UNIPROT:P07898; UNIPARC:UPI000013177F; GB:L21913; NID:g416133; PIDN:f  
B;Chandrasekaran, L.; Tanzer, M.L.  
Biochem. J. 296, 885-887, 1993  
A;Reference number: S39796; MUID: 94107258; PMID: 8280087  
A;Contents: annotation; erratum  
A;Accession: S39796  
A;Molecule type: mRNA

A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1602,'A'  
A;Cross-references: UNIPARC:UPI0000173C73; GB:M88101  
R;Chandrasekaran, L.; Tanzer, M.L.  
Biochem. J. 288, 903-910, 1992  
A;Title: Molecular cloning of chicken aggrecan. Structural analyses.  
A;Reference number: S27356; MUID:93111968; PMID:1339285  
A;Accession: S27356  
A;Molecule type: mRNA  
A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1549,'T'  
A;Cross-references: UNIPARC:UPI0000173C74; UNIPARC:UPI0000173C75; EMBL:M88101  
R;Sai, S.; Tanaka, T.; Koshier, R.A.; Tanzer, M.L.  
Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986  
A;Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteogly  
A;Reference number: A25442; MUID:86259736; PMID:3460082  
A;Accession: A25442  
A;Molecule type: mRNA  
A;Residues: 1693-1795,'G',1797-1855,1894-2109 <SAI>  
A;Cross-references: UNIPARC:UPI00001712F6; GB:M13993; NID:g211654; PIDN:AAA48720.1; PID:  
A;Experimental source: sternal cartilage  
R;Tanaka, T.; Har-El, R.; Tanzer, M.L.  
J. Biol. Chem. 263, 15831-15835, 1988  
A;Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.  
A;Reference number: A32002; MUID:89008500; PMID:3170613  
A;Accession: A32002  
A;Molecule type: DNA  
A;Residues: 1893-1987,'S',1989-2022 <TAN>  
A;Cross-references: UNIPARC:UPI0000173C76  
A;Note: the authors translated the codon TCC for residue 1787 as Phe  
R;Kruoger, R.C.  
J. Biol. Chem. 265, 12088-12097, 1990  
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide s  
A;Reference number: I50216; MUID:90307744; PMID:1694853  
A;Accession: I50216  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 'FA',1044-1559 <XRU>  
A;Cross-references: UNIPARC:UPI00001712F8; GB:M38187; NID:g211685; PIDN:AAA48731.1; PID:  
R;Kruoger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.  
J. Biol. Chem. 265, 12075-12087, 1990  
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation an  
A;Reference number: A37072; MUID:90307743; PMID:2365711  
A;Accession: A37072  
A;Molecule type: protein  
A;Residues: 998-1015,'X',1017-1019,'X',1021-1023 <KR2>  
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A;Note: amino end of 86K core peptide CS-A  
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A;Cross-references: UNIPARC:UPI0000173C78  
A;Note: amino end of 75K core peptide CS-B  
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C;Keywords: alternative splicing  
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F;21-2109/Product: aggrecan #status predicted <MAT>  
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F;166-243/Domain: link protein repeat homology <LNK1>  
F;264-346/Domain: link protein repeat homology <LNK2>  
F;537-614/Domain: link protein repeat homology <LNK3>  
F;635-716/Domain: link protein repeat homology <LNK4>  
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QY 92 KNGVGV-LIWKVPV-----SRQFAACYNNSDWTNNSCIP-----EIIITTKDPIFNT 137

Db 316 GNLVGVRTVYLNPNANQGYPHPSRYDAICYSDD--FEALVPGLFTDEVGTELGSFTI 373  
QY 138 QTATQT-----TEFIVSDTSYVASPYSTIPATTTTPAPASTSIPRRKKLICVT 187  
DB 374 QTVTQTEVELPLPRNVTE---EEARGSIATLEPMEITATATELYEATVLPD----LPAT 426  
QY 188 EFMETSTMTSTETEPFVENKAAPKNEAAGFGGVPSTALLVLALLFFGAAAGLFCYVKRYV 247  
DB 427 SVTVETAS-----PREEN--VTREITGIWAVPE-----VTTSV 459  
QY 248 KAPFTNKQKQKEMIEKVKVKEKANDSNPNES 281  
DB 460 SGTAFTT-----GMAEVSSVEEAIAVTATPGLS 488

Search completed: March 20, 2006, 14:09:54  
Job time : 16.7123 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 14:08:48 ; Search time 66.0354 Seconds  
(without alignments)  
3269.333 Million cell updates/sec

Title: US-10-063-510-6\_COPY\_17\_322  
Perfect score: 1575  
Sequence: 1 TRLLVQSLRAEELSIQVSC.....NPBEKSPSKTTVRCLEAEV 306

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1055	67.0	318	2 Q99NE4_MOUSE	Q99NE4 mus musculus
7	726.5	46.1	201	2 Q7YS22_PIG	Q7YS22 sus scrofa
8	245	15.6	392	2 Q5815_XENLA	Q5815 xenopus lae
9	241	15.3	441	2 Q6GM56_XENLA	Q6GM56 xenopus lae
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11	229.5	14.6	437	2 Q6P8A2_XENTR	Q6P8A2 xenopus tro
12	222.5	14.1	362	1 CD44_PAPHA	P14745 papio hamad
13	222	14.1	364	2 Q70509_RAT	Q70509 rattus norv
14	217	13.8	503	1 CD44_RAT	CD44 rat
15	214.5	13.6	780	2 Q08779_RAT	Q08779 rattus norv
16	212.5	13.5	431	1 CD44_MESAU	Q60522 m cd44 anti
17	211	13.4	265	2 Q98RS5_ANAPL	Q98RS5 anas platyr
18	209.5	13.3	398	2 Q90ZL8_ANAPL	Q90ZL8 anas platyr
19	209.5	13.3	778	1 CD44_MOUSE	P15379 mus musculus
20	208.5	13.2	366	1 CD44_BOVIN	Q29423 bos taurus
21	204	13.0	361	2 Q86T72_HUMAN	Q86T72 homo sapien
22	203.5	12.9	364	2 Q97569_CERSI	Q97569 ceratotheri
23	203.5	12.9	396	2 Q9W6S4_CHICK	Q9W6S4 gallus gall
24	203	12.9	742	2 Q9UQ36_HUMAN	Q9UQ36 homo sapien
25	202	12.8	351	1 CD44_CANFA	Q28284 canis fami
26	202	12.8	361	2 Q8N694_HUMAN	Q8N694 homo sapien
27	202	12.8	742	1 CD44_HUMAN	P16070 h cd44 anti
28	200.5	12.7	580	2 Q80X37_MOUSE	Q80X37 mus musculus
29	199.5	12.7	493	2 Q86227_HUMAN	Q86227 homo sapien
30	199.5	12.7	493	2 Q5R9V4_PONPY	Q5R9V4 pongo pygma
31	199	12.6	338	2 Q9H5A4_HUMAN	Q9H5A4 homo sapien

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Q9H5A5	HUMAN	2	719	12.5	197	33
Q92493	HUMAN	2	294	12.4	196	34
Q9H5A7	HUMAN	2	676	12.2	191.5	35
Q9H5A3	HUMAN	2	271	12.1	191	36
Q9H5A6	HUMAN	2	470	12.1	191	37
Q05078	equus caball	1	359	11.8	186	38
Q48195	tetraodon n	2	153	11.0	173.5	39
Q29011	sus scrofa	1	537	9.5	150	40
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P07898	gallus gall	1	2109	9.4	148.5	42
Q9BGH3	sus scrofa	2	494	9.2	145.5	43
Q90953	gallus gall	1	3562	9.2	145.5	44
P98066	homo sapien	1	277	9.2	145	45
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Q28343	canis fami	1	2333	8.9	139.5	55
P98065	oryctolagus	1	276	8.7	137	56
Q8r4u0	mus musculus	1	2559	8.6	136	57
Q62913	rattus norv	2	514	8.4	133	58
Q8c6m6	rattus norv	1	1431	8.4	133	59
Q8wq88	h scabalin-	1	2551	8.4	133	60
Q6WpD9	homo sapien	2	721	8.4	132.5	61
Q481v9	tetraodon n	2	1046	8.4	132	62
P07897	rattus norv	1	2124	8.3	131.5	63
Q48e78	tetraodon n	2	314	8.3	131	64
Q61282	mus musculus	1	2132	8.3	131	65
Q61361	mus musculus	1	883	8.3	130.5	66
P55068	rattus norv	1	883	8.3	130.5	67
Q80wt7	mus musculus	2	883	8.3	130.5	68
Q90wm2	xenopus lae	2	1152	8.3	130.5	69
P16112	homo sapien	1	2415	8.3	130.5	70
Q9ny15	homo sapien	1	2570	8.3	130.5	71
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Q4rv64	tetraodon n	2	845	8.1	128	73
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Q96gw7	homo sapien	1	911	8.1	127.5	76
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Q4SE77	TETNG	2	1091	7.7	121.5	88
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Q75Z13	BRARE	2	1570	7.7	120.5	90
Q4SHL9	TETNG	2	313	7.6	120	91
Q702X4	HV1	2	411	7.6	119.5	92
Q7ZX17	XENLA	2	359	7.6	119	93
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Q55V99	HUMAN	2	3410	7.5	118.5	95
Q702X3	HV1	2	397	7.5	117.5	96
Q41QU7	GBZE	2	537	7.4	117	97
Q55DV2	DICDI	2	1452	7.4	117	98
Q8BS97	MOUSE	2	368	7.4	116	99
Q4VA91	MOUSE	2	368	7.4	116	100
CSFG2_RAT		1	2738	7.4	116	101
Q4RLD6	TETNG	2	744	7.3	115.5	102
Q7M2W7	PIG	2	370	7.3	115	103
Q6DCI6	XENLA	2	394	7.3	115	104



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106	114.5	7.3	1039	2	Q4S473_TETNG	Q4S473	tetraodon n	179	102	6.5	404	2	Q702Y3_HHV1	Q702Y3 human herpe
107	114.5	7.3	1257	1	CSFG3_RAT	P5067	rattus norv	180	102	6.5	527	2	Q54V00_DICDI	Q54V00 dictyosteli
108	114	7.2	610	2	Q9N3C0_CAEBL	Q9N3C0	caenorhabdi	181	102	6.5	1879	2	Q4VZL0_CUCSA	Q4VZL0 cucumis sat
109	113.5	7.2	289	2	Q60T22_CAEBR	Q60t22	caenorhabdi	182	101.5	6.4	380	2	O02343_CAEBL	O02343 caenorhabdi
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111	113.5	7.2	1290	2	Q9W6E1_CHICK	Q9w6el	gallus gall	184	101.5	6.4	1893	2	Q9NKC9_DROME	Q9nkc9 drosophila
112	113	7.2	459	2	Q54G90_DICDI	Q54g90	dictyosteli	185	101.5	6.4	4370	2	Q4QJQ2_LEIMA	Q4qlq2 leishmania
113	113	7.2	892	1	LDLR2_XENLA	Q99088	xenopus lae	186	101	6.4	700	2	Q8TG00_ASPFU	Q8tg00 aspergillus
114	112.5	7.1	340	1	HPLN2_HUMAN	Q99z7	homo sapien	187	101	6.4	700	2	Q4WS89_ASPFU	Q4ws89 aspergillus
115	112.5	7.1	340	1	Q5T3J0_HUMAN	Q5t3j0	homo sapien	188	101	6.4	708	2	Q18175_CAEBL	Q18175 caenorhabdi
116	112.5	7.1	417	1	PGCB_FELCA	P41725	felis silve	189	101	6.4	1777	2	Q54FB8_DICDI	Q54fb8 dictyosteli
117	112	7.1	210	2	Q8C9U7_MOUSE	Q8c9u7	mus musculus	190	101	6.4	2535	2	Q755B8_ASHGO	Q755b8 ashbya goss
118	112	7.1	390	1	VGLI1_HHV1	P66487	human herpe	191	100.5	6.4	353	2	Q4IH62_GIBZE	Q4ih62 gibberella
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122	111	7.0	359	2	QSR1X6_RAT	Q8rlx6	rattus norv	195	100.5	6.4	1121	2	Q59YM6_CANAL	Q59ym6 candida alb
123	110	7.0	363	2	Q5NV41_BRARE	Q5nv41	brachydanio	196	100.5	6.4	1121	2	Q7Z884_CANAL	Q7z884 candida alb
124	109	6.9	816	2	Q70474_RAT	Q70474	rattus norv	197	100	6.3	319	2	Q4S1V7_TETNG	Q4s1v7 tetraodon n
125	109	6.9	1321	1	CSFG3_HUMAN	Q14594	homo sapien	198	100	6.3	403	2	Q702W8_HHV1	Q702w8 human herpe
126	109	6.9	1335	2	Q4LE67_HUMAN	Q4le67	homo sapien	199	100	6.3	404	2	Q702W6_HHV1	Q702w6 human herpe
127	108.5	6.9	341	1	HPLN2_RAT	Q9esm2	rattus norv	200	100	6.3	404	2	Q702Y0_HHV1	Q702y0 human herpe
128	108.5	6.9	397	2	Q702X6_HHV1	Q702x6	human herpe	201	100	6.3	441	2	Q5BA48_EMENI	Q5ba48 aspergillus
129	108.5	6.9	1441	2	Q4S3C4_TETNG	Q4s3c4	tetraodon n	202	100	6.3	486	2	Q8FRY2_COREF	Q8fry2 corynebacte
130	108	6.9	354	1	HPLN1_HUMAN	P10915	homo sapien	203	100	6.3	738	2	Q5WN81_CAEBR	Q5wn81 caenorhabdi
131	108	6.9	359	1	HPLN3_MOUSE	Q80wm5	mus musculus	204	99.5	6.3	335	2	Q60H44_BRARE	Q60h44 brachydanio
132	108	6.9	624	2	Q19780_CAEBL	Q19780	caenorhabdi	205	99.5	6.3	478	2	Q7YX15_CAEBL	Q7yx15 caenorhabdi
133	107.5	6.8	739	2	O02360_CAEBL	O02360	caenorhabdi	206	99.5	6.3	577	2	Q52GY0_CAEBL	Q52gy0 caenorhabdi
134	107	6.8	354	1	HPLN1_RAT	P03994	rattus norv	207	99.5	6.3	1092	1	NCA12_XENLA	P36335 xenopus lae
135	107	6.8	355	1	HPLN1_CHICK	P07354	gallus gall	208	99.5	6.3	1117	2	Q54SZ6_DICDI	Q54sz6 dictyosteli
136	107	6.8	356	1	HPLN1_MOUSE	Q9eqp5	mus musculus	209	99.5	6.3	1165	2	Q60NC3_CAEBR	Q60nc3 caenorhabdi
137	107	6.8	543	2	Q4YVC9_PLABE	Q4yvc9	plasmodium	210	99.5	6.3	2297	2	Q5PZ43_BRARE	Q5pz43 brachydanio
138	107	6.8	862	2	Q3UF98_HUMAN	Q3uf98	homo sapien	211	99	6.3	178	2	Q8FQJ3_COREF	Q8fqj3 corynebacte
139	107	6.8	956	2	Q60MG7_CAEBR	Q60mg7	caenorhabdi	212	99	6.3	388	2	Q4H2F0_HPV27	Q4h2f0 human papil
140	107	6.8	1268	1	CSPG3_MOUSE	P5066	mus musculus	213	99	6.3	604	2	Q6E9B8_LISMO	Q6e9b8 listeria mo
141	107	6.8	1321	1	CSPG3_PANTR	Q5is41	pan troglod	214	99	6.3	896	2	O02253_CAEBL	Q02253 caenorhabdi
142	107	6.8	1795	2	Q76894_DROME	Q76894	drosophila	215	99	6.3	1100	2	Q8CCT8_MOUSE	Q8ccct8 mus musculus
143	106.5	6.8	1390	2	Q4XGK9_DICDI	Q4xgk9	dictyosteli	216	99	6.3	5376	1	ZAN_MOUSE	Q88799 mus musculus
144	106	6.7	1059	2	Q51SN4_MACFA	Q51sn4	macaca fasc	217	98.5	6.3	204	2	Q9N5Z8_CAEBL	Q9n5z8 caenorhabdi
145	106	6.7	1153	2	Q4IAN9_GIBZE	Q4ian9	gibberella	218	98.5	6.3	346	2	Q7S973_NEUCR	Q7s973 neurospora
146	105.5	6.7	374	2	Q9Z209_CHIGR	Q9z209	cricetulus	219	98.5	6.3	397	2	Q702W7_HHV1	Q702w7 human herpe
147	105.5	6.7	573	2	Q8CJD9_RAT	Q8cjd9	rattus norv	220	98.5	6.3	397	2	Q702X1_HHV1	Q702x1 human herpe
148	105.5	6.7	830	2	Q6CAY0_YARLI	Q6cay0	yarrowia li	221	98.5	6.3	425	2	Q702W3_HHV1	Q702w3 human herpe
149	105	6.7	354	1	HPLN1_BOVIN	P52522	bos taurus	222	98.5	6.3	578	2	Q63ZX6_MOUSE	Q63zx6 mus musculus
150	105	6.7	438	2	Q4X548_PLACH	Q4x548	plasmodium	223	98.5	6.3	1126	2	Q9VGK5_DROME	Q9vgk5 drosophila
151	105	6.7	463	2	Q7RNE3_PLAYO	Q7rne3	cryptospori	224	98.5	6.3	1203	2	Q6Z056_MOUSE	Q6z056 mus musculus
152	105	6.7	480	2	Q5CGY9_CRYHO	Q5cgy9	cryptospori	225	98	6.2	390	2	Q702W4_HHV1	Q702w4 human herpe
153	105	6.7	612	2	Q8CD44_YARLI	Q8cd44	yarrowia li	226	98	6.2	604	2	Q8GMR7_LISMO	Q8gmr7 listeria mo
154	104.5	6.6	862	1	CSFG2_MACNE	Q28858	macaca neme	227	98	6.2	604	2	Q6E9T6_LISMO	Q6e9t6 listeria mo
155	104	6.6	139	2	Q95370_HUMAN	Q95370	homo sapien	228	98	6.2	604	2	Q8GMR1_LISMO	Q8gmr1 listeria mo
156	104	6.6	354	1	HPLN1_HORSE	Q28381	equus cabal	229	98	6.2	1015	2	Q54V57_DICDI	Q54v57 dictyosteli
157	104	6.6	354	1	HPLN1_PIG	P10859	sus scrofa	230	98	6.2	2112	2	Q9VEL9_DROME	Q9vel9 drosophila
158	104	6.6	627	2	Q8MPJ9_DICDI	Q8mpj9	dictyosteli	231	97.5	6.2	297	2	Q7PR65_ANOGA	Q7pr65 anopheles g
159	104	6.6	681	2	Q55519_DICDI	Q55519	dictyosteli	232	97.5	6.2	385	2	Q9NHU9_DROMI	Q9nhu9 drosophila
160	104	6.6	1716	2	Q9I708_DROME	Q9i7q8	drosophila	233	97.5	6.2	505	2	Q4FYQ6_LEIMA	Q4fyq6 leishmania
161	104	6.6	1912	2	Q3VVS9_DROME	Q3vvs9	drosophila	234	97.5	6.2	553	2	Q8F932_LEPIN	Q8f932 leptospira
162	103.5	6.6	288	2	Q6PC93_9ADEN	Q6pcp9	simian aden	235	97.5	6.2	557	2	Q72V13_LEPIC	Q72v13 leptospira
163	103.5	6.6	616	2	Q58E94_BRARE	Q58ee4	brachydanio	236	97.5	6.2	836	2	Q55DF3_DICDI	Q55df3 dictyosteli
164	103.5	6.6	952	2	Q86A40_DICDI	Q86a40	dictyosteli	237	97.5	6.2	909	1	LDLR1_XENLA	Q55df3 dictyosteli
165	103.5	6.6	1197	2	Q3IS86_9PRIM	Q3is86	saimiri bol	238	97	6.2	294	2	Q54FY4_DICDI	Q54fy4 dictyosteli
166	103.5	6.6	1254	2	Q94185_CAEBL	Q94185	caenorhabdi	239	97	6.2	404	2	Q702Y6_HHV1	Q702y6 human herpe
167	103.5	6.6	1592	2	Q5AWR8_EMENI	Q5awr8	aspergillus	240	97	6.2	604	2	Q6E9K8_LISMO	Q6e9k8 listeria mo
168	103	6.5	80	2	Q86U21_HUMAN	Q86u21	homo sapien	241	97	6.2	604	2	Q6E9X2_LISMO	Q6e9x2 listeria mo
169	103	6.5	231	2	Q5T316_HUMAN	Q5t3i6	homo sapien	242	97	6.2	604	2	Q6EA16_LISMO	Q6ea16 listeria mo
170	103	6.5	232	2	Q5BD11_EMENI	Q5bdd1	aspergillus	243	97	6.2	889	2	Q4RUP0_TETNG	Q4rup0 tetraodon n
171	102.5	6.5	182	2	Q8I0D8_DROME	Q8i0d8	drosophila	244	97	6.2	1159	2	Q55GQ9_DICDI	Q55gq9 dictyosteli
172	102.5	6.5	183	2	Q9VT37_DROME	Q9vt37	drosophila	245	97	6.2	1604	2	Q4SNA3_TETNG	Q4sna3 tetraodon n
173	102.5	6.5	497	2	Q8QVC4_9REOV	Q8qvc4	eyach virus	246	96.5	6.1	268	2	Q5ATR9_EMENI	Q5atr9 aspergillus
174	102.5	6.5	590	2	Q5BG25_EMENI	Q5bg25	aspergillus	247	96.5	6.1	276	2	Q4NG33_DICDI	Q4ng33 dictyosteli
175	102.5	6.5	595	2	Q5UPW9_MIMIV	Q5upw9	mimivirus	248	96.5	6.1	385	2	Q9N666_DROMI	Q9n666 drosophila
176	102.5	6.5	699	2	Q8QV89_9REOV	Q8qve9	eyach virus	249	96.5	6.1	385	2	Q9NHU6_DROMI	Q9nhu6 drosophila
177	102	6.5	391	2	Q753G3_ASHGO	Q753g3	ashbya goss	250	96.5	6.1	397	2	Q702Y5_HHV1	Q702y5 human herpe

251	96.5	6.1	407	2	Q564S9_CABEL	Q564B9	caenorhabdi	324	94.5	6.0	1390	2	Q17602_CABEL	Q17602	caenorhabdi
252	96.5	6.1	465	1	YHU6_YEAST	P38845	saccharomyc	325	94.5	6.0	1622	2	Q54G21_DICDI	Q54G21	dictyosteli
253	96.5	6.1	604	2	Q8GNS1_LISMO	Q8GNS1	listeria mo	326	94.5	6.0	1942	2	Q8G1Z7_LACDL	Q8G1Z7	lactobacill
254	96.5	6.1	731	1	NOG2_CRYGA	O6T9J8	cryptococcu	327	94.5	6.0	3370	2	Q81IN9_PLAF7	Q81IN9	plasmodium
255	96.5	6.1	961	2	Q5ATY9_EMENI	Q5ATY9	aspergillus	328	94	6.0	239	2	Q5SC69_DICDI	Q5SC69	dictyosteli
256	96.5	6.1	961	2	Q92223_EMENI	Q92223	emericella	329	94	6.0	639	2	Q8GNS8_LISMO	Q8GNS8	listeria mo
257	96.5	6.1	1065	2	Q50ZFI_ENTHI	Q50ZFI	entamoeba h	330	94	6.0	639	2	Q6E8W8_LISMO	Q6E8W8	listeria mo
258	96.5	6.1	1403	1	LARP_DROME	Q9VAW5	drosoophila	331	94	6.0	639	2	Q6E922_LISMO	Q6E922	listeria mo
259	96	6.1	173	2	Q4KTX2_CEREL	Q4KX2	cervus elap	332	94	6.0	639	2	Q6E9G6_LISMO	Q6E9G6	listeria mo
260	96	6.1	232	2	Q4V322_DROME	Q4V322	drosoophila	333	94	6.0	639	2	Q6EA26_LISMO	Q6EA26	listeria mo
261	96	6.1	236	2	Q4V400_DROME	Q4V400	drosoophila	334	94	6.0	639	2	Q6EA68_LISMO	Q6EA68	listeria mo
262	96	6.1	429	2	Q76430_CABEL	Q76430	caenorhabdi	335	94	6.0	639	2	Q6EAP0_LISMO	Q6EAP0	listeria mo
263	96	6.1	449	2	Q71UN8_CABEL	Q71UN8	caenorhabdi	336	94	6.0	769	2	Q00816_TOXGO	Q00816	toxoplasma
264	96	6.1	481	2	Q5XUF4_CABEL	Q5XUF4	caenorhabdi	337	94	6.0	989	2	Q83U76_CHLTR	Q83U76	chlamydia t
265	96	6.1	545	2	Q5A7A3_CANAL	Q5A7A3	candida alb	338	94	6.0	989	2	Q84FU9_CHLTR	Q84FU9	chlamydia t
266	96	6.1	549	2	Q54WC8_DICDI	Q54WC8	dictyosteli	339	94	6.0	1067	2	Q5BGE6_EMENI	Q5BGE6	aspergillus
267	96	6.1	555	2	Q95X13_CABEL	Q95X13	caenorhabdi	340	94	6.0	1241	1	PER_DROPS	P12348	drosoophila
268	96	6.1	604	2	Q6E9R2_LISMO	Q6E9R2	listeria mo	341	93.5	5.9	278	2	Q4WIP3_ASFFU	Q4WIP3	aspergillus
269	96	6.1	604	2	Q6E9R8_LISMO	Q6E9R8	listeria mo	342	93.5	5.9	383	2	Q702W5_HHV1	Q702W5	human herpe
270	96	6.1	604	2	Q6EAJ7_LISMO	Q6EAJ7	listeria mo	343	93.5	5.9	385	2	Q9NHU8_DROMI	Q9NHU8	drosoophila
271	96	6.1	604	2	Q724K9_LISMF	Q724K9	listeria mo	344	93.5	5.9	498	2	Q6FWR9_CANGA	Q6FWR9	candida gla
272	96	6.1	620	2	Q5A7H9_CANAL	Q5A7H9	candida alb	345	93.5	5.9	556	2	Q6DEK7_BRARE	Q6DEK7	brachydanio
273	96	6.1	625	2	Q58SF3_DROSI	Q58SF3	drosoophila	346	93.5	5.9	607	2	Q8GNS0_LISMO	Q8GNS0	listeria mo
274	96	6.1	625	2	Q58SH8_DROSI	Q58SH8	drosoophila	347	93.5	5.9	613	2	Q5ITE4_MACGR	Q5ITE4	magnaporthe
275	96	6.1	625	2	Q5ELN3_DROSI	Q5ELN3	drosoophila	348	93.5	5.9	802	2	Q60LR3_CABER	Q60LR3	caenorhabdi
276	96	6.1	625	2	Q6V6E1_DROSI	Q6V6E1	dictyosteli	349	93.5	5.9	980	2	Q54T19_DICDI	Q54T19	dictyosteli
277	96	6.1	732	2	Q54FU3_DICDI	Q54FU3	dictyosteli	350	93.5	5.9	1033	2	Q4HYJ6_GIBZE	Q4HYJ6	gibberella
278	96	6.1	804	2	Q54L26_DICDI	Q54L26	dictyosteli	351	93.5	5.9	1595	2	Q5SBM3_LACSK	Q5SBM3	lactobacill
279	96	6.1	1038	2	Q4T3K8_TETNG	Q4T3K8	tetradodon n	352	93	5.9	261	2	Q70CC2_EIMTE	Q70CC2	eimeria ten
280	96	6.1	1088	1	NCA11_XENLA	P16170	xenopus lae	353	93	5.9	385	2	Q8T817_DROPS	Q8T817	drosoophila
281	96	6.1	1155	2	Q4JAZ20_SULAC	Q4JAZ20	sulfolobus	354	93	5.9	385	2	Q8T819_DROPS	Q8T819	drosoophila
282	96	6.1	1569	2	Q54DM4_DICDI	Q54DM4	dictyosteli	355	93	5.9	405	2	Q66H22_BRARE	Q66H22	brachydanio
283	96	6.1	3178	1	YS89_CABEL	Q09624	caenorhabdi	356	93	5.9	448	2	Q5BPF27_CHICK	Q5BPF27	gallus gall
284	95.5	6.1	266	2	Q4HZD3_GIBZE	Q4HZD3	gibberella	357	93	5.9	572	2	Q58SM0_DROME	Q58SM0	drosoophila
285	95.5	6.1	385	2	Q9NHU5_DROMI	Q9NHU5	drosoophila	358	93	5.9	572	2	Q58SM7_DROME	Q58SM7	drosoophila
286	95.5	6.1	385	2	Q9NHU7_DROMI	Q9NHU7	drosoophila	359	93	5.9	608	2	Q24017_DROME	Q24017	drosoophila
287	95.5	6.1	469	2	Q54P62_DICDI	Q54P62	dictyosteli	360	93	5.9	629	2	Q24017_DROME	Q24017	drosoophila
288	95.5	6.1	585	2	Q5SE79_9MONO	Q5SE79	avian pneum	361	93	5.9	629	2	Q5ELT0_DROME	Q5ELT0	drosoophila
289	95.5	6.1	596	2	Q5BF33_EMENI	Q5BF33	aspergillus	362	93	5.9	629	2	Q5ELT4_DROME	Q5ELT4	drosoophila
290	95.5	6.1	1259	2	Q869X4_DICDI	Q869X4	dictyosteli	363	93	5.9	629	2	Q5ELV0_DROME	Q5ELV0	drosoophila
291	95.5	6.1	5374	2	Q99ND0_MOUSE	Q99ND0	mus musculus	364	93	5.9	639	2	Q8GNS5_LISMO	Q8GNS5	listeria mo
292	95	6.0	273	2	Q61002_MOUSE	Q61002	mus musculus	365	93	5.9	639	2	Q8GNS6_LISMO	Q8GNS6	listeria mo
293	95	6.0	281	2	Q4KS19_9ADEN	Q4KS19	human adeno	366	93	5.9	639	2	Q6E8X4_LISMO	Q6E8X4	listeria mo
294	95	6.0	390	2	Q702W9_HHV1	Q702W9	human herpe	367	93	5.9	758	2	Q54UR7_DICDI	Q54UR7	dictyosteli
295	95	6.0	424	2	Q9FGW0_ARATH	Q9FGW0	arabidopsis	368	93	5.9	791	2	Q51UQ4_MACGR	Q51UQ4	magnaporthe
296	95	6.0	538	2	Q69379_LISMO	Q69379	listeria mo	369	93	5.9	916	2	Q7YZI0_MONBE	Q7YZI0	monosiga br
297	95	6.0	601	2	Q5ZKL1_CHICK	Q5ZKL1	gallus gall	370	93	5.9	928	2	Q4SL40_TETNG	Q4SL40	tetradodon n
298	95	6.0	604	2	Q9RQ13_LISMO	Q9RQ13	listeria mo	371	93	5.9	1034	2	Q613E9_CABER	Q613E9	caenorhabdi
299	95	6.0	604	2	Q6EAD8_LISMO	Q6EAD8	listeria mo	372	93	5.9	1285	2	Q4RXD7_TETNG	Q4RXD7	tetradodon n
300	95	6.0	639	2	Q8GNS2_LISMO	Q8GNS2	listeria mo	373	93	5.9	1349	2	Q8WQ04_HUMAN	Q8WQ04	homo sapien
301	95	6.0	639	2	Q6E904_LISMO	Q6E904	listeria mo	374	93	5.9	1413	2	Q54FI2_DICDI	Q54FI2	dictyosteli
302	95	6.0	639	2	Q6E982_LISMO	Q6E982	listeria mo	375	92.5	5.9	215	2	Q614I3_CABER	Q614I3	caenorhabdi
303	95	6.0	639	2	Q6E9Q6_LISMO	Q6E9Q6	listeria mo	376	92.5	5.9	247	2	Q8MKY7_DROME	Q8MKY7	drosoophila
304	95	6.0	639	2	Q6PPF4_BRARE	Q6PPF4	brachydanio	377	92.5	5.9	299	2	Q4HYT1_GIBZE	Q4HYT1	gibberella
305	95	6.0	1203	3	Q6C028_YARLI	Q6C028	yarrowia li	378	92.5	5.9	300	1	JAM1_MOUSE	JAM1	mouse
306	95	6.0	1317	1	YQ03_CABEL	Q09550	caenorhabdi	379	92.5	5.9	318	2	Q86HN3_DICDI	Q86HN3	dictyosteli
307	95	6.0	1578	2	Q55C84_DICDI	Q55C84	dictyosteli	380	92.5	5.9	385	2	Q9NHV2_DROMI	Q9NHV2	drosoophila
308	95	6.0	1748	2	Q54FL9_DICDI	Q54FL9	dictyosteli	381	92.5	5.9	400	1	HPLN4_MOUSE	HPLN4	mus musculus
309	94.5	6.0	359	1	TIM01_HUMAN	Q96442	homo sapien	382	92.5	5.9	446	2	Q8EMV3_OCEIH	Q8EMV3	oceanobacill
310	94.5	6.0	383	2	Q702X5_HHV1	Q702X5	human herpe	383	92.5	5.9	453	2	Q5KCR5_CRYNE	Q5KCR5	cryptococcu
311	94.5	6.0	383	2	Q702Y4_HHV1	Q702Y4	human herpe	384	92.5	5.9	466	2	Q55IY7_CRYNE	Q55IY7	cryptococcu
312	94.5	6.0	395	2	Q70220_HHV1	Q70220	human herpe	385	92.5	5.9	466	2	Q5KCR4_CRYNE	Q5KCR4	cryptococcu
313	94.5	6.0	405	2	Q4INQ5_GIBZE	Q4INQ5	gibberella	386	92.5	5.9	487	2	Q54G14_DICDI	Q54G14	dictyosteli
314	94.5	6.0	494	2	Q4WG24_ASFFU	Q4WG24	aspergillus	387	92.5	5.9	569	2	Q9KGV9_LISMO	Q9KGV9	listeria mo
315	94.5	6.0	510	2	Q5YFP0_9VIRU	Q5YFP0	singapore g	388	92.5	5.9	604	2	Q6EAE4_LISMO	Q6EAE4	listeria mo
316	94.5	6.0	519	2	Q7YXTR_CABEL	Q7YXTR	caenorhabdi	389	92.5	5.9	623	2	Q55F14_DICDI	Q55F14	dictyosteli
317	94.5	6.0	539	2	Q54GL8_DICDI	Q54GL8	dictyosteli	390	92.5	5.9	708	2	Q55F14_DICDI	Q55F14	dictyosteli
318	94.5	6.0	698	2	Q61SH2_CABER	Q61SH2	caenorhabdi	391	92.5	5.9	638	2	Q73H41_WOLPM	Q73H41	wolbachia p
319	94.5	6.0	814	2	Q5AG78_CANAL	Q5AG78	candida alb	392	92.5	5.9	784	2	Q7S3V6_NEUCR	Q7S3V6	neurospora
320	94.5	6.0	1007	2	Q55CR8_DICDI	Q55CR8	dictyosteli	393	92.5	5.9	812	2	Q55D98_DICDI	Q55D98	dictyosteli
321	94.5	6.0	1007	2	Q5POE5_AZOSE	Q5POE5	azocarcus sp	394	92.5	5.9	927	2	Q21811_CABEL	Q21811	caenorhabdi
322	94.5	6.0	1066	2	Q76NW3_DICDI	Q76NW3	dictyosteli	395	92.5	5.9	1491	2	Q4QDK4_LEIAMA	Q4QDK4	leishmania
323	94.5	6.0	1079	2	Q9N4S7_CABEL	Q9N4S7	caenorhabdi	396	92.5	5.9	1636	1	BUD3_YEAST	BUD3	saccharomyc

397	92.5	5.9	2338	2	Q75983	ASHGO	Q75983	ashbya coss
398	92	5.8	347	2	Q8SYW5	DROME	Q8SYW5	drosophila
399	92	5.8	500	2	Q864U8	BOVIN	Q864U8	bos taurus
400	92	5.8	504	2	Q54F08	DICDI	Q54F08	dictyosteli
401	92	5.8	567	2	Q4P6Q2	USTMA	Q4P6Q2	ustilago ma
402	92	5.8	574	2	Q58SM3	DROME	Q58SM3	drosophila
403	92	5.8	586	2	Q5B1V4	EMENI	Q5B1V4	aspergillus
404	92	5.8	604	2	Q3JUN2	LISMO	Q3JUN2	listeria mo
405	92	5.8	629	2	Q5ELR9	DROME	Q5ELR9	drosophila
406	92	5.8	629	2	Q5ELJ5	DROME	Q5ELJ5	drosophila
407	92	5.8	629	2	Q5ELU4	DROME	Q5ELU4	drosophila
408	92	5.8	639	2	Q6EA92	LISMO	Q6EA92	listeria mo
409	92	5.8	644	2	Q6CF33	YARLI	Q6CF33	yarrowia li
410	92	5.8	659	2	Q55XK2	CABEL	Q55XK2	caenorhabdi
411	92	5.8	741	2	Q6CHB8	YARLI	Q6CHB8	yarrowia li
412	92	5.8	828	2	Q5B819	EMENI	Q5B819	aspergillus
413	92	5.8	846	2	Q01699	CABEL	Q01699	caenorhabdi
414	92	5.8	907	2	Q6CT08	KLULA	Q6CT08	kluyveromyc
415	92	5.8	966	1	SSN6	YEAST	PI4922	saccharomyc
416	92	5.8	1170	2	Q54PR2	DICDI	Q54PK2	dictyosteli
417	92	5.8	1241	2	Q75J00	DICDI	Q75J00	dictyosteli
418	92	5.8	1269	2	Q54CA1	DICDI	Q54CAL	dictyosteli
419	92	5.8	1343	2	Q54XT5	DICDI	Q54XT5	dictyosteli
420	92	5.8	1720	2	Q81486	PLAF7	Q81486	plasmodium
421	91.5	5.8	161	2	Q6CP23	KLULA	Q6CP23	kluyveromyc
422	91.5	5.8	198	2	QWRH11	LISMO	QWRH11	listeria mo
423	91.5	5.8	296	2	Q7X384	LISMO	Q7X384	listeria mo
424	91.5	5.8	298	2	Q6P9X9	RAT	Q6P9X9	rattus norv
425	91.5	5.8	300	2	Q9Z0P0	RAT	Q9Z0P0	rattus norv
426	91.5	5.8	308	2	Q8VC39	MOUSE	Q8VC39	mus musculus
427	91.5	5.8	305	2	Q8R193	MOUSE	Q8R183	mus musculus
428	91.5	5.8	338	2	Q6EAH4	LISMO	Q6EAH4	listeria mo
429	91.5	5.8	383	2	Q51693	HRV1	Q51693	human herpe
430	91.5	5.8	383	2	Q702X8	HRV1	Q702X8	human herpe
431	91.5	5.8	385	2	Q9NHV1	DROMI	Q9NHV1	drosophila
432	91.5	5.8	497	2	Q8QVC5	GREOV	Q8QVC5	eyach virus
433	91.5	5.8	538	2	Q76H84	STRMU	Q76H84	streptococc
434	91.5	5.8	573	2	Q69380	LISTERIA	Q69380	listeria mo
435	91.5	5.8	579	2	Q5CYK7	CRYPV	Q5CYK7	cryptospori
436	91.5	5.8	588	2	Q5ANGO	CANAL	Q5ANGO	candida alb
437	91.5	5.8	604	2	Q8GNR3	LISMO	Q8GNR3	listeria mo
438	91.5	5.8	604	2	Q6E8U4	LISMO	Q6E8U4	listeria mo
439	91.5	5.8	633	2	Q3JMY6	LISMO	Q3JMY6	listeria mo
440	91.5	5.8	633	2	Q4TV06	LISMO	Q4TV06	listeria mo
441	91.5	5.8	639	1	ACTA	LISMO	ACTA	listeria mo
442	91.5	5.8	639	2	Q8GNR9	LISMO	Q8GNR9	listeria mo
443	91.5	5.8	639	2	Q6E8V0	LISMO	Q6E8V0	listeria mo
444	91.5	5.8	639	2	Q6E914	LISMO	Q6E914	listeria mo
445	91.5	5.8	639	2	Q6E9X8	LISMO	Q6E9X8	listeria mo
446	91.5	5.8	639	2	Q6EA56	LISMO	Q6EA56	listeria mo
447	91.5	5.8	639	2	Q6EAA4	LISMO	Q6EAA4	listeria mo
448	91.5	5.8	639	2	Q8GNR2	LISMO	Q8GNR2	listeria mo
449	91.5	5.8	639	2	Q6E8T8	LISMO	Q6E8T8	listeria mo
450	91.5	5.8	651	2	Q61Y25	CABER	Q61Y25	caenorhabdi
451	91.5	5.8	860	2	Q7RZN3	NEUCR	Q7RZN3	neurospora
452	91.5	5.8	930	2	Q7YBL5	ARPE	Q7YBL5	aeropyrum p
453	91.5	5.8	1148	2	Q6CBJ2	YARLI	Q6CBJ2	yarrowia li
454	91.5	5.8	1167	2	Q7RW07	NEUCR	Q7RW07	neurospora
455	91.5	5.8	1481	2	Q4P152	USTMA	Q4P152	ustilago ma
456	91.5	5.8	1783	2	Q51UR4	MAGGR	Q51UR4	magnaporthe
457	91	5.8	174	2	Q7YTP1	CABEL	Q7YTP1	caenorhabdi
458	91	5.8	198	2	Q7X3M4	LISMO	Q7X3M4	listeria mo
459	91	5.8	213	2	Q5T317	HUMAN	Q5T317	homo sapien
460	91	5.8	246	2	Q9UAV4	CABEL	Q9UAV4	caenorhabdi
461	91	5.8	316	2	Q9U9J0	TOXCA	Q9U9J0	toxocara ca
462	91	5.8	450	2	Q8CV85	OCEIH	Q8CV85	oceanobacil
463	91	5.8	488	2	Q09586	CABEL	Q09586	caenorhabdi
464	91	5.8	576	2	Q6IMDL	CABER	Q6IMDL	caenorhabdi
465	91	5.8	591	2	Q4WHJ8	ASPFU	Q4WHJ8	aspergillus
466	91	5.8	596	2	Q6P1T0	XENTR	Q6P1T0	xenopus tro
467	91	5.8	600	2	Q4VBE0	XENTR	Q4VBE0	xenopus tro
468	91	5.8	620	2	Q8SVR3	ENCCU	Q8SVR3	encephalito
469	91	5.8	629	2	Q5ELR5	DROME	Q5ELR5	drosophila

470	91	5.8	629	2	Q5ELR7	DROME	Q5ELR7	drosophila
471	91	5.8	629	2	Q5ELJ3	DROME	Q5ELJ3	drosophila
472	91	5.8	639	2	Q6E964	LISMO	Q6E964	listeria mo
473	91	5.8	639	2	Q6EAI0	LISMO	Q6EAI0	listeria mo
474	91	5.8	644	2	Q54D31	DICDI	Q54D31	dictyosteli
475	91	5.8	693	2	Q7PYV7	ANOCA	Q7PYV7	anopheles g
476	91	5.8	701	2	Q8ZWG4	PYRAE	Q8ZWG4	pyrobaculum
477	91	5.8	730	2	Q86AZ8	DICDI	Q86AZ8	dictyosteli
478	91	5.8	876	2	Q619L5	CABER	Q619L5	caenorhabdi
479	91	5.8	1398	2	Q869T5	DICDI	Q869T5	dictyosteli
480	91	5.8	1842	2	Q4N830	THEPA	Q4N830	theileria p
481	91	5.8	2162	2	Q09515	CABEL	Q09515	caenorhabdi
482	91	5.8	2176	2	Q54VP0	DICDI	Q54VP0	dictyosteli
483	91	5.8	4262	2	Q685U2	HUMAN	Q685U2	homo sapien
484	91	5.8	4493	2	Q685J3	HUMAN	Q685J3	homo sapien
485	90.5	5.7	306	2	Q54UW3	DICDI	Q54UW3	dictyosteli
486	90.5	5.7	336	2	Q4Z0P5	PLABE	Q4Z0P5	plasmodium
487	90.5	5.7	360	2	Q4WG94	ASPFU	Q4WG94	aspergillus
488	90.5	5.7	384	2	Q9DW41	ECMYM	Q9DW41	rat cytomeg
489	90.5	5.7	385	2	Q9NHV0	DROMI	Q9NHV0	drosophila
490	90.5	5.7	385	2	Q9NHV3	DROMI	Q9NHV3	drosophila
491	90.5	5.7	406	2	Q528W4	MAGGR	Q528W4	magnaporthe
492	90.5	5.7	408	2	Q6UDF5	9HERP	Q6UDF5	peittacidi h
493	90.5	5.7	411	2	Q6P6W1	RAT	Q6P6W1	rattus norv
494	90.5	5.7	461	2	Q6C2X8	YARLI	Q6C2X8	yarrowia li
495	90.5	5.7	496	2	Q5SD06	DICDI	Q5SD06	dictyosteli
496	90.5	5.7	575	1	CH61	CUCMA	Q50545	cucurbita m
497	90.5	5.7	595	2	Q5ANA0	CANAL	Q5ANA0	candida alb
498	90.5	5.7	659	2	Q59R26	CANAL	Q59R26	candida alb
499	90.5	5.7	678	2	Q54U48	DICDI	Q54U48	dictyosteli
500	90.5	5.7	690	2	Q66S18	9UROC	Q66S18	oikopleura
501	90.5	5.7	862	2	Q615W4	CABER	Q615W4	caenorhabdi
502	90.5	5.7	972	2	Q60Q42	CABER	Q60Q42	caenorhabdi
503	90.5	5.7	1084	2	Q55A66	DICDI	Q55A66	dictyosteli
504	90.5	5.7	1084	2	Q86LA6	DICDI	Q86LA6	dictyosteli
505	90.5	5.7	1126	2	Q5C1S2	CRYHO	Q5C1S2	cryptospori
506	90.5	5.7	1175	2	Q9VRL7	DROME	Q9VRL7	drosophila
507	90.5	5.7	1400	2	Q5FBC4	DICDI	Q5FBC4	dictyosteli
508	90.5	5.7	1505	2	Q54VU4	DICDI	Q54VU4	dictyosteli
509	90.5	5.7	1711	1	NU214	DROME	Q9W1X4	drosophila
510	90.5	5.7	1976	2	Q9V918	DROME	Q9V918	drosophila
511	90.5	5.7	2300	2	Q7SFP6	NEUCR	Q7SFP6	neurospora
512	90	5.7	294	2	Q4V3X0	DROME	Q4V3X0	drosophila
513	90	5.7	296	2	Q923D3	MOUSE	Q923D3	mus musculu
514	90	5.7	388	1	VE2	HPV27	P36789	human papil
515	90	5.7	448	2	Q61C01	CABER	Q61C01	caenorhabdi
516	90	5.7	488	2	Q4V3Z8	DROME	Q4V3Z8	drosophila
517	90	5.7	508	2	Q54BP8	DICDI	Q54BP8	dictyosteli
518	90	5.7	511	2	Q5A7R7	CANAL	Q5A7R7	candida alb
519	90	5.7	540	2	Q7SFI7	NEUCR	Q7SFI7	neurospora
520	90	5.7	560	2	Q54LP6	DICDI	Q54LP6	dictyosteli
521	90	5.7	572	2	Q58SM4	DROME	Q58SM4	drosophila
522	90	5.7	572	2	Q58SM6	DROME	Q58SM6	drosophila
523	90	5.7	598	2	Q5ELV8	DROSI	Q5ELV8	drosophila
524	90	5.7	604	2	Q6E9Q0	LISMO	Q6E9Q0	listeria mo
525	90	5.7	612	2	Q7QJB6	ANOCA	Q7QJB6	anopheles g
526	90	5.7	616	2	Q4WC60	ASPFU	Q4WC60	aspergillus
527	90	5.7	626	2	Q81QJ5	DROME	Q81QJ5	drosophila
528	90	5.7	629	2	Q5ELS7	DROME	Q5ELS7	drosophila
529	90	5.7	629	2	Q9V3H7	DROME	Q9V3H7	drosophila
530	90	5.7	630	2	Q5ELS1	DROME	Q5ELS1	drosophila
531	90	5.7	639	2	Q6E866	LISMO	Q6E866	listeria mo
532	90	5.7	740	2	Q54H84	DICDI	Q54H84	dictyosteli
533	90	5.7	812	2	Q61KE5	CABER	Q61KE5	caenorhabdi
534	90	5.7	823	2	Q54Y28	DICDI	Q54Y28	dictyosteli
535	90	5.7	877	2	Q9H3Q6	HUMAN	Q9H3Q6	homo sapien
536	90	5.7	878	2	Q9H3Q7	HUMAN	Q9H3Q7	homo sapien
537	90	5.7	948	2	Q6EAV9	DICDI	Q6EAV9	dictyosteli
538	90	5.7	954	2	Q610Z8	CABER	Q610Z8	caenorhabdi
539	90	5.7	957	2	Q14651	HUMAN	Q14651	homo sapien
540	90	5.7	965	2	Q22286	CABEL	Q22286	caenorhabdi
541	90	5.7	1086	2	Q54X99	DICDI	Q54X99	dictyosteli
542	90	5.7	1170	2	Q4IC26	GIBZE	Q4IC26	gibberella

543	90	5.7	1217	2	Q9UKW9_HUMAN	Q9UKW9	homo sapien	616	88.5	5.6	389	2	Q611Z9_CABER	Q611Z9	caenorhabdi
544	90	5.7	1293	1	Q4Q6D9_LEIMA	Q4Q6D9	leishmania	617	88.5	5.6	448	2	Q6AQD8_DESPS	Q6AQD8	desulfocale
545	90	5.7	1367	1	MUCL1_YEAST	P08640	saccharomyc	618	88.5	5.6	481	2	Q9VWK3_DROME	Q9VWK3	drosofila
546	90	5.7	1367	2	Q6LCS8_SACDI	Q6LCS8	saccharomyc	619	88.5	5.6	494	2	Q618M1_CABER	Q618M1	caenorhabdi
547	90	5.7	2282	2	Q9NKS6_DROME	Q9NKS6	drosofila	620	88.5	5.6	518	2	Q8NJS3_CANAL	Q8NJS3	candida alb
548	89.5	5.7	276	2	Q52BL6_WAGGR	Q52BL6	magnaporthe	621	88.5	5.6	569	2	Q71X10_LISMF	Q71X10	listeria mo
549	89.5	5.7	305	1	C8VBW0_MOUSE	Q8VBW0	mus musculus	622	88.5	5.6	582	2	Q81R74_DROME	Q81R74	drosofila
550	89.5	5.7	319	1	JU07H8_MOUSE	Q8BP27	mus musculus	623	88.5	5.6	596	1	UBQL4_MOUSE	Q99NB8	mus musculus
551	89.5	5.7	326	2	Q7SCW5_NEUCR	Q7SCW5	neutrospora	624	88.5	5.6	598	2	Q9JMY5_LISMO	Q9JMY5	listeria mo
552	89.5	5.7	359	2	Q5KCH0_CRYNE	Q5KCH0	cryptococcu	625	88.5	5.6	615	2	Q9M6E8_PHAUV	Q9M6E8	phaeolus v
553	89.5	5.7	411	1	LAMP2_RAT	PI7046	rattus norv	626	88.5	5.6	622	2	Q58SF6_DROSI	Q58SF6	drosofila
554	89.5	5.7	440	2	Q9P566_NEUCR	Q9P566	neutrospora	627	88.5	5.6	653	2	Q81JX0_PLAF7	Q81JX0	plasmodium
555	89.5	5.7	443	2	Q6P111_BRARE	Q6P111	brachydanio	628	88.5	5.6	699	2	Q6CSM7_KLULA	Q6CSM7	kluyveromyc
556	89.5	5.7	456	2	Q25242_LUCCU	Q25242	lucilia cup	629	88.5	5.6	721	2	Q97UG7_SULSO	Q97UG7	sulfolobus
557	89.5	5.7	471	2	Q9VMG7_DROME	Q9VMG7	drosofila	630	88.5	5.6	722	2	Q59644_SULSO	Q59644	sulfolobus
558	89.5	5.7	480	2	Q25241_LUCCU	Q25241	lucilia cup	631	88.5	5.6	722	2	Q6FTP4_CANGA	Q6FTP4	candida gla
559	89.5	5.7	492	2	Q6CGC6_YARLI	Q6CGC6	aspergillus	632	88.5	5.6	752	2	Q52CR1_MAGGR	Q52CR1	magnaporthe
560	89.5	5.7	510	2	Q6SCU8_ASPPU	Q6SCU8	aspergillus	633	88.5	5.6	764	2	Q4WY10_ASPPU	Q4WY10	aspergillus
561	89.5	5.7	548	2	Q61CS6_CABER	Q61CS6	caenorhabdi	634	88.5	5.6	901	2	Q84FU6_CHLTR	Q84FU6	chlamydia t
562	89.5	5.7	558	2	Q4JK70_DERPT	Q4JK70	dermatophag	635	88.5	5.6	980	2	Q84FU6_CHLTR	Q84FU6	chlamydia t
563	89.5	5.7	604	2	Q6E9W0_LISMO	Q6E9W0	listeria mo	636	88.5	5.6	980	2	Q84FU6_CHLTR	Q84FU6	chlamydia t
564	89.5	5.7	606	2	Q5ZLH8_CHICK	Q5ZLH8	gallus gall	637	88.5	5.6	981	2	Q84FU7_CHLTR	Q84FU7	chlamydia t
565	89.5	5.7	659	2	Q55616_DICDI	Q55616	dictyosteli	638	88.5	5.6	1101	1	GUNC_CELFI	GUNC	celulomona
566	89.5	5.7	659	2	Q86A18_DICDI	Q86A18	dictyosteli	639	88.5	5.6	1106	2	Q41AX5_GIBZE	Q41AX5	gibberella
567	89.5	5.7	917	2	Q7QJ16_ANOGA	Q7QJ16	anopheles g	640	88.5	5.6	1224	2	Q54PM6_DICDI	Q54PM6	dictyosteli
568	89.5	5.7	1145	2	Q8JKT0_9VIRU	Q8JKT0	heliothis z	641	88.5	5.6	1230	2	Q54JY4_DICDI	Q54JY4	dictyosteli
569	89.5	5.7	1368	2	Q23821_CAEVU	Q23821	caenorhabdi	642	88.5	5.6	1292	2	Q4RHM3_TENG	Q4RHM3	tetradodon n
570	89.5	5.7	1773	2	Q4N437_THEPA	Q4N437	thelateria p	643	88.5	5.6	1346	2	Q54SH1_DICDI	Q54SH1	dictyosteli
571	89.5	5.7	1816	2	Q4N6E9_THEPA	Q4N6E9	thelateria p	644	88.5	5.6	2122	2	Q54R92_DICDI	Q54R92	dictyosteli
572	89	5.7	195	2	Q9QX82_RAT	Q9QX82	rattus norv	645	88	5.6	103	2	Q9TTB3_PIG	Q9TTB3	sus scrofa
573	89	5.7	307	1	SGS3_DROME	P02840	drosofila	646	88	5.6	161	2	Q9CVT7_MOUSE	Q9CVT7	mus musculus
574	89	5.7	369	2	Q91E39_9ALPH	Q91E39	phocid herp	647	88	5.6	302	2	Q55XK5_CRYNE	Q55XK5	cryptococcu
575	89	5.7	392	2	Q59F20_HUMAN	Q59F20	homo sapien	648	88	5.6	302	2	Q5KMC9_CRYNE	Q5KMC9	cryptococcu
576	89	5.7	416	1	LAMP1_HUMAN	PI1279	homo sapien	649	88	5.6	347	2	Q9TZV4_PLAFA	Q9TZV4	plasmodium
577	89	5.7	417	2	Q8WU33_HUMAN	Q8WU33	homo sapien	650	88	5.6	362	2	Q9TZV3_PLAFA	Q9TZV3	plasmodium
578	89	5.7	421	2	Q6KCA6_CANDU	Q6KCA6	candida dub	651	88	5.6	382	2	Q6C971_YARLI	Q6C971	yarrowia li
579	89	5.7	422	2	Q5CNT4_CRYHO	Q5CNT4	cryptospori	652	88	5.6	385	2	Q8T812_DROPB	Q8T812	drosofila
580	89	5.7	429	2	P79046_9ASCO	P79046	humicola gr	653	88	5.6	385	2	Q8T814_DROPB	Q8T814	drosofila
581	89	5.7	477	2	Q14887_HUMAN	Q14887	homo sapien	654	88	5.6	385	2	Q8T816_DROPB	Q8T816	drosofila
582	89	5.7	482	2	Q6BSZ9_DEBHA	Q6BSZ9	debaromyce	655	88	5.6	385	2	Q8T8J0_DROPB	Q8T8J0	drosofila
583	89	5.7	503	1	NAS14_CABEL	Q19269	caenorhabdi	656	88	5.6	385	2	Q8T8J1_DROPB	Q8T8J1	drosofila
584	89	5.7	589	2	Q4N7T4_THEPA	Q4N7T4	thelateria p	657	88	5.6	385	2	Q8T8K3_DROPE	Q8T8K3	drosofila
585	89	5.7	603	2	Q6CE49_YARLI	Q6CE49	yarrowia li	658	88	5.6	447	2	Q6CCR1_YARLI	Q6CCR1	yarrowia li
586	89	5.7	648	2	Q4QJ32_LEIMA	Q4QJ32	leishmania	659	88	5.6	449	2	Q6CWZ6_KLULA	Q6CWZ6	kluyveromyc
587	89	5.7	666	2	Q7QXK0_GIALA	Q7QXK0	giardia lam	660	88	5.6	456	2	Q9U2W2_CABEL	Q9U2W2	caenorhabdi
588	89	5.7	714	2	Q9NGW9_DICDI	Q9NGW9	dictyosteli	661	88	5.6	487	2	Q4U479_ANOGA	Q4U479	anopheles g
589	89	5.7	770	2	Q55G55_DICDI	Q55G55	dictyosteli	662	88	5.6	543	2	Q7QK86_ANOGA	Q7QK86	anopheles g
590	89	5.7	833	2	Q8IRC1_DROME	Q8IRC1	drosofila	663	88	5.6	564	2	Q01627_CABEL	Q01627	caenorhabdi
591	89	5.7	851	2	Q9VZ10_DROME	Q9VZ10	drosofila	664	88	5.6	577	2	Q6FSJ1_CANGA	Q6FSJ1	candida gla
592	89	5.7	860	2	Q5WNQ1_CABER	Q5WNQ1	caenorhabdi	665	88	5.6	587	2	Q51R09_MAGGR	Q51R09	magnaporthe
593	89	5.7	880	2	Q54UK3_DICDI	Q54UK3	dictyosteli	666	88	5.6	588	2	Q813F9_BACCR	Q813F9	bacillus ce
594	89	5.7	887	2	Q917T2_DROME	Q917T2	drosofila	667	88	5.6	601	2	Q6V6S2_DROME	Q6V6S2	drosofila
595	89	5.7	898	2	Q8IRC0_DROME	Q8IRC0	drosofila	668	88	5.6	602	2	Q8YV91_ANASP	Q8YV91	anabaena sp
596	89	5.7	917	2	Q4X105_ASPPU	Q4X105	aspergillus	669	88	5.6	604	2	Q6E916_LISMO	Q6E916	listeria mo
597	89	5.7	951	2	Q9FVX8_ORYSA	Q9FVX8	oryza sativ	670	88	5.6	716	2	Q9NVE4_HUMAN	Q9NVE4	homo sapien
598	89	5.7	952	2	Q9U3P1_CABEL	Q9U3P1	caenorhabdi	671	88	5.6	931	2	Q51LJ1_MAGGR	Q51LJ1	magnaporthe
599	89	5.7	958	2	Q4WTT4_ASPPU	Q4WTT4	aspergillus	672	88	5.6	995	2	Q91638_XENLA	Q91638	xenopus lae
600	89	5.7	983	2	Q8IRB9_DROME	Q8IRB9	drosofila	673	88	5.6	1051	2	Q6C1J9_YARLI	Q6C1J9	yarrowia li
601	89	5.7	1081	2	Q59EAL_HUMAN	Q59EAL	homo sapien	674	88	5.6	1409	2	Q5ALT5_CANAL	Q5ALT5	candida alb
602	89	5.7	1116	2	Q5AJH8_CANAL	Q5AJH8	candida alb	675	88	5.6	1630	1	MSP1_PLAFK	MSP1	plasmodium
603	89	5.7	1473	2	Q54TV0_DICDI	Q54TV0	dictyosteli	676	88	5.6	1790	2	Q81816_APLCA	Q81816	aplysia cal
604	89	5.7	1483	2	Q7KWU3_DICDI	Q7KWU3	dictyosteli	677	88	5.6	2195	2	Q4SA07_TENG	Q4SA07	tetradodon n
605	89	5.7	1493	2	Q55917_DICDI	Q55917	dictyosteli	678	88	5.6	5703	1	MUC5B_HUMAN	MUC5B	homo sapien
606	89	5.7	1521	2	Q7Q1W8_ANOGA	Q7Q1W8	anopheles g	679	88	5.6	147	2	Q61043_TRYCR	Q61043	trypanosoma
607	89	5.7	1708	2	Q7XWZ9_ORYSA	Q7XWZ9	oryza sativ	680	87.5	5.6	244	2	Q54RQ4_DICDI	Q54RQ4	dictyosteli
608	89	5.7	2273	2	Q63HU2_BURPS	Q63HU2	burkholderi	681	87.5	5.6	283	2	Q5XUY9_ARATH	Q5XUY9	arabidopsis
609	89	5.7	6994	2	Q17343_CABEL	Q17343	caenorhabdi	682	87.5	5.6	283	2	Q9PKU2_ARATH	Q9PKU2	arabidopsis
610	89	5.7	6994	2	Q17490_CABEL	Q17490	caenorhabdi	683	87.5	5.6	289	2	Q41UR0_GIBZE	Q41UR0	gibberella
611	88.5	5.6	133	2	Q23366_ARATH	Q23366	arabidopsis	684	87.5	5.6	299	2	Q5H2T1_XANOR	Q5H2T1	xanthomonas
612	88.5	5.6	264	2	Q80X55_MOUSE	Q80X55	mus musculus	685	87.5	5.6	338	2	Q6CY50_KLULA	Q6CY50	kluyveromyc
613	88.5	5.6	321	2	Q25939_PLAFA	Q25939	plasmodium	686	87.5	5.6	345	2	Q56WV8_ARATH	Q56WV8	arabidopsis
614	88.5	5.6	359	2	Q55JER_CRYNE	Q55JER	cryptococcu	687	87.5	5.6	366	2	Q6FSI8_CANGA	Q6FSI8	candida gla
615	88.5	5.6	376	1	MID2_YEAST	P36027	saccharomyc	688	87.5	5.6	383	2	Q702Y9_HHVI	Q702Y9	human herpe

689	87.5	5.6	442	2	Q7S223_NEUCR	Q7a2z3 neurospora	762	87	5.5	1506	2	P79927_XENLA	P79927 xenopus lae
690	87.5	5.6	462	2	Q8TUS0_METAC	Q8tue0 methanosarc	763	87	5.5	1537	1	FLO1_YEAST	P32758 saccharomyc
691	87.5	5.6	463	2	Q8A3K1_CANAL	Q8a3k1 candida alb	764	87	5.5	1537	2	Q58HH7_YEAST	Q58hh7 saccharomyc
692	87.5	5.6	498	2	Q6FV08_CANGA	Q6fvc8 candida gla	765	87	5.5	6586	2	Q52FL1_MAGGR	Q52fl1 magnaporth
693	87.5	5.6	542	2	Q4V4X7_DROME	Q4v4x7 drosophila	766	86.5	5.5	197	2	Q92317_MOUSE	Q92317 mus musculu
694	87.5	5.6	545	2	Q9U6R7_DERFA	Q9u6r7 dermatophag	767	86.5	5.5	197	2	Q9R0L9_MOUSE	Q9r0l9 mus musculu
695	87.5	5.6	563	2	Q5LKG3_STIPO	Q5lkg3 silicibacte	768	86.5	5.5	249	2	Q6BVX5_DEBHA	Q6bv5 debaryomyce
696	87.5	5.6	571	2	Q4YH01_PLABE	Q4yh01 plasmodium	769	86.5	5.5	277	2	Q4KMD4_BRARE	Q4kmd4 brachydanio
697	87.5	5.6	622	2	Q58S02_DROSI	Q58sg2 drosophila	770	86.5	5.5	300	2	Q73J08_TREDE	Q73jv8 treponema d
698	87.5	5.6	622	2	Q58S09_DROSI	Q58sh9 drosophila	771	86.5	5.5	400	1	MUAI_XENLA	P10667 xenopus lae
699	87.5	5.6	622	2	Q5EL05_DROSI	Q5elq5 drosophila	772	86.5	5.5	401	2	Q6BV71_DEBHA	Q6bv71 debaryomyce
700	87.5	5.6	622	2	Q5EL09_DROSI	Q5elq9 drosophila	773	86.5	5.5	442	2	Q7M8Z3_WOLSU	Q7m8z3 wolinnella s
701	87.5	5.6	623	2	Q6T547_LISMO	Q6t547 listeria mo	774	86.5	5.5	451	2	Q6DF68_XENTR	Q6df68 xenopus tro
702	87.5	5.6	625	2	Q5ELP7_DROSI	Q5elp7 drosophila	775	86.5	5.5	461	2	Q21004_CAEEL	Q21004 caenorhabdi
703	87.5	5.6	626	2	Q5ND01_LEITR	Q5nd01 leishmania	776	86.5	5.5	483	2	Q5AT96_EMENI	Q5at96 aspergillus
704	87.5	5.6	634	2	Q7RW80_NEUCR	Q7rwb0 neurospora	777	86.5	5.5	484	1	PAPO2_XENLA	P51005 xenopus lae
705	87.5	5.6	639	2	Q6T548_LISMO	Q6t548 listeria mo	778	86.5	5.5	493	2	Q23330_CAEEL	Q23330 caenorhabdi
706	87.5	5.6	648	2	Q44109_CAEEL	Q44109 caenorhabdi	779	86.5	5.5	503	1	WSC2_YEAST	P53832 saccharomyc
707	87.5	5.6	653	2	Q59YC5_CANAL	Q59yc5 candida alb	780	86.5	5.5	582	2	Q58SG7_DROSI	Q58sg7 drosophila
708	87.5	5.6	653	2	Q59YC5_CANAL	Q59yc5 candida alb	781	86.5	5.5	582	2	Q58SG8_DROSI	Q58sg8 drosophila
709	87.5	5.6	665	2	Q4IIM3_GIBZE	Q4iim3 gibberella	782	86.5	5.5	582	2	Q58SG9_DROSI	Q58sg9 drosophila
710	87.5	5.6	682	2	Q60PP2_CAEER	Q60pp2 caenorhabdi	783	86.5	5.5	582	2	Q58SH3_DROSI	Q58sh3 drosophila
711	87.5	5.6	717	2	Q8NAJ6_HUMAN	Q8naj6 homo sapien	784	86.5	5.5	598	2	Q5ELV4_DROSI	Q5elv4 drosophila
712	87.5	5.6	752	2	Q8MNE2_DICDI	Q8me2 dictyosteli	785	86.5	5.5	598	2	Q5ELV5_DROSI	Q5elv5 drosophila
713	87.5	5.6	785	2	Q7Q0T5_GIALA	Q7q0t5 giardia lam	786	86.5	5.5	598	2	Q5ELW0_DROSI	Q5elw0 drosophila
714	87.5	5.6	825	2	Q9LZ46_ARATH	Q9lza6 arabidopsis	787	86.5	5.5	601	2	Q6V6S4_DROME	Q6v6s4 drosophila
715	87.5	5.6	867	2	Q90X49_BRAND	Q90x49 brachydanio	788	86.5	5.5	604	2	Q6E8Z8_LISMO	Q6e8z8 listeria mo
716	87.5	5.6	906	2	Q8UUV1_XENLA	Q8uuv1 xenopus lae	789	86.5	5.5	604	2	Q6E9Z8_LISMO	Q6e9z8 listeria mo
717	87.5	5.6	908	2	Q59PF9_CANAL	Q59pf9 candida alb	790	86.5	5.5	624	2	Q58SF9_DROSI	Q58sf9 drosophila
718	87.5	5.6	968	2	Q4SSC4_TETNG	Q4ssc4 tetradodon n	791	86.5	5.5	629	2	Q4QJ30_LEIMA	Q4qj30 leishmania
719	87.5	5.6	971	2	Q6W3C4_CAEEL	Q6w3c4 caenorhabdi	792	86.5	5.5	639	2	Q8GNR0_LISMO	Q8gnr0 listeria mo
720	87.5	5.6	989	2	Q19930_CAEEL	Q19930 caenorhabdi	793	86.5	5.5	639	2	Q6E9S2_LISMO	Q6e9s2 listeria mo
721	87.5	5.6	997	1	VGNM_APMV	P38485 andean pota	794	86.5	5.5	639	2	Q6E976_LISMO	Q6e976 listeria mo
722	87.5	5.6	1085	1	CASR_BOVIN	P35384 bos taurus	795	86.5	5.5	681	2	VGP_MABVP	P35254 marburg vir
723	87.5	5.6	1091	1	NCAMI_CHICK	P13590 gallus gall	796	86.5	5.5	681	2	Q71VM1_9MONO	Q71vm1 lake victor
724	87.5	5.6	1118	2	Q550H5_DICDI	Q550h5 dictyosteli	797	86.5	5.5	687	2	Q6NHU1_CORDI	Q6nhu1 corynebacte
725	87.5	5.6	1370	2	Q6C3B8_YARLI	Q6c3b8 yarrowia li	798	86.5	5.5	733	2	Q55R25_DICDI	Q55e25 dictyosteli
726	87.5	5.6	1799	2	Q7KUT0_DROME	Q7ku0 drosophila	799	86.5	5.5	739	1	GAG_SMRVH	P21411 squirrel mo
727	87.5	5.6	1802	1	HKR1_YEAST	P41809 saccharomyc	800	86.5	5.5	768	2	Q60279_HUMAN	Q60279 homo sapien
728	87.5	5.6	2048	2	Q55GCI_DICDI	Q55gci dictyosteli	801	86.5	5.5	779	2	Q5TRJ3_ANOGA	Q5trj3 anopheles g
729	87.5	5.6	2314	2	Q55F23_DICDI	Q55f23 dictyosteli	802	86.5	5.5	788	2	O18510_TRINI	O18510 trichoplusi
730	87.5	5.6	2829	1	APC_XENLA	P70039 xenopus lae	803	86.5	5.5	790	2	Q8TBZ7_HUMAN	Q8tbz7 homo sapien
731	87	5.5	167	2	Q65742_CICAR	Q65742 cicier ariet	804	86.5	5.5	807	2	O18511_TRINI	O18511 trichoplusi
732	87	5.5	235	2	Q63349_RAT	Q63349 rattus norv	805	86.5	5.5	838	2	Q7UNP4_RHOBA	Q7unp4 rhodopirell
733	87	5.5	259	2	Q70CD5_EIMTE	Q70cd5 emieria ten	806	86.5	5.5	843	2	Q4RQ04_TETNG	Q4rqm0 tetradodon n
734	87	5.5	363	2	Q91YX8_MOUSE	Q91yx8 mus musculu	807	86.5	5.5	853	2	Q54S28_DICDI	Q54s28 dictyosteli
735	87	5.5	385	2	Q8T8J9_DROSI	Q8t8j9 drosophila	808	86.5	5.5	941	2	Q9LTH0_ARATH	Q9lth0 arabidopsis
736	87	5.5	406	2	Q4I3G6_GIBZE	Q4i3g6 gibberella	809	86.5	5.5	970	2	Q4W973_ASPFU	Q4w973 aspergillus
737	87	5.5	442	2	Q75805_ASHGO	Q758q5 ashbya goss	810	86.5	5.5	1546	2	Q80SS4_MOUSE	Q80ss4 mus musculu
738	87	5.5	456	2	Q5B7G2_EMENI	Q5b7g2 aspergillus	811	86.5	5.5	1579	2	Q99MP1_MOUSE	Q99mp1 mus musculu
739	87	5.5	478	2	Q5SR11_KYNE	Q5srt1 cryptococcu	812	86.5	5.5	1683	2	Q810D4_MOUSE	Q810d4 mus musculu
740	87	5.5	484	2	Q4FK07_9TRYP	Q4fkq7 trypanosoma	813	86.5	5.5	1684	2	Q9WTQ5_MOUSE	Q9wtq5 mus musculu
741	87	5.5	532	2	Q4JK69_DERPT	Q4jk69 dermatophag	814	86.5	5.5	1822	2	Q7R0W4_GIALA	Q7r0w4 giardia lam
742	87	5.5	567	2	Q60XG6_CAEER	Q60xg6 caenorhabdi	815	86.5	5.5	1844	2	Q22579_CAEEL	Q22579 caenorhabdi
743	87	5.5	585	2	Q58SH0_DROSI	Q58sh0 drosophila	816	86.5	5.5	2546	2	Q54ER5_DICDI	Q54er5 dictyosteli
744	87	5.5	627	2	Q7RW72_NEUCR	Q7rwt2 neurospora	817	86.5	5.5	2781	2	Q9UIG2_HUMAN	Q9uig2 homo sapien
745	87	5.5	639	2	Q6E8S0_LISMO	Q6e8s0 listeria mo	818	86.5	5.5	4509	2	Q54T85_DICDI	Q54t85 dictyosteli
746	87	5.5	661	2	O13444_CIAFU	O13444 cladosporiu	819	86	5.5	337	2	Q5AF14_CANAL	Q5af14 candida alb
747	87	5.5	686	2	Q61XJ6_CAEER	Q61xj6 caenorhabdi	820	86	5.5	347	2	Q9TZV5_PLAFA	Q9tzv5 plasmodium
748	87	5.5	689	2	Q72400_LISMF	Q724q0 listeria mo	821	86	5.5	347	2	Q9TZV6_PLAFA	Q9tzv6 plasmodium
749	87	5.5	752	2	Q3YC61_AERPE	Q3yc61 aeropyrum p	822	86	5.5	385	2	O8TK84_DROPE	Q8tk84 drosophila
750	87	5.5	841	2	Q6AX38_XENLA	Q6ax88 xenopus lae	823	86	5.5	390	2	Q70LM3_PHLRA	Q70lm3 phlebia rad
751	87	5.5	881	2	Q8IMS9_DROME	Q8ims9 drosophila	824	86	5.5	390	2	Q96T85_PHLRA	Q96t85 phlebia rad
752	87	5.5	919	2	Q51BH5_ENTHI	Q51bh5 entamoeba h	825	86	5.5	431	2	O51WX9_MAGGR	Q51wx9 magnaporth
753	87	5.5	991	2	Q83UW2_CHLTR	Q83uw2 chlamydia t	826	86	5.5	434	2	Q872V2_NEUCR	Q872v2 neurospora
754	87	5.5	991	2	Q84FV0_CHLTR	Q84fv0 chlamydia t	827	86	5.5	435	2	Q7VNN0_HAEDU	Q7vnn0 haemophilus
755	87	5.5	991	2	Q84FV1_CHLTR	Q84fv1 chlamydia t	828	86	5.5	476	2	Q03996_PLACH	Q03996 plasmodium
756	87	5.5	1016	1	PNPH_CHLTR	Q84880 chlamydia t	829	86	5.5	477	2	Q03996_PLACH	Q03996 homo sapien
757	87	5.5	1048	2	Q3LAU3_LEGPN	Q3lau3 legionella	830	86	5.5	495	2	Q6AK33_DESPS	Q6ak33 desulfotale
758	87	5.5	1055	2	Q55G65_DICDI	Q55g65 dictyosteli	831	86	5.5	537	2	Q5AHC9_CANAL	Q5ahc9 candida alb
759	87	5.5	1173	2	Q61A60_CAEER	Q61a60 caenorhabdi	832	86	5.5	537	2	Q5AHQ5_CANAL	Q5ahq5 candida alb
760	87	5.5	1246	2	Q51FG7_ENTHI	Q51fg7 entamoeba h	833	86	5.5	551	1	PODXL_RABIT	Q28645 oryctolagus
761	87	5.5	1447	2	Q5B4Q8_EMENI	Q5b4q8 aspergillus	834	86	5.5	572	2	Q58SM1_DROME	Q58sm1 drosophila

835	Q4TVQ7_LISMO	2	598	5.5	86	Q4TVQ7 listeria mo	908	85.5	5.4	878	2	Q55GH4_DICDI	2	Q55GH4 dictyosteli
836	Q8GNQ9_LISMO	2	604	5.5	86	Q8GNQ9 listeria mo	909	85.5	5.4	895	2	Q80973_ARATH	2	Q80973 arabidopsis
837	Q6E9N2_LISMO	2	604	5.5	86	Q6E9N2 listeria mo	910	85.5	5.4	895	2	Q6R8J3_BRARE	2	Q6R8J3 brachydanio
838	Q58SG0_DROSI	2	625	5.5	86	Q58SG0 drosophila	911	85.5	5.4	935	2	Q55FS4_DICDI	2	Q55FS4 dictyosteli
839	Q5EL88_DROME	2	629	5.5	86	Q5EL88 drosophila	912	85.5	5.4	954	2	Q6R8J2_BRARE	2	Q6R8J2 brachydanio
840	Q6BR84_LISMO	2	639	5.5	86	Q6BR84 listeria mo	913	85.5	5.4	977	2	Q6GQ19_XENLA	2	Q6GQ19 xenopus lae
841	Q7S009_NEUCR	2	697	5.5	86	Q7S009 neurospora	914	85.5	5.4	981	2	Q91G49_IRV6	2	Q91G49 chilo iride
842	Q4P7V7_USTWA	2	709	5.5	86	Q4P7V7 ustilago ma	915	85.5	5.4	1052	2	Q4SP88_TETNG	2	Q4SP88 tetraodon n
843	Q59TK9_CANAL	2	714	5.5	86	Q59TK9 candida alb	916	85.5	5.4	1209	2	Q8MU69_9VIRU	2	Q8MU69 cacao swoll
844	Q59TP1_CANAL	2	714	5.5	86	Q59TP1 candida alb	917	85.5	5.4	1888	2	Q8MU69_9VIRU	2	Q8MU69 cacao swoll
845	Q869R9_DICDI	2	734	5.5	86	Q869R9 dictyosteli	918	85.5	5.4	2448	2	Q8MU69_9VIRU	2	Q8MU69 cacao swoll
846	Q9HF24_CANAL	2	750	5.5	86	Q9HF24 candida alb	919	85.5	5.4	2482	2	Q8MU69_9VIRU	2	Q8MU69 cacao swoll
847	Q9LK78_ARATH	2	780	5.5	86	Q9LK78 arabidopsis	920	85.5	5.4	3346	2	Q8RI27_BRARE	2	Q8RI27 brachydanio
848	Q8EXF5_LEPIN	2	799	5.5	86	Q8EXF5 leptospira	921	85.5	5.4	4862	2	Q5RI27_BRARE	2	Q5RI27 brachydanio
849	Q75R17_LEPIC	2	799	5.5	86	Q75R17 leptospira	922	85.5	5.4	6995	2	Q86RK2_HUMAN	2	Q86RK2 homo sapien
850	Q7X106_ORYSA	2	843	5.5	86	Q7X106 oryza sativ	923	85.5	5.4	172	2	Q8VC95_MOUSE	2	Q8VC95 mus musculu
851	Q55C58_DICDI	2	855	5.5	86	Q55C58 dictyosteli	924	85.5	5.4	235	2	Q86HS8_DICDI	2	Q86HS8 dictyosteli
852	Q80XL8_MOUSE	2	866	5.5	86	Q80XL8 mus musculu	925	85.5	5.4	265	2	Q9GZES_CABEL	2	Q9GZES caenorhabdi
853	Q55MM6_CRYNE	2	955	5.5	86	Q55MM6 cryptococcu	926	85.5	5.4	300	2	Q95XH5_CABEL	2	Q95XH5 caenorhabdi
854	Q5KB01_CRYNE	2	955	5.5	86	Q5KB01 cryptococcu	927	85.5	5.4	317	2	Q8BEK4_COWPX	2	Q8BEK4 cowpox viru
855	Q59X21_CANAL	2	1042	5.5	86	Q59X21 candida alb	928	85.5	5.4	326	2	Q9VW89_DROME	2	Q9VW89 drosophila
856	Q80U87_MOUSE	2	1080	5.5	86	Q80U87 mus musculu	929	85.5	5.4	343	1	HXDAAR_BRARE	1	HXDAAR brachydanio
857	Q6CAR3_YARLI	2	1266	5.5	86	Q6CAR3 yarrowia li	930	85.5	5.4	345	2	Q691Y8_ANOSA	2	Q691Y8 anolis sagr
858	Q262F7_CAEBR	2	1266	5.5	86	Q262F7 caenorhabdi	931	85.5	5.4	456	2	Q5R8Q6_PONPY	2	Q5R8Q6 pongo pygma
859	Q8MMQ2_DICDI	2	1324	5.5	86	Q8MMQ2 dictyosteli	932	85.5	5.4	474	2	Q417B2_GIBZE	2	Q417B2 gibberella
860	Q51DL9_ENTHI	2	1609	5.5	86	Q51DL9 entamoeba h	933	85.5	5.4	477	2	Q7MR34_WOLSU	2	Q7MR34 wolinnella s
861	Q80Z18_MOUSE	2	1674	5.5	86	Q80Z18 mus musculu	934	85.5	5.4	478	2	Q5XG84_CRYNE	2	Q5XG84 cryptococcu
862	Q61ZV2_CAEBR	2	1716	5.5	86	Q61ZV2 caenorhabdi	935	85.5	5.4	503	2	Q8VCF0_MOUSE	2	Q8VCF0 mus musculu
863	Q25685_PLACH	2	1785	5.5	86	Q25685 plasmodium e	936	85.5	5.4	510	2	Q8NJT3_KJULA	2	Q8NJT3 kluyveromyc
864	Q4H2P9_GIBZE	2	2044	5.5	86	Q4H2P9 gibberella	937	85.5	5.4	516	2	Q5CM29_CRYHO	2	Q5CM29 cryptospori
865	Q55FT4_DICDI	2	2247	5.5	86	Q55FT4 dictyosteli	938	85.5	5.4	526	2	Q51V78_MAGR	2	Q51V78 magnaporth
866	Q8LB00_ARATH	2	193	5.5	86	Q8LB00 arabidopsis	939	85.5	5.4	531	2	Q5TXG4_ANGOA	2	Q5TXG4 anopheles g
867	Q6TVK4_9POXV	2	206	5.5	86	Q6TVK4 orf virus	940	85.5	5.4	573	2	Q8H7K9_ORYSA	2	Q8H7K9 oryza sativ
868	Q8KKT9_RHIEI	2	224	5.5	86	Q8KKT9 rhizobium e	941	85.5	5.4	576	2	Q86G04_YEAST	2	Q86G04 saccharomyc
869	Q9U9J2_TOXCA	2	289	5.5	86	Q9U9J2 toxocara ca	942	85.5	5.4	597	2	Q5AA66_CANAL	2	Q5AA66 candida alb
870	Q6DG19_BRARE	2	271	5.5	86	Q6DG19 brachydanio	943	85.5	5.4	599	2	Q6C2K2_YARLI	2	Q6C2K2 yarrowia li
871	Q5R230_92YGO	2	346	5.5	86	Q5R230 phycomyces	944	85.5	5.4	601	2	Q6V6S1_DROME	2	Q6V6S1 drosophila
872	Q7KRX4_DROME	2	370	5.5	86	Q7KRX4 drosophila	945	85.5	5.4	612	2	Q622S9_CAEBR	2	Q622S9 caenorhabdi
873	Q8R089_MOUSE	2	378	5.5	86	Q8R089 mus musculu	946	85.5	5.4	625	2	Q58SP8_DROSI	2	Q58SP8 drosophila
874	Q81050_DROME	2	379	5.5	86	Q81050 drosophila	947	85.5	5.4	627	1	PKMB_LACLA	1	PKMB lactococcu
875	Q81GQ0_DROME	2	390	5.5	86	Q81GQ0 drosophila	948	85.5	5.4	639	2	Q6E9T0_LISMO	2	Q6E9T0 listeria mo
876	Q51P11_MAGGR	2	405	5.5	86	Q51P11 magnaporth	949	85.5	5.4	655	2	Q54QL5_TETNG	2	Q54QL5 tetraodon n
877	Q5T227_BRARE	2	419	5.5	86	Q5T227 brachydanio	950	85.5	5.4	657	2	Q54E45_DICDI	2	Q54E45 dictyosteli
878	Q4STA8_TETNG	2	427	5.5	86	Q4STA8 tetraodon n	951	85.5	5.4	761	2	Q22271_ARATH	2	Q22271 arabidopsis
879	Q4IGB4_GIBZE	2	453	5.5	86	Q4IGB4 gibberella	952	85.5	5.4	782	2	Q8GX37_ARATH	2	Q8GX37 arabidopsis
880	Q5WG39_BACSK	2	459	5.5	86	Q5WG39 bacillus cl	953	85.5	5.4	852	2	Q6CIA5_YARLI	2	Q6CIA5 yarrowia li
881	CH62_CUCMA	1	575	5.5	86	CH62 cucurbita m	954	85.5	5.4	879	2	Q7KWL1_DICDI	2	Q7KWL1 dictyosteli
882	Q58SG4_DROSI	2	585	5.5	86	Q58SG4 drosophila	955	85.5	5.4	911	2	Q52P88_MAGGR	2	Q52P88 magnaporth
883	Q7R2J1_GIALA	2	595	5.5	86	Q7R2J1 giardia lam	956	85.5	5.4	927	2	Q9M1E4_ARATH	2	Q9M1E4 arabidopsis
884	Q8R0X0_MOUSE	2	616	5.5	86	Q8R0X0 mus musculu	957	85.5	5.4	989	2	Q91803_XENLA	2	Q91803 xenopus lae
885	Q6V6D8_DROSI	2	622	5.5	86	Q6V6D8 drosophila	958	85.5	5.4	990	2	Q83JT6_CHLTR	2	Q83JT6 chlamydia t
886	Q6V6E4_DROSI	2	622	5.5	86	Q6V6E4 drosophila	959	85.5	5.4	993	2	Q60YJ3_CAEBR	2	Q60YJ3 caenorhabdi
887	Q89QR8_BRAJA	2	623	5.5	86	Q89QR8 bradyrhizob	960	85.5	5.4	1002	2	Q4RRX1_TETNG	2	Q4RRX1 tetraodon n
888	Q58SF2_DROSI	2	624	5.5	86	Q58SF2 drosophila	961	85.5	5.4	1004	2	Q6KCB8_KJULA	2	Q6KCB8 kluyveromyc
889	Q58SG1_DROSI	2	624	5.5	86	Q58SG1 drosophila	962	85.5	5.4	1013	2	Q626Q9_CAEBR	2	Q626Q9 caenorhabdi
890	Q5ELN1_DROSI	2	624	5.5	86	Q5ELN1 drosophila	963	85.5	5.4	1025	2	Q960E6_DROME	2	Q960E6 drosophila
891	Q5ELN5_DROSI	2	624	5.5	86	Q5ELN5 drosophila	964	85.5	5.4	1049	2	Q9V6L1_DROME	2	Q9V6L1 drosophila
892	Q5ELN9_DROSI	2	624	5.5	86	Q5ELN9 drosophila	965	85.5	5.4	1049	2	Q9V6L1_DROME	2	Q9V6L1 drosophila
893	Q9LCV8_STAAU	2	625	5.5	86	Q9LCV8 staphylococ	966	85.5	5.4	1061	2	Q54Z39_DICDI	2	Q54Z39 dictyosteli
894	Q5JH19_PYRKO	2	643	5.5	86	Q5JH19 pyrococcus	967	85.5	5.4	1139	2	Q54Z39_PONPY	2	Q54Z39 pongo pygma
895	Q49445_ARATH	2	649	5.5	86	Q49445 arabidopsis	968	85.5	5.4	1170	2	Q95011_CABEL	2	Q95011 caenorhabdi
896	Q8BUE7_MOUSE	2	656	5.5	86	Q8BUE7 mus musculu	969	85.5	5.4	1286	2	Q9VKA7_DROME	2	Q9VKA7 drosophila
897	Q54LR1_DICDI	2	693	5.5	86	Q54LR1 dictyosteli	970	85.5	5.4	1354	2	Q61Y04_MAGGR	2	Q61Y04 caenorhabdi
898	Q54BAL_DICDI	2	716	5.5	86	Q54BAL dictyosteli	971	85.5	5.4	1429	2	Q51ZG9_CAEBR	2	Q51ZG9 magnaporth
899	Q7S939_NEUCR	2	734	5.5	86	Q7S939 neurospora	972	85.5	5.4	1499	2	Q52374_9FIRM	2	Q52374 caldicellul
900	Q54N84_DICDI	2	746	5.5	86	Q54N84 dictyosteli	973	85.5	5.4	1693	2	Q52YM2_PROCL	2	Q52YM2 procambur
901	LMBL3_HUMAN	1	780	5.5	86	LMBL3 human	974	84.5	5.4	17352	2	Q5CYR7_CRYPV	2	Q5CYR7 cryptospori
902	Q4VXEL_HUMAN	2	780	5.5	86	Q4VXEL homo sapien	975	84.5	5.4	187	2	Q5EQG0_MOUSE	2	Q5EQG0 mus musculu
903	Q21027_CAEBR	2	786	5.5	86	Q21027 caenorhabdi	976	84.5	5.4	220	2	Q564Z3_CABEL	2	Q564Z3 caenorhabdi
904	Q6R8J4_BRARE	2	841	5.5	86	Q6R8J4 brachydanio	977	84.5	5.4	245	2	Q5AP52_CANAL	2	Q5AP52 candida alb
905	Q9VYH8_DROME	2	843	5.5	86	Q9VYH8 drosophila	978	84.5	5.4	250	2	Q54W22_DICDI	2	Q54W22 dictyosteli
906	Q851G7_ORYSA	2	863	5.5	86	Q851G7 oryza sativ	979	84.5	5.4	274	2	Q51QC1_MAGGR	2	Q51QC1 magnaporth
907	Q4PDE9_USTWA	2	866	5.5	86	Q4PDE9 ustilago ma	980	-84.5	5.4	278	2	Q8BEJ1_9POXV	2	Q8BEJ1 skunkbox vi



981	84.5	5.4	320	2	Q4SCG1_TETNG	Q4scg1 tetraodon n	1054	84	5.3	399	2	Q5MJ02_TETPY	O5mj02 tetrahymena
982	84.5	5.4	333	2	Q60J76_CAEBR	Q60j76 caenorhabdi	1055	84	5.3	420	2	Q8N7W9_HUMAN	Q8n7w9 homo sapien
983	84.5	5.4	378	2	Q6FNP6_CANGA	Q6fnp6 candida gla	1056	84	5.3	420	2	Q8YMH1_ANASP	Q8ymh1 anabena sp
984	84.5	5.4	396	2	Q51T12_MAGGR	Q51t12 magnaporth	1057	84	5.3	456	1	NRX133_BOVIN	Q2m143 bos taurus
985	84.5	5.4	456	2	Q8R5M8_MOUSE	Q8r5m8 mus musculu	1058	84	5.3	464	2	Q9VX42_DROME	Q9vx42 drosophila
986	84.5	5.4	463	2	Q8R5M8_MOUSE	Q8r5m8 mus musculu	1058	84	5.3	464	2	Q9VX42_DROME	Q9vx42 drosophila
987	84.5	5.4	493	1	TNR8_RAT	Q9jx25 neiseria m	1059	84	5.3	475	2	Q8FQJ1_COREF	Q8fqj1 corynebacte
988	84.5	5.4	506	2	Q53Q78_HUMAN	P97525 rattus norv	1060	84	5.3	487	2	Q8E1P9_STRAS	Q8el19 streptococc
989	84.5	5.4	522	2	Q4VAS1_HUMAN	Q33qt8 homo sapien	1061	84	5.3	487	2	Q8E1P9_STRAS	Q8el19 streptococc
990	84.5	5.4	524	2	Q54B97_DICDI	Q4vas1 homo sapien	1062	84	5.3	543	2	Q14879_HUMAN	Q14879 homo sapien
991	84.5	5.4	532	2	Q6P7V2_MOUSE	Q54b97 dictyosteli	1063	84	5.3	598	2	Q5ELV9_DROSI	Q5elv9 drosophila
992	84.5	5.4	542	2	Q54PF2_DICDI	Q6p7v2 mus musculu	1064	84	5.3	625	2	Q58SH7_DROSI	Q58sh7 drosophila
993	84.5	5.4	547	2	Q4R5X1_MACFA	Q54pf2 dictyosteli	1065	84	5.3	636	1	Q5ELP1_DROSI	Q5elp1 drosophila
994	84.5	5.4	560	2	Q4VAS3_HUMAN	Q4r5x1 macaca fasc	1066	84	5.3	636	1	ENV_MCFE	P15073 mink cell f
995	84.5	5.4	562	2	NUPL_HUMAN	Q4vas3 homo sapien	1067	84	5.3	639	2	Q6E3J4_LISMO	Q6e3j4 listeria mo
996	84.5	5.4	562	1	Q4VASO_HUMAN	P52594 homo sapien	1068	84	5.3	640	2	Q5SG71_DICDI	Q5sg71 dictyosteli
997	84.5	5.4	566	2	Q4UKT5_RICFE	Q4vas0 homo sapien	1069	84	5.3	641	2	Q6AJU8_DESPS	Q6aju8 desulfotale
998	84.5	5.4	570	2	Q6GM29_XENLA	Q4ukt5 rickettsia	1070	84	5.3	648	2	Q55XQ0_CAEBL	Q55xq0 caenorhabdi
999	84.5	5.4	582	2	Q58SG6_DROSI	Q6gm29 xenopus lae	1071	84	5.3	662	1	MUC1_XENLA	Q50049 xenopus lae
1000	84.5	5.4	622	2	Q5V6R2_DROSI	Q58sg6 drosophila	1072	84	5.3	668	2	Q5B5D4_EMENI	Q5b5d4 aspergillus
1001	84.5	5.4	624	2	Q58SF7_DROSI	Q5v6r2 drosophila	1073	84	5.3	688	2	Q4QK4_LEINA	Q4qk4 leishmania
1002	84.5	5.4	624	2	Q675N0_CORSU	Q58sf7 drosophila	1074	84	5.3	677	2	Q5B9K5_EMENI	Q5b9k5 aspergillus
1003	84.5	5.4	625	2	Q58SF7_DROSI	Q675n0 cornus suec	1075	84	5.3	713	2	Q55RT5_CRYNE	Q55rt5 cryptococcu
1004	84.5	5.4	632	2	Q5ELU2_DROME	Q58sf7 drosophila	1076	84	5.3	730	2	Q6CFU9_KLUJA	Q6cfu9 kluyveromyc
1005	84.5	5.4	653	2	Q4P8I9_USTWA	Q5elu2 drosophila	1077	84	5.3	758	2	Q51JF4_MAGGR	Q51jf4 magnaporth
1006	84.5	5.4	657	2	Q86ID0_DICDI	Q4p8i9 utiilago ma	1078	84	5.3	793	2	Q8VAG7_LISMO	Q8vag7 listeria mo
1007	84.5	5.4	658	1	SHK1_SCHPO	Q86id0 dictyosteli	1079	84	5.3	809	2	Q54J73_DICDI	Q54j73 dictyosteli
1008	84.5	5.4	709	2	Q16783_CAEBL	P50527 schizosacch	1080	84	5.3	812	2	Q5TT09_ANOGA	Q5tt09 anopheles g
1009	84.5	5.4	729	2	Q51WE3_MAGGR	Q16783 caenorhabdi	1081	84	5.3	836	2	Q56DP0_PLABE	Q56dp0 plasmodium
1010	84.5	5.4	773	2	Q8TGH3_9BASI	Q51we3 magnaporth	1082	84	5.3	855	2	Q4P3C5_USTWA	Q4p3c5 utiilago ma
1011	84.5	5.4	803	1	IF2_COXBU	Q8tgh3 malassezia	1083	84	5.3	864	1	AT7L11_HUMAN	Q9ulk2 homo sapien
1012	84.5	5.4	806	2	Q3VC07_DROME	Q3bcl1 coxiella bu	1084	84	5.3	880	2	Q7YU85_DROME	Q7yu85 drosophila
1013	84.5	5.4	814	2	Q6C247_YARLI	Q3vcq7 drosophila	1085	84	5.3	933	2	Q6ZM25_HUMAN	Q6zm25 h cda flj1
1014	84.5	5.4	834	2	Q877B7_ASPOR	Q6c247 yarrowia li	1086	84	5.3	961	1	ENCL_MOUSE	Q35914 mus musculu
1015	84.5	5.4	931	2	Q5LHK9_BACFN	Q877b7 aspergillus	1087	84	5.3	996	1	LRP8_MOUSE	Q924x6 mus musculu
1016	84.5	5.4	931	2	Q64Y17_BACFR	Q5lhk9 bacteroides	1088	84	5.3	1021	2	Q6CXI2_KLUJA	Q6cxi2 kluyveromyc
1017	84.5	5.4	956	2	Q4P076_USTWA	Q64y17 bacteroides	1089	84	5.3	1075	1	FLO5_YEAST	Q38894 saccharomyc
1018	84.5	5.4	956	2	Q4SF84_TETNG	Q4p076 utiilago ma	1090	84	5.3	1085	2	Q5BLF7_BRARE	Q5blf7 brachydanio
1019	84.5	5.4	1047	2	Q874I3_CANAL	Q4sf84 tetraodon n	1091	84	5.3	1331	1	MANE_CALSA	P22533 caldocellum
1020	84.5	5.4	1057	2	Q5KE83_CRYNE	Q874i3 candida alb	1092	84	5.3	1343	2	Q960V6_DROME	Q960v6 drosophila
1021	84.5	5.4	1102	2	Q08964_YEAST	Q5ke83 cryptococcu	1093	84	5.3	1343	2	Q9W2G6_DROME	Q9w2g6 drosophila
1022	84.5	5.4	1103	2	Q6CA70_YARLI	Q08964 saccharomyc	1094	84	5.3	1362	2	Q9V294_PYRAB	Q9v294 pyrococcus
1023	84.5	5.4	1161	1	DAN4_YEAST	Q6ca70 yarrowia li	1095	84	5.3	1366	2	Q86AM2_DICDI	Q86am2 dictyosteli
1024	84.5	5.4	1186	2	Q54I34_DICDI	P47179 saccharomyc	1096	84	5.3	1601	2	Q54L90_DICDI	Q54l90 dictyosteli
1025	84.5	5.4	1189	2	Q54CM2_DICDI	Q54i34 dictyosteli	1097	84	5.3	1645	2	Q9U263_CAEBL	Q9u263 caenorhabdi
1026	84.5	5.4	1218	2	Q54Y26_DICDI	Q54cm2 dictyosteli	1098	84	5.3	1649	2	Q54LW8_DICDI	Q54lw8 dictyosteli
1027	84.5	5.4	1355	2	Q86AM1_DICDI	Q54y26 dictyosteli	1099	84	5.3	1832	2	Q96503_CRYPV	Q96503 cryptocospori
1028	84.5	5.4	1380	2	Q556L7_DICDI	Q86am1 dictyosteli	1100	84	5.3	2044	2	Q55CR5_DICDI	Q55cr5 dictyosteli
1029	84.5	5.4	1420	2	Q4FWR7_LEIMA	Q556l7 dictyosteli	1101	84	5.3	2215	2	Q8I1Z6_PLAF7	Q8i1z6 plasmodium
1030	84.5	5.4	1629	2	Q4IB96_GIBZE	Q4fwr7 leishmania	1102	84	5.3	2233	2	Q7PRT5_ANOGA	Q7prt5 anopheles g
1031	84.5	5.4	1743	2	Q8I1L9_PLAVI	Q4ib96 gibbrellia	1103	84	5.3	2306	2	Q4WY2_ASPPU	Q4wy2 aspergillus
1032	84.5	5.4	1827	2	Q4Y6M8_PLACH	Q8i1l9 plasmodium	1104	84	5.3	2447	2	Q4RIS7_TETNG	Q4ris7 tetraodon n
1033	84.5	5.4	1878	2	Q6CP24_KLUJA	Q4y6m8 plasmodium	1105	83.5	5.3	203	2	Q4VHF5_9MONO	Q4vhf5 bovine resp
1034	84.5	5.4	2163	2	Q61TS1_CAEBR	Q6cp24 kluyveromyc	1106	83.5	5.3	216	2	Q28501_MACMU	Q28501 macaca mula
1035	84.5	5.4	2180	2	Q3VAS8_DROME	Q61ts1 caenorhabdi	1107	83.5	5.3	274	2	Q9EX24_STRCO	Q9ex24 streptomyce
1036	84.5	5.4	2205	2	Q54C75_DICDI	Q3vas8 drosophila	1108	83.5	5.3	279	2	Q14888_HUMAN	Q14888 homo sapien
1037	84.5	5.4	2206	2	Q4RC74_TETNG	Q54c75 dictyosteli	1109	83.5	5.3	292	2	Q68668_BACME	Q68668 bacillus me
1038	84.5	5.4	2481	2	Q99QR6_STAAM	Q4rc74 tetraodon n	1110	83.5	5.3	306	2	Q88V34_LACPL	Q88v34 lactobacill
1039	84.5	5.4	2481	2	Q99QR6_STAAM	Q99qr6 staphylococ	1111	83.5	5.3	306	2	Q9QYL4_MOUSE	Q9qyl4 mus musculu
1040	84.5	5.4	2152	2	Q8WXI7_HUMAN	Q99qr6 staphylococ	1112	83.5	5.3	385	2	Q8T8L3_DROMI	Q8t8l3 drosophila
1041	84	5.3	197	2	Q54G93_DICDI	Q8wxi7 homo sapien	1113	83.5	5.3	385	2	Q83NC5_TROW8	Q83nc5 tropheryma
1042	84	5.3	259	2	Q3N3B9_CABEL	Q54gr3 dictyosteli	1114	83.5	5.3	405	2	Q95XV0_CAEBL	Q95xv0 caenorhabdi
1043	84	5.3	262	2	P74577_SYNP3	Q3nb9 caenorhabdi	1115	83.5	5.3	446	2	Q9Y849_KLUJA	Q9y849 kluyveromyc
1044	84	5.3	305	2	Q4WU27_ASPFU	P74577 synechocyst	1116	83.5	5.3	448	2	Q83FT5_TROWT	Q83ft5 tropheryma
1045	84	5.3	309	2	Q63549_RAT	Q4wuz7 aspergillus	1117	83.5	5.3	455	2	Q4INK6_GIBZE	Q4ink6 gibbrellia
1046	84	5.3	335	2	Q9C7W2_ARATH	Q63549 rattus norv	1118	83.5	5.3	476	2	Q7SEJ2_NEUCR	Q7sej2 neuropeora
1047	84	5.3	359	1	MTDH_MEOSA	Q9c7w2 arabidopsis	1119	83.5	5.3	476	2	Q6AYP5_RAT	Q6ayp5 rattus norv
1048	84	5.3	359	2	Q54X16_MEDSA	Q92515 medicago sa	1120	83.5	5.3	498	1	TNR8_MOUSE	Q60846 mus musculu
1049	84	5.3	376	2	Q54N82_DICDI	Q53xl6 medicago sa	1121	83.5	5.3	498	2	Q6C977_YARLI	Q6c977 yarrowia li
1050	84	5.3	385	2	Q8T8I3_DROPB	Q54n82 dictyosteli	1122	83.5	5.3	575	2	Q58SM2_DROME	Q58sm2 drosophila
1051	84	5.3	385	2	Q8T8I5_DROPB	Q8t8i3 drosophila	1123	83.5	5.3	585	2	Q5S881_9MONO	Q5s881 avian pneum
1052	84	5.3	385	2	Q8T8K2_DROPE	Q8t8i5 drosophila	1124	83.5	5.3	585	2	Q5S881_9MONO	Q5s881 avian pneum
1053	84	5.3	385	2	Q8T8L0_DROPE	Q8t8k2 drosophila	1125	83.5	5.3	623	2	Q7XND3_ORYSA	Q7xnd3 oryza sativ
						Q8t8l0 drosophila	1126	83.5	5.3	624	2	Q58SF5_DROSI	Q58sf5 drosophila

1127	83.5	5.3	624	2	Q5ELP3_DROSI	Q5elp3 drosophila	1200	83	5.3	601	2	Q5VVA1_HUMAN	Q5vva1 homo sapien
1128	83.5	5.3	624	2	Q5VVF5_8ASTE	Q5vfj5 cornus cf.	1201	83	5.3	605	1	W5C4_YEAST	W5c4 yeast
1129	83.5	5.3	632	2	Q5ELT8_DROME	Q5elt8 drosophila	1202	83	5.3	632	2	Q5ELU0_DROME	Q5elu0 drosophila
1130	83.5	5.3	636	2	Q66H25_BRARE	Q66h25 brachydanio	1203	83	5.3	632	2	Q5ELU8_DROME	Q5elu8 drosophila
1131	83.5	5.3	641	2	Q66SD2_CIOIN	Q66sd2 clona intes	1204	83	5.3	639	2	Q6EB22_LISMO	Q6eb22 listeria mo
1132	83.5	5.3	669	2	Q7EZV9_ORYSA	Q7ezv9 oryza sativ	1205	83	5.3	653	1	NUMB_MOUSE	Numb mouse
1133	83.5	5.3	674	2	Q6APL0_DESPS	Q6apl0 desulfotale	1206	83	5.3	661	2	Q9V8S2_DROME	Q9v8s2 drosophila
1134	83.5	5.3	789	2	Q57ZS5_9TRYP	Q57z55 trypanosoma	1207	83	5.3	679	2	Q59DM1_CABEL	Q59dm1 caenorhabdi
1135	83.5	5.3	791	2	Q66VC3_GALPH	Q66vc3 equid herpe	1208	83	5.3	737	1	KNS1_YEAST	Kns1 yeast
1136	83.5	5.3	800	2	Q8TFG4_SCHPO	Q8tf4 echinosacch	1209	83	5.3	762	2	Q8GAG3_DICDI	Q8gag3 dictyostelli
1137	83.5	5.3	812	2	Q86AW3_DICDI	Q86aw3 dictyostelli	1210	83	5.3	769	2	Q17921_CABEL	Q17921 caenorhabdi
1138	83.5	5.3	822	2	Q34252_DICDI	Q34252 dictyostelli	1211	83	5.3	771	2	Q4WCD2_ASPFU	Q4wcd2 aspergillus
1139	83.5	5.3	838	2	Q90YMI_BRARE	Q90ym1 brachydanio	1212	83	5.3	786	2	Q9FDM5_STRAG	Q9fdm5 streptococ
1140	83.5	5.3	899	2	Q58CJ5_DROME	Q58cj5 drosophila	1213	83	5.3	794	2	Q55CQ4_DICDI	Q55cq4 dictyostelli
1141	83.5	5.3	915	2	Q54BC9_DICDI	Q54bc9 dictyostelli	1214	83	5.3	797	1	VGLX_EHV1B	Vglx ehv1b
1142	83.5	5.3	935	2	Q9VGN4_DROME	Q9vgn4 drosophila	1215	83	5.3	806	2	Q5R6R3_PONPY	Q5r6r3 pongo pygma
1143	83.5	5.3	984	2	Q4UEB9_THEAN	Q4ueb9 thelleria a	1216	83	5.3	814	2	Q55AJ1_DICDI	Q55aj1 dictyostelli
1144	83.5	5.3	1043	2	Q7EB41_CLOAB	Q7eb41 clostridium	1217	83	5.3	826	2	Q8VOL5_9ALPH	Q8vol5 equid herpe
1145	83.5	5.3	1056	2	Q55P74_CRYNE	Q55p74 cryptococcus	1218	83	5.3	832	2	Q60J61_CABER	Q60j61 caenorhabdi
1146	83.5	5.3	1153	2	Q6A1Q0_DROME	Q6alq0 drosophila	1219	83	5.3	858	2	Q9H8D9_HUMAN	Q9h8d9 homo sapien
1147	83.5	5.3	1214	2	Q54LH4_DICDI	Q54lh4 dictyostelli	1220	83	5.3	866	1	VGLX_EHV1V	Vglx ehv1v
1148	83.5	5.3	1255	2	Q54HF3_DICDI	Q54hf3 dictyostelli	1221	83	5.3	866	2	Q39781_9ALPH	Q39781 equid herpe
1149	83.5	5.3	1286	2	Q9TXR6_CABEL	Q9txr6 caenorhabdi	1222	83	5.3	867	2	Q39782_9ALPH	Q39782 equid herpe
1150	83.5	5.3	1570	2	Q61L27_CABER	Q61l27 caenorhabdi	1223	83	5.3	904	2	Q5SW65_HUMAN	Q5sw65 homo sapien
1151	83.5	5.3	1589	2	Q54I34_DICDI	Q54i34 dictyostelli	1224	83	5.3	955	2	Q5SQZ9_HUMAN	Q5sqz9 homo sapien
1152	83.5	5.3	1607	2	Q54WL2_DICDI	Q54wl2 dictyostelli	1225	83	5.3	963	1	LRP8_HUMAN	Lrp8 human
1153	83.5	5.3	1765	2	Q54WL2_DICDI	Q54wl2 dictyostelli	1226	83	5.3	963	2	Q5SW67_HUMAN	Q5sw67 homo sapien
1154	83.5	5.3	1820	2	Q54P55_DICDI	Q54p55 dictyostelli	1227	83	5.3	985	2	Q5KL22_CRYNE	Q5kl22 cryptococcu
1155	83.5	5.3	1855	2	Q4L3P2_STAHR	Q4l3p2 staphylococ	1228	83	5.3	985	2	Q55V60_CRYNE	Q55v60 cryptococcu
1156	83.5	5.3	2623	2	Q54S21_DICDI	Q54s21 dictyostelli	1229	83	5.3	1002	2	Q6CBD5_YARLI	Q6cbd5 yarrowia li
1157	83.5	5.3	2656	2	Q4UEK8_THEAN	Q4uek8 thelleria a	1230	83	5.3	1030	2	Q7QV30_GIALA	Q7qv30 giardia lam
1158	83.5	5.3	2764	2	Q7Z7D6_HUMAN	Q7z7d6 homo sapien	1231	83	5.3	1069	2	Q519R3_ENTHI	Q519r3 entamoeba h
1159	83.5	5.3	3026	2	Q8ILS9_PLAF7	Q8ils9 plasmodium	1232	83	5.3	1080	2	Q510Y4_ENTHI	Q510y4 entamoeba h
1160	83.5	5.3	3372	2	Q86498_FELCA	Q86498 felis silve	1233	83	5.3	1126	2	Q8E6U1_STRA3	Q8e6u1 streptococ
1161	83.5	5.3	5179	1	MUC2_HUMAN	Q02817 homo sapien	1234	83	5.3	1183	2	Q8GCD1_CHLAU	Q8gcd1 chloroflexu
1162	83	5.3	197	2	Q7JL62_GVCF	Q7jl62 choristoneu	1235	83	5.3	1184	2	Q41HX0_GIBZE	Q41hx0 gibberella
1163	83.5	5.3	198	2	Q7QB72_ANOGA	Q7qb72 anopheles g	1236	83	5.3	1221	2	Q4X1D8_ASPFU	Q4x1d8 aspergillus
1164	83	5.3	207	2	Q4X015_ASPFU	Q4x015 aspergillus	1237	83	5.3	1265	2	Q9P2G7_HUMAN	Q9p2g7 homo sapien
1165	83	5.3	257	2	Q54HH8_DICDI	Q54hh8 dictyostelli	1238	83	5.3	1266	2	Q4X245_ASPFU	Q4x245 aspergillus
1166	83	5.3	262	2	Q7PRG9_ANOGA	Q7prg9 anopheles g	1239	83	5.3	1377	2	Q54ND2_DICDI	Q54nd2 dictyostelli
1167	83	5.3	277	2	Q5A5U6_CANAL	Q5a5u6 candida alb	1240	83	5.3	1458	2	Q5CFZ6_CRYHO	Q5cfz6 cryptocopori
1168	83	5.3	291	2	Q6QPG5_9ADEN	Q6qpg5 simian aden	1241	83	5.3	1686	2	Q7R2E6_NEUCR	Q7r2e6 neurospora
1169	83	5.3	309	2	Q6IEL3_ORYSA	Q6iel3 oryza sativ	1242	83	5.3	2081	2	Q5SQZ8_HUMAN	Q5sqz8 homo sapien
1170	83	5.3	309	2	Q7XNY3_ORYSA	Q7xny3 oryza sativ	1243	83	5.3	2162	2	Q8N3U0_HUMAN	Q8n3u0 homo sapien
1171	83	5.3	314	2	Q9H8R7_HUMAN	Q9h8r7 homo sapien	1244	83	5.3	2210	2	Q7Z3E7_HUMAN	Q7z3e7 homo sapien
1172	83	5.3	316	2	Q8TD14_HUMAN	Q8td14 homo sapien	1245	83	5.3	2478	2	Q9LCH2_STAAR	Q9lch2 staphylococ
1173	83	5.3	337	2	Q7Z5K8_HUMAN	Q7z5k8 dictyostelli	1246	83	5.3	2478	2	Q5HE44_STAAC	Q5he44 staphylococ
1174	83	5.3	342	2	Q54LV1_DICDI	Q54lv1 dictyostelli	1247	83	5.3	3300	2	Q4N127_THERPA	Q4n127 thelleria p
1175	83	5.3	362	2	Q6CGU2_YARLI	Q6cgu2 yarrowia li	1248	83	5.3	6011	2	Q4U447_POLCB	Q4u447 polyangium
1176	83	5.3	378	2	Q8SX55_DROME	Q8sx55 drosophila	1249	83	5.3	184	2	Q7PRM2_ANOGB	Q7prm2 anopheles g
1177	83	5.3	382	2	Q9XZ28_LITSI	Q9xz28 litomosoid	1250	83	5.3	197	2	Q26878_TRYCR	Q26878 trypanosoma
1178	83	5.3	385	2	Q8TRK5_DROPE	Q8trk5 drosophila	1251	82.5	5.2	231	2	Q86LC2_9CNID	Q86lc2 zoanthus sp
1179	83	5.3	409	1	RD23B_HUMAN	F54727 homo sapien	1252	82.5	5.2	252	2	Q6GZ06_9MONO	Q6gz06 avian pneum
1180	83	5.3	409	2	Q53F10_HUMAN	Q53f10 homo sapien	1253	82.5	5.2	258	2	Q7SGP8_NEUCR	Q7sgp8 neurospora
1181	83	5.3	410	2	Q5AYD3_EMENI	Q5ayd3 aspergillus	1254	82.5	5.2	308	2	Q7XA59_LILLO	Q7xa59 lilium long
1182	83	5.3	419	2	Q8TD11_HUMAN	Q8td11 homo sapien	1255	82.5	5.2	326	2	Q9NFX5_CERCA	Q9nfx5 ceratitis c
1183	83	5.3	422	2	Q8TD13_HUMAN	Q8td13 homo sapien	1256	82.5	5.2	346	2	Q5CE07_CRYHO	Q5ce07 cryptocopori
1184	83	5.3	433	2	Q42665_SCHPO	Q42665 schizosacch	1257	82.5	5.2	346	2	Q5J888_9SAUR	Q5j888 heteronotia
1185	83	5.3	485	2	Q9VB80_DROME	Q9vb80 drosophila	1258	82.5	5.2	383	1	VEJ_HPV57	VEJ176 heteronotia
1186	83	5.3	487	2	Q4UHA9_THEAN	Q4uha9 thelleria a	1259	82.5	5.2	389	2	Q64BB8_9ARCH	Q64bb8 human papil
1187	83	5.3	512	2	Q4I756_GIBZE	Q4i756 gibberella	1260	82.5	5.2	389	2	Q6GXX0_9VIRU	Q6gxx0 swine hepat
1188	83	5.3	542	2	Q54SA9_DICDI	Q54sa9 dictyostelli	1261	82.5	5.2	389	2	Q6GXX3_9VIRU	Q6gxx3 swine hepat
1189	83	5.3	547	2	Q623V9_CABER	Q623v9 caenorhabdi	1262	82.5	5.2	391	2	Q54XF0_DICDI	Q54xf0 dictyostelli
1190	83	5.3	552	2	Q4NGB9_THERPA	Q4nqb9 thelleria p	1263	82.5	5.2	400	2	Q9SQF7_BRAJU	Q9sqf7 brassica ju
1191	83	5.3	559	2	Q9VN36_DROME	Q9vn36 drosophila	1264	82.5	5.2	416	2	Q9K8G4_BACHD	Q9k8g4 bacillus ha
1192	83	5.3	564	2	Q5CCQ1_CRYPV	Q5ccq1 cryptocopori	1265	82.5	5.2	425	2	Q54VC3_DICDI	Q54vc3 dictyostelli
1193	83	5.3	585	2	Q58SG3_DROSI	Q58sg3 drosophila	1266	82.5	5.2	452	2	Q6CE56_YARLI	Q6ce56 yarrowia li
1194	83	5.3	585	2	Q58SG5_DROSI	Q58sg5 drosophila	1267	82.5	5.2	456	1	Y883_HAEIN	Y883 haemophilus
1195	83	5.3	585	2	Q58SH2_DROSI	Q58sh2 drosophila	1268	82.5	5.2				
1196	83	5.3	599	2	Q5ELY7_DROME	Q5ely7 drosophila	1269	82.5	5.2				
1197	83	5.3	599	2	Q5ELY8_DROME	Q5ely8 drosophila	1270	82.5	5.2				
1198	83	5.3	600	2	Q59FP94_HUMAN	Q59fp94 homo sapien	1271	82.5	5.2				
1199	83	5.3	601	1	UBQL4_HUMAN	Q9nrr5 homo sapien	1272	82.5	5.2				



1273	82.5	5.2	456	2	Q4QM25_HAEI8	Q4gm25	haemophilus	1346	82	5.2	208	2	Q8IWS2_HUMAN	Q8iws2	homo sapien
1274	82.5	5.2	459	2	Q55S28_CRYNE	Q55s28	cryptococcus	1347	82	5.2	208	2	Q8NI31_HUMAN	Q8ni31	homo sapien
1275	82.5	5.2	464	2	Q55S28_CRYNE	Q55s28	cryptococcus	1348	82	5.2	226	2	Q5AIY4_CANAL	Q5aiy4	candida alb
1276	82.5	5.2	465	2	Q84DR0_NEUCR	Q8c247	neurospora	1349	82	5.2	235	2	Q5TM43_MACMU	Q5tm43	macaca mula
1277	82.5	5.2	508	2	Q6VNX4_DROSA	Q6vnx4	drosophila	1350	82	5.2	236	2	Q9LM00_PINTA	Q9lm00	pinus taeda
1278	82.5	5.2	517	2	Q5AF50_CANAL	Q5af50	candida alb	1351	82	5.2	250	2	Q8FSI6_COREF	Q8fsi6	corynebacte
1279	82.5	5.2	540	1	CH60_STRAP	Q8kj20	streptococc	1352	82	5.2	255	2	Q8IINI_DROER	Q8iini	drosophila
1280	82.5	5.2	540	2	Q7UPM2_RHOBA	Q7upm2	rhodospirell	1353	82	5.2	282	2	Q9FSR0_ORYSA	Q9fsr0	oryza sativ
1281	82.5	5.2	569	2	Q9SL10_ARATH	Q9sl10	arabidopsis	1354	82	5.2	288	2	Q4YH55_PLABE	Q4yh55	plasmodium
1282	82.5	5.2	582	2	Q54W91_DICDI	Q54w91	dictyosteli	1355	82	5.2	301	2	Q4I1K5_GIBZE	Q4i1k5	gibberella
1283	82.5	5.2	598	2	Q5ELW5_DROSI	Q5elw5	drosophila	1356	82	5.2	302	2	Q4IS83_GIBZE	Q4is83	gibberella
1284	82.5	5.2	599	2	Q5ELX0_DROME	Q5ely0	drosophila	1357	82	5.2	311	2	Q55I24_CRYNE	Q55i24	cryptococcus
1285	82.5	5.2	602	2	Q4V707_DROME	Q4v707	drosophila	1358	82	5.2	311	2	Q5K884_CRYNE	Q5k884	cryptococcus
1286	82.5	5.2	607	2	Q8GNR4_LISMO	Q8gnr4	listeria mo	1359	82	5.2	323	2	Q9W1I7_DROME	Q9w1i7	drosophila
1287	82.5	5.2	623	2	Q5LYX7_STRT1	Q5lyx7	streptococc	1360	82	5.2	338	2	Q8T8J5_DROPS	Q8t8j5	drosophila
1288	82.5	5.2	623	2	Q5M3J0_STRT2	Q5m3j0	streptococc	1361	82	5.2	339	2	Q9VUX8_DROME	Q9vux8	drosophila
1289	82.5	5.2	624	2	Q5VFJ4_CORSU	Q5vfj4	cornus suec	1362	82	5.2	345	2	Q4FKI2_9TRYP	Q4fki2	trypanosoma
1290	82.5	5.2	624	2	Q5VFJ6_CORSU	Q5vfj6	cornus suec	1363	82	5.2	345	2	Q69W2_2ANOSA	Q69w2	anolis sagr
1291	82.5	5.2	624	2	Q5VFJ7_CORSU	Q5vfj7	cornus suec	1364	82	5.2	361	2	Q5I4P3_ENTHI	Q5i4p3	entamebea h
1292	82.5	5.2	624	2	Q5VFJ9_9ASTE	Q5vfj9	cornus unal	1365	82	5.2	367	2	Q59KD1_CANAL	Q59kd1	candida alb
1293	82.5	5.2	624	2	Q5VFK1_9ASTE	Q5vfk1	cornus cf.	1366	82	5.2	385	2	Q8T8K9_DROPE	Q8t8k9	drosophila
1294	82.5	5.2	624	2	Q675N1_CORSU	Q675n1	cornus suec	1367	82	5.2	385	2	Q8T8L2_DROPE	Q8t8l2	drosophila
1295	82.5	5.2	635	2	Q66065_FIBSU	Q66065	fibrobacter	1368	82	5.2	388	2	Q60KQ3_CAEBR	Q60kq3	caenorhabdi
1296	82.5	5.2	639	2	Q5E910_LISMO	Q5e910	listeria mo	1369	82	5.2	389	2	Q76573_CAEBL	Q76573	caenorhabdi
1297	82.5	5.2	639	2	Q5E940_LISMO	Q5e940	listeria mo	1370	82	5.2	392	2	Q5A484_CANAL	Q5a484	candida alb
1298	82.5	5.2	641	2	Q5KHD0_CRYNE	Q5khd0	cryptococcus	1371	82	5.2	397	2	Q55DL3_DICDI	Q55dl3	dictyosteli
1299	82.5	5.2	646	2	Q4J684_SULAC	Q4j6e4	sulfolobus	1372	82	5.2	410	2	Q4R5B5_MACFA	Q4r5b5	macaca fasc
1300	82.5	5.2	686	2	Q8NV84_STAAR	Q8nve4	staphylococ	1373	82	5.2	466	2	Q4PCZ4_USTWA	Q4pcz4	ustilago ma
1301	82.5	5.2	698	2	Q74LM8_LACJO	Q74lm8	lactobacill	1374	82	5.2	475	2	Q50ST5_ENTHI	Q50st5	entamebea h
1302	82.5	5.2	711	2	Q7YYX9_CRYPV	Q7yyx9	cryptospori	1375	82	5.2	475	1	MYBPH_HUMAN	Q13203	homo sapien
1303	82.5	5.2	726	1	NF11_YEAST	Q12216	saccharomyc	1376	82	5.2	479	2	Q61AU9_CAEBR	Q61au9	caenorhabdi
1304	82.5	5.2	728	2	Q7NB51_MYCGLA	Q7nb51	mycoplasma	1377	82	5.2	483	2	Q9W4M2_DROME	Q9w4m2	drosophila
1305	82.5	5.2	782	2	Q6CNV3_KULULA	Q6cnv3	kluyveromyc	1378	82	5.2	486	2	Q84DR1_LISMO	Q84dr1	listeria mo
1306	82.5	5.2	790	1	ADA30_HUMAN	Q9ukf2	homo sapien	1379	82	5.2	490	2	Q7PW84_ANOGA	Q7pw84	anopheles g
1307	82.5	5.2	790	2	Q5T3X6_HUMAN	Q5t3x6	homo sapien	1380	82	5.2	491	2	Q5ORL8_ENTHI	Q5orl8	entamebea h
1308	82.5	5.2	808	2	Q81123_CAEBL	Q81123	caenorhabdi	1381	82	5.2	495	2	Q4R228_TETNG	Q4r228	tetradodon n
1309	82.5	5.2	825	2	Q03088_YEAST	Q03088	saccharomyc	1382	82	5.2	520	2	Q4XP68_PLACH	Q4xp68	plasmodium
1310	82.5	5.2	833	2	Q602I7_METCA	Q602i7	methylococc	1383	82	5.2	538	2	Q75US0_DICDI	Q75us0	dictyosteli
1311	82.5	5.2	848	2	Q6GP20_XENLA	Q6gp20	xenopus lae	1384	82	5.2	544	2	Q81G67_CAEBL	Q81g67	caenorhabthe
1312	82.5	5.2	871	1	POB1_SCHPO	Q74653	schizosacch	1385	82	5.2	562	2	Q51ND8_MAGGR	Q51nd8	magnaporthe
1313	82.5	5.2	876	2	Q5XLB5_BRARE	Q6xli5	brachydanio	1386	82	5.2	584	1	CEJ1_CAEBL	Q17802	caenorhabdi
1314	82.5	5.2	896	2	Q52B52_MAGGR	Q52b52	magnaporthe	1387	82	5.2	588	2	Q4S6V8_TETNG	Q4s6v8	tetradodon n
1315	82.5	5.2	988	2	Q8UVU2_XENLA	Q8uvu2	xenopus lae	1388	82	5.2	599	2	Q5ELX9_DROME	Q5elx9	drosophila
1316	82.5	5.2	1042	2	Q54IH7_DICDI	Q54ih7	dictyosteli	1389	82	5.2	599	2	Q9V680_DROME	Q9v680	drosophila
1317	82.5	5.2	1091	2	Q7SDT8_NEUCR	Q7sdt8	neurospora	1390	82	5.2	599	2	Q5ELY3_DROME	Q5ely3	drosophila
1318	82.5	5.2	1124	2	Q50XX8_ENTHI	Q50xx8	entamebea h	1391	82	5.2	601	2	Q4PHL9_USTWA	Q4phl9	ustilago ma
1319	82.5	5.2	1163	2	Q7PY32_ANOGA	Q7py32	anopheles g	1392	82	5.2	602	2	Q6V6S0_DROME	Q6v6s0	drosophila
1320	82.5	5.2	1167	2	Q54CK8_DICDI	Q54ck8	dictyosteli	1393	82	5.2	625	2	Q5VFL0_9ASTE	Q5vfl0	cornus cf.
1321	82.5	5.2	1181	2	Q52A92_MAGGR	Q52a92	magnaporthe	1394	82	5.2	630	2	Q96YH6_SULTO	Q96yh6	sulfolobus
1322	82.5	5.2	1206	1	FWN1B_MOUSE	Q55859	mus musculus	1395	82	5.2	641	2	Q83363_9GAMR	Q83363	murine leuk
1323	82.5	5.2	1258	2	Q4HVR5_GIBZE	Q4hvr5	gibberella	1396	82	5.2	670	2	Q9YWM0_GALV	Q9ywm0	gibbon ape
1324	82.5	5.2	1258	2	Q86IA2_DICDI	Q86ia2	dictyosteli	1397	82	5.2	673	2	Q91VK6_MOUSE	Q91vk6	mus musculus
1325	82.5	5.2	1260	2	Q614L3_CAEBR	Q614l3	caenorhabdi	1398	82	5.2	693	2	Q27394_CAEBL	Q27394	caenorhabdi
1326	82.5	5.2	1269	2	Q55G51_DICDI	Q55g51	dictyosteli	1399	82	5.2	713	2	Q5KG88_CRYNE	Q5kg88	cryptococcus
1327	82.5	5.2	1261	2	Q7R2F4_GIALA	Q7r2f4	giardia lam	1400	82	5.2	720	1	NUP2_YEAST	P32499	saccharomyc
1328	82.5	5.2	1267	2	Q54VU8_DICDI	Q54vu8	dictyosteli	1401	82	5.2	746	2	Q82GM0_STRAW	Q82gm0	streptomyce
1329	82.5	5.2	1343	2	Q61MH3_CAEBR	Q61mh3	caenorhabdi	1402	82	5.2	763	2	Q5A8K3_CANAL	Q5a8k3	candida alb
1330	82.5	5.2	1371	2	Q3VU22_DROME	Q3vu22	drosophila	1403	82	5.2	771	2	Q86NN7_DROME	Q86nn7	drosophila
1331	82.5	5.2	1383	2	Q5B1U5_EWENI	Q5b1u5	aspergillus	1404	82	5.2	776	2	Q4RHT1_TETNG	Q4rht1	tetradodon n
1332	82.5	5.2	1460	1	PMPC_CHLMU	Q3piy1	chlamydia m	1405	82	5.2	780	2	Q5CH10_CRYHO	Q5ch10	cryptospori
1333	82.5	5.2	1468	1	FWN1A_MOUSE	Q55860	mus musculus	1406	82	5.2	789	2	Q9VY98_DROME	Q9vy98	drosophila
1334	82.5	5.2	1472	2	Q6V9R4_STRPU	Q6v9r4	strongyloce	1407	82	5.2	824	2	Q6CY28_KLUULA	Q6cy28	kluyveromyc
1335	82.5	5.2	1478	1	LPN22_BOVIN	Q97817	bos taurus	1408	82	5.2	847	2	Q6ZQ82_MOUSE	Q6zq82	mus musculus
1336	82.5	5.2	1809	2	Q4Q829_LEIMA	Q4q829	leishmania	1409	82	5.2	894	2	Q7FL10_ARATH	Q7fl10	arabidopsis
1337	82.5	5.2	1851	2	Q9ESP3_RAT	Q9esp3	rattus norv	1410	82	5.2	894	2	Q9C816_ARATH	Q9c816	arabidopsis
1338	82.5	5.2	1969	2	Q7SE25_NEUCR	Q7se25	neurospora	1411	82	5.2	911	2	Q8GWK9_ARATH	Q8gwk9	arabidopsis
1339	82.5	5.2	2311	1	ROS_CHICK	P08941	gallus galli	1412	82	5.2	911	2	Q9SA18_ARATH	Q9sa18	arabidopsis
1340	82.5	5.2	2381	2	Q54QC0_DICDI	Q54qc0	dictyosteli	1413	82	5.2	926	1	XYI8_SCHPO	Q9uul5	schizosacch
1341	82.5	5.2	2483	2	Q51QB7_MAGGR	Q51qb7	magnaporthe	1414	82	5.2	926	2	Q7LDM3_HUMAN	Q7ldm3	homo sapien
1342	82	5.2	166	2	Q5IE00_PINTA	Q5ie00	pinus taeda	1415	82	5.2	957	2	Q9UKN0_HUMAN	Q9ukn0	homo sapien
1343	82	5.2	166	2	Q5IE20_PINTA	Q5ie20	pinus taeda	1416	82	5.2	963	2	Q99MX4_GLAVO	Q99mx4	glaucomys v
1344	82	5.2	166	2	Q56VT9_9STRA	Q56vt9	pythium aph	1417	82	5.2	971	2	Q6A036_MOUSE	Q6a036	mus musculus
1345	82	5.2	198	2	Q4WAE1_ASPPFU	Q4wae1	aspergillus	1418	82	5.2	973	2	Q7CZHI_AGR15	Q7czhi	agrobacteri

1419	82	1419	82	5.2	977	2	Q8UFQ8	agrobacteri	Q8ufq8	agrobacteri	1492	81.5	5.2	860	1	VG12	BPB03	Q37893	bacterioph
1420	82	5.2	981	2	Q54SW0	DICDI	Q54sw0	dictyosteli	Q54sw0	dictyosteli	1493	81.5	5.2	869	2	O01262	CABEL	Q01262	caenorhabdi
1421	82	5.2	1019	2	Q9Y6L9	HUMAN	Q9y6l9	homo sapien	Q9y6l9	homo sapien	1494	81.5	5.2	880	1	PHTF	DRONE	Q9v9a8	thelateria
1422	82	5.2	1023	2	Q7M009	SCMVC	Q7m009	simian cyto	Q7m009	simian cyto	1495	81.5	5.2	884	2	Q4ZJ94	9APIC	Q4zj94	thelateria
1423	82	5.2	1074	2	Q8C0P8	MOUSE	Q8c0p8	mus musculus	Q8c0p8	mus musculus	1496	81.5	5.2	913	2	Q7NP28	GLOVI	Q7np28	gloeobacter
1424	82	5.2	1082	1	YK02	SCHPO	Q9hdj9	schizosacch	Q9hdj9	schizosacch	1497	81.5	5.2	915	2	Q54YM3	DICDI	Q54ym3	dictyosteli
1425	82	5.2	1083	2	Q06108	YEAST	Q06108	saccharomyc	Q06108	saccharomyc	1498	81.5	5.2	917	2	Q7RA65	PLAYO	Q7ra65	plasmodium
1426	82	5.2	1099	2	Q7TUJ6	PROMM	Q8cgf7	mus musculus	Q8cgf7	mus musculus	1499	81.5	5.2	939	2	Q5SF31	HAELN	Q5sf31	haemophilus
1427	82	5.2	1100	1	TCRG1	MOUSE	Q7pmd5	anopheles g	Q7pmd5	anopheles g	1500	81.5	5.2	976	2	Q6NTV5	XENLA	Q6ntv5	xenopus lae
1428	82	5.2	1113	2	Q7PMD5	ANOGA	Q7pmd5	anopheles g	Q7pmd5	anopheles g									
1429	82	5.2	1126	2	Q9EQJ9	MOUSE	Q9eqj9	mus musculus	Q9eqj9	mus musculus									
1430	82	5.2	1147	2	Q4248	CABEL	Q94248	caenorhabdi	Q94248	caenorhabdi									
1431	82	5.2	1170	2	Q69ZB1	MOUSE	Q69ze1	mus musculus	Q69ze1	mus musculus									
1432	82	5.2	1215	1	GP158	HUMAN	Q5t848	homo sapien	Q5t848	homo sapien									
1433	82	5.2	1234	2	Q4Y8D6	PLACH	Q4y8d6	plasmodium	Q4y8d6	plasmodium									
1434	82	5.2	1256	2	Q54RH9	DICDI	Q54rh9	dictyosteli	Q54rh9	dictyosteli									
1435	82	5.2	1262	2	Q5AI49	CANAL	Q5ai49	candida alb	Q5ai49	candida alb									
1436	82	5.2	1275	2	Q5B0V1	EMENI	Q5b0v1	aspergillus	Q5b0v1	aspergillus									
1437	82	5.2	1320	2	Q54QP0	DICDI	Q54qp0	dictyosteli	Q54qp0	dictyosteli									
1438	82	5.2	1339	2	Q35788	RAT	Q35788	rattus norv	Q35788	rattus norv									
1439	82	5.2	1399	2	Q54GM7	DICDI	Q54gm7	dictyosteli	Q54gm7	dictyosteli									
1440	82	5.2	1423	2	Q6CRU1	KULIA	Q6cru1	kluyveromyc	Q6cru1	kluyveromyc									
1441	82	5.2	1526	2	Q5AAL9	CANAL	Q5aal9	candida alb	Q5aal9	candida alb									
1442	82	5.2	1564	2	Q95VZ5	DROME	Q95vz5	drosofila	Q95vz5	drosofila									
1443	82	5.2	1598	2	Q60RK8	CAEBR	Q60rk8	caenorhabdi	Q60rk8	caenorhabdi									
1444	82	5.2	1599	2	Q4QDX1	LEIMA	Q4qdx1	leishmania	Q4qdx1	leishmania									
1445	82	5.2	1672	1	PMPB	CHLMU	Q9pjy2	chlamydia m	Q9pjy2	chlamydia m									
1446	82	5.2	1689	2	Q5EEN9	VRIRU	Q5een9	crimean-con	Q5een9	crimean-con									
1447	82	5.2	1854	2	Q7ZA78	CANAL	Q7za78	candida alb	Q7za78	candida alb									
1448	82	5.2	2523	2	Q4IEB9	GIBZE	Q4ieb9	gibberella	Q4ieb9	gibberella									
1449	82	5.2	2981	1	Q6CEB2	YARLI	Q6ceb2	yarrowia li	Q6ceb2	yarrowia li									
1450	82	5.2	3146	2	Q9VUB5	DROME	Q9vub5	drosofila	Q9vub5	drosofila									
1451	82	5.2	3529	2	Q9GP30	THEPA	Q9gp30	thelateria p	Q9gp30	thelateria p									
1452	82	5.2	3529	2	Q4N9U4	THEPA	Q4n9u4	thelateria p	Q4n9u4	thelateria p									
1453	82	5.2	26926	2	Q4UIZ6	HUMAN	Q4uiz6	homo sapien	Q4uiz6	homo sapien									
1454	81.5	5.2	146	2	Q5W0S5	HUMAN	Q5w0s5	homo sapien	Q5w0s5	homo sapien									
1455	81.5	5.2	171	1	NUOE	BUCBP	Q5w0s5	homo sapien	Q5w0s5	homo sapien									
1456	81.5	5.2	234	2	Q6FXA6	CANGA	Q6fxa6	buchnera ap	Q6fxa6	buchnera ap									
1457	81.5	5.2	235	2	Q9ML82	ARATH	Q9ml82	arabidopsis	Q9ml82	arabidopsis									
1458	81.5	5.2	245	2	Q7SB16	NEUCR	Q7sb16	neurospora	Q7sb16	neurospora									
1459	81.5	5.2	245	2	Q61P73	CAEBR	Q61pf3	caenorhabdi	Q61pf3	caenorhabdi									
1460	81.5	5.2	246	2	Q60MW7	CAEBR	Q60mw7	caenorhabdi	Q60mw7	caenorhabdi									
1461	81.5	5.2	268	2	Q7QW74	ANOGA	Q7qw74	anopheles g	Q7qw74	anopheles g									
1462	81.5	5.2	345	2	Q6UJM5	9SAUR	Q6ujm5	diploclactyl	Q6ujm5	diploclactyl									
1463	81.5	5.2	364	2	Q521P9	MAGGR	Q521p9	magnaporthe	Q521p9	magnaporthe									
1464	81.5	5.2	381	2	Q5B2S4	EMENI	Q5b2s4	aspergillus	Q5b2s4	aspergillus									
1465	81.5	5.2	386	2	Q7G338	CLOAB	Q7g338	clostridium	Q7g338	clostridium									
1466	81.5	5.2	390	2	Q6PND6	EMENI	Q6pnd6	emerixella	Q6pnd6	emerixella									
1467	81.5	5.2	412	2	Q9P603	NEUCR	Q9p603	neurospora	Q9p603	neurospora									
1468	81.5	5.2	432	2	Q6NUR0	HUMAN	Q6nur0	homo sapien	Q6nur0	homo sapien									
1469	81.5	5.2	460	2	Q18984	CERAE	Q18984	cercopithec	Q18984	cercopithec									
1470	81.5	5.2	463	2	Q5FSW2	NEIGL	Q5fsw2	neisseria g	Q5fsw2	neisseria g									
1471	81.5	5.2	463	2	Q9KLH4	NEIMB	Q9klh4	neisseria m	Q9klh4	neisseria m									
1472	81.5	5.2	467	2	Q59PE2	CANAL	Q59pe2	candida alb	Q59pe2	candida alb									
1473	81.5	5.2	467	2	Q59PL2	CANAL	Q59pl2	candida alb	Q59pl2	candida alb									
1474	81.5	5.2	475	2	Q5CVA2	CRYPV	Q5cva2	cryptospori	Q5cva2	cryptospori									
1475	81.5	5.2	540	2	Q54T81	DICDI	Q54t81	dictyosteli	Q54t81	dictyosteli									
1476	81.5	5.2	551	2	Q7S436	NEUCR	Q7s436	neurospora	Q7s436	neurospora									
1477	81.5	5.2	567	2	Q6FRS1	CANGA	Q6frs1	candida gla	Q6frs1	candida gla									
1478	81.5	5.2	579	2	Q4RLQ7	TETNG	Q4rlq7	tetradodon n	Q4rlq7	tetradodon n									
1479	81.5	5.2	599	2	Q5ELX2	DROME	Q5elx2	drosofila	Q5elx2	drosofila									
1480	81.5	5.2	599	2	Q5ELY5	DROME	Q5ely5	drosofila	Q5ely5	drosofila									
1481	81.5	5.2	599	2	Q9U3W0	DROME	Q9u3w0	drosofila	Q9u3w0	drosofila									
1482	81.5	5.2	633	2	Q519D6	ENTHI	Q519d6	entamoeba h	Q519d6	entamoeba h									
1483	81.5	5.2	636	1	YNR6	YEAST	Y53882	saccharomyc	Y53882	saccharomyc									
1484	81.5	5.2	638	2	Q4ZJ93	9APIC	Q4zj93	thelateria l	Q4zj93	thelateria l									
1485	81.5	5.2	640	2	Q55CW3	DICDI	Q55cw3	dictyosteli	Q55cw3	dictyosteli									
1486	81.5	5.2	687	1	SRB4	YEAST	Q35269	saccharomyc	Q35269	saccharomyc									
1487	81.5	5.2	687	2	Q6B1B4	YEAST	Q6b1b4	saccharomyc	Q6b1b4	saccharomyc									
1488	81.5	5.2	700	2	Q5B6C0	EMENI	Q5b6c0	aspergillus	Q5b6c0	aspergillus									
1489	81.5	5.2	773	2	Q6IDE4	DROME	Q6ide4	drosofila	Q6ide4	drosofila									
1490	81.5	5.2	846	2	Q6ZKY0	ORYSA	Q6zky0	oryza sativ	Q6zky0	oryza sativ									
1491	81.5	5.2	860	1	MUTS	LISIN	Q92bv3	listeria in	Q92bv3	listeria in									

## RESULT 1

## Q9UNF4\_HUMAN

ID Q9UNF4\_HUMAN PRELIMINARY; PRT; 322 AA.

## AC Q9UNF4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Hyaluronic acid receptor (XLKDL).

GN Name: HAR; ORFNames: UNQ230;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;

OC Homo

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Winkelmann J.C., Basu S., Ozdemir E., Blough R.I.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Lewis A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Seshagiri S., Simmons L., Watanabe C., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,

RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RT bioinformatics assessment."

RL Genome Res. 13:2265-2270(2003).

RL EMBL; AF127670; AAD49220.2; -; mRNA.

DR EMBL; AY358925; AAQ89284.1; -; mRNA.

DR HSSP; P98066; 1078.

DR Ensembl; ENSG00000133800; Homo sapiens.

DR GO; GO:0005540; F:hyaluronic acid binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR000538; Link.

DR Pfam; PF00193; Xlink; 1.

DR PRINTS; PR01265; LINKMODULE.

DR ProDom; PD000918; Link; 1.

DR PROSITE; PS50963; LINK\_2; 1.

KW Receptor.

SQ

SEQUENCE 322 AA; 35213 MW; 8B4D6D623F52D559 CRC64;

Query Match 100.0%; Score 1575; DB 2; Length 322;

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Db 77 ALKASFETCSYGVGDGFVVISRISPNPKCKNGKGVGLIWKVPVSRQFAAYCYNSSDTWT 136
Qy 121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
Db 137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196
Qy 181 KKLICVTEVFVETSTMSTETEPFVENKAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 240
Db 197 KKLICVTEVFVETSTMSTETEPFVENKAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 256
Qy 241 CYVKRYVKAFFPTNKNQCKEMIEYKVVKEEKANDSNPNNEESKTKDKNPEESKSPSKTTVR 300
Db 257 CYVKRYVKAFFPTNKNQCKEMIEYKVVKEEKANDSNPNNEESKTKDKNPEESKSPSKTTVR 316
Qy 301 CLEAEV 306
Db 317 CLEAEV 322

RESULT 2
Q8TC18 HUMAN
ID Q8TC18 HUMAN PRELIMINARY; PRT; 322 AA.
AC Q8TC18;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Extracellular link domain containing 1.
GN Name=XLKD1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026231; AAB26231.1; -; mRNA.
DR HSSP; P98066; 107B.
DR HGNC; HGNC:14687; XLKD1.
DR Ensembl; ENSG00000133800; Homo sapiens.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; F:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
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DR PROSITE; PSS0963; LINK_2; 1.
SQ SEQUENCE 322 AA; 35183 MW; 0B1EBDBD7CE4610A CRC64;

Query Match 99.1%; Score 1561; DB 2; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.5e-118;
Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TRLLVQGSLSRAEELSISQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQDVET 60
Db 17 TRLLVQGSLSRAEELSISQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQDVET 76
Qy 61 ALKASFETCSYGVGDGFVVISRISPNPKCKNGKGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 77 ALKASFETCSYGVGDGFVVISRISPNPKCKNGKGVGLIWKVPVSRQFAAYCYNSSDTWT 136
Qy 121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 180
Db 137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPRR 196
Qy 181 KKLICVTEVFVETSTMSTETEPFVENKAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 240
Db 197 KKLICVTEVFVETSTMSTETEPFVENKAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 256
Qy 241 CYVKRYVKAFFPTNKNQCKEMIEYKVVKEEKANDSNPNNEESKTKDKNPEESKSPSKTTVR 300
Db 257 CYVKRYVKAFFPTNKNQCKEMIEYKVVKEEKANDSNPNNEESKTKDKNPEESKSPSKTTVR 316
Qy 301 CLEAEV 306
Db 317 CLEAEV 322

RESULT 3
Q9Y5Y7 HUMAN
ID Q9Y5Y7 HUMAN PRELIMINARY; PRT; 322 AA.
AC Q9Y5Y7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA Jackson D.G.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RT receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801 (1999).
DR EMBL; AF118108; AAD42764.1; -; mRNA.
DR HSSP; P98066; 107B.
DR GO; GO:0005867; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR GO; GO:0009653; P:morphogenesis; TAS.
DR GO; GO:0009611; P:response to wounding; TAS.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PSS0963; LINK_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35238 MW; 0EBEA56729CEFF77 CRC64;

Query Match 98.8%; Score 1556; DB 2; Length 322;
Best Local Similarity 99.0%; Pred. No. 3.8e-118;
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Matches 303; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 TRLLVQSLRAEELSIQVSCRMIGITLVSKKANQQLNFTAEKACRLGLSLAGKQVET 60
DB 17 TRLLVQSLRAEELSIQVSCRMIGITLVSKKANQQLNFTAEKACRLGLSLAGKQVET 76
QY 61 ALKASFETCSYGVWGDGFWVLSRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
DB 77 ALKASFETCSYGVWGDGFWVLSRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
QY 121 NSCIPEIITTKDPIFNQTQTATQTFEFIVSDSTYSVASPYSTIPAPTTTPAPASTSI 180
DB 137 NSRIPEIITTKDPIFNQTQTATQTFEFIVSDSTYSVASPYSTIPAPTTTPAPASTSI 196
QY 181 KKLICVTEVFMTSTMTSTETETEPFVENKAAPKNEAAGFGVPTALLVLLALLFFGAAGLGF 240
DB 197 KKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAAGFGVPTALLVLLALLFFGAAGLGF 256
QY 241 CYVKRYVKAFPTNKNQKQKEMIETKVYKEKANDSNPNESKKTDKNPEESKSPSKTTVR 300
DB 257 CYVKRYVKAFPTNKNQKQKEMIETKVYKEKANDSNPNESKKTDKNPEESKSPSKTTVR 316
QY 301 CLEAEV 306
DB 317 CLEAEV 322
RESULT 4
Q6UC88_BOVIN
ID Q6UC88_BOVIN PRELIMINARY; PRT; 322 AA.
AC Q6UC88;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Cell surface retention sequence binding protein-1.
OS Bos taurus (Bovinae).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RX MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
RA Huang J.S.;
RT "Cloning, expression, characterization and role in autocrine cell
RT growth of cell surface retention sequence binding protein-1.";
RL J. Biol. Chem. 278:43855-43869(2003).
DR EMBL; AY372937; AAQ85130.1; -; mRNA.
DR GO; GO:0005540; F-hyaluronic acid binding; IEA.
DR GO; GO:0007155; P-cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN 1.
DR PROSITE; PSS0963; LINK 2; 1.
SQ SEQUENCE 322 AA; 35561 MW; 4901DA1BF92648AE CRC64;
Query Match 71.0%; Score 1118; DB 2; Length 322;
Best Local Similarity 70.9%; Pred. No. 1.6e-82;
Matches 217; Conservative 33; Mismatches 56; Indels 0; Gaps 0;
QY 1 TRLLVQSLRAEELSIQVSCRMIGITLVSKKANQQLNFTAEKACRLGLSLAGKQVET 60
DB 17 TRLLVQSLRAEELSIQVSCRMIGITLVSKKANQQLNFTAEKACRLGLSLAGKQVET 76
QY 61 ALKASFETCSYGVWGDGFWVLSRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
DB 77 ARKFGFETCSYGVWQKQVFIPIRIINPNKCGKNGVGIWRSLSRHRHSYCHNSSDIWI 136
QY 121 NSCIPEIITTKDPIFNQTQTATQTFEFIVSDSTYSVASPYSTIPAPTTTPAPASTSI 190
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137 NSCLPEIITDDPLFNTETATYTKLWVSDSTHSELSTDGPDVVTTTVAPPLASTSTPRK 196
QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAPKNEAAGFGVPTALLVLLALLFFGAAGLGF 240
DB 197 RKLCICITEAFMDTSATVATERESDIQRPAFPKNEAVGGVPTALLVLLALLFFGAAGLAV 256
QY 241 CYVKRYVKAFPTNKNQKQKEMIETKVYKEKANDSNPNESKKTDKNPEESKSPSKTTVR 300
DB 257 CYVKRYVKAFPTNKNQKQKEMIETKVYKEKANDSNPNESKKTDKNPEESKSPSKTTVR 316
QY 301 CLEAEV 306
DB 317 CLEAEV 322
RESULT 5
Q8BHC0_MOUSE
ID Q8BHC0_MOUSE PRELIMINARY; PRT; 318 AA.
AC Q8BHC0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Extra cellular link domain-containing 1 (Mus musculus adult male lung
DE cDNA, RIKEN full-length enriched library, clone:1200012G08
DE product:extra cellular link domain-containing 1, full insert
DE sequence).
GN Name=Xlkd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.L., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
NUCLEOTIDE SEQUENCE.
RP STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
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RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2001).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki R., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
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RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pesole G.,  
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RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes";  
RL Genome Res. 10:1617-1630(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hashima M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

"RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa S., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC038653; AAH38653.1; -; mRNA.  
DR EMBL; BC038892; AAH38892.1; -; mRNA.  
DR EMBL; AK004726; BAC25094.1; -; mRNA.  
DR HSSP; P98066; 107B.  
DR Ensembl; ENSMUSG0000030787; Mus musculus.  
DR MGI; MGI:2136348; Xlkd1.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005886; C:plasma membrane; IDA.  
DR GO; GO:0005540; F:plasma membrane; IDA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.  
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.  
DR InterPro; IPR000538; Link.  
DR Pfam; PF00193; Xlink; 1.  
DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; Link; 1.  
DR PROSITE; PS01241; LINK 1; UNKNOWN 1.  
DR PROSITE; PS0963; LINK 2; 1.  
DR PROSITE; PS0963; LINK 2; 1.  
SQ SEQUENCE 318 AA; 34573 MW; 34AA31AEF5430B08 CRC64;

Query Match 67.0%; Score 1055; DB 2; Length 318;  
Best Local Similarity 69.0%; Pred. No. 2.1e-77;  
Matches 211; Conservative 30; Mismatches 61; Indels 4; Gaps 3;

Qy 1 TRLLVQSLRAEELISQVSCRMIGITIVSKANQOLNFTFEAKCRLLGLSLAGKDOVET 60  
Db 17 TRHPVQAGADLVQDLSTIS-TCRIMGVALVGRNKNPQMNFTNEANEACMLGUTLASRDQVES 75  
Qy 61 ALKASFTCSYGVWGDGFVVISRISPNPKCKGKGVGLIWKVPVSRQFAAYCYNNSDWT 120  
Db 76 AQKSGFTCSYGVWGEQFVIFSNPRCKGKGVGLIWNAPSSQKFKAYCHNSSDTWV 135  
Qy 121 NSCPIEITTKDPIFNPTQTATOTTEFTIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR 180  
Db 136 NSCPIEIVTTFYPVLDIQ--TPATEFSVSSSAVLASSPDSTTPVSATT-RAPPLTSMARK 192  
Qy 181 KKLICVTEVPMETSTMTSETETEPVENKAAFKNEAAGCGVPTALLVLAILPFGAAGLGF 240  
Db 193 TKKICITEVTEPITMATETAEFAVGAAGFKNEAAGCGVPTALLVLAILPFGAAGLGF 252  
Qy 241 CYKRVYKAPFPFNKNOCKEMIEETKVVKEEKANDSNENEEKSKTDKNPEESKSPSKTTVR 300  
Db 253 CYKRVYKAPFPFNKNOCKEMIEETKVVKEEKADDVNANEESKTKTKNPEEAKSPKTTVR 312  
Qy 301 CLEAEV 306  
Db 313 CLEAEV 318

RESULT 6  
Q99NE4 MOUSE  
ID Q99NE4 MOUSE PRELIMINARY; PRT; 318 AA.  
AC Q99NE4  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)





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RN RA HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F.,
RP DIATCHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L.,
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA STRAUSBERG R.L., FEINGOLD E.A., GROUSE L.H., DERGE J.G.,
RA KLAUSNER R.D., COLLINS F.S., WAGNER L., SHENMEN C.M., SCHULER G.D.,
RA ALTECHUL S.F., ZEEBERG B., BUETOW K.H., SCHAEFER C.F., BHAT N.K.,
RA HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F.,
RA DIATCHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L.,
RA STAPLETON M., SOARES M.B., BONALDO M.F., CASAVANT T.L., SCHEETZ T.E.,
RA BROWNSTEIN M.J., USLIN T.B., TOSHIYUKI S., CARNINCI P., PRANGE C.,
RA RAHA S.S., LOQUELLANO N.A., PETERS G.J., ABRAMSON R.D., MULLAHY S.J.,
RA BOSAK S.A., MCEWAN P.J., MCKERNAN K.J., MALEK J.A., GUNARATNE P.H.,
RA RICHARDS S., WORLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W.,
RA VILLALON D.K., MUZNY D.M., SODERGREN E.J., LU X., GIBBS R.A.,
RA FAHEY J., HELTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A.,
RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BOUFFARD G.G.,
RA BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C.,
RA BOSAK S.A., MCEWAN P.J., MCKERNAN K.J., MALEK J.A., GUNARATNE P.H.,
RA RICHARDS S., WORLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W.,
RA VILLALON D.K., MUZNY D.M., SODERGREN E.J., LU X., GIBBS R.A.,
RA FAHEY J., HELTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A.,
RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BOUFFARD G.G.,
RA BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C.,
RA BUTERFIELD Y.S.N., KRZYWINSKI M.I., SKALEKA U., SMAILUS D.E.,
RA SCHNERCH A., SCHEIN J.E., JONES S.J.M., MARRA M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA KLEIN S.L., STRAUSBERG R.L., WAGNER L., PONTIUS J., CLIFTON S.W.,
RA RICHARDSON P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX SUBMITTED (JUN-2004) TO THE EMBL/GenBank/DBJ DATABASES.
RA EMBL; BC074228; AAH74228.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR INTERPRO; IPR001231; CD44 antigen.
DR INTERPRO; IPR00538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS00963; LINK_2; 1.
FT NON_TER 1
SQ SEQUENCE 392 AA; 43658 MW; AF47C05AC550C6A1 CRC64;

Query Match 15.6%; Score 245; DB 2; Length 392;
Best Local Similarity 34.9%; Pred. No. 2.1e-11;
Matches 58; Conservative 18; Mismatches 70; Indels 20; Gaps 3;

QY 18 VSCRIMGITLVSKKANQOLNFTFAKEACRLGLSLAGKQVETALKASFETCSYGVGDG 77
DB 33 ISCRFGVHFVEKNDYSLNQEDAVKLCGLMNTTASYAQLAIDFGFCRYGWIEDR 92
QY 78 FVVISRISPNPKCGKGVGLVWKVPVSRQFAAYCYNSSDTWTNSCIPEI----- 127
DB 93 -VLIPRIKPNPICAAANYTGITLGNESRLYDVYCNASETEKSCULPVLLNEDFSHN 151
QY 128 -ITTKDPIFNQTATQTTEFIVSDSYSVASPYSTIPAPTTTPAP 172
DB 152 TDSYDPLDTQIQNSDKSGYQGSV-----TDPAPAMITPDP 189

RESULT 9
O6GM56_XENLA PRELIMINARY; PRT; 441 AA.
AC O6GM56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC443701 protein (fragment).
GN Name=LOC443701;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA STRAUSBERG R.L., FEINGOLD E.A., GROUSE L.H., DERGE J.G.,
RA KLAUSNER R.D., COLLINS F.S., WAGNER L., SHENMEN C.M., SCHULER G.D.,
RA ALTECHUL S.F., ZEEBERG B., BUETOW K.H., SCHAEFER C.F., BHAT N.K.,
RA HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F.,
RA DIATCHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L.,
RA STAPLETON M., SOARES M.B., BONALDO M.F., CASAVANT T.L., SCHEETZ T.E.,
RA BROWNSTEIN M.J., USLIN T.B., TOSHIYUKI S., CARNINCI P., PRANGE C.,
RA RAHA S.S., LOQUELLANO N.A., PETERS G.J., ABRAMSON R.D., MULLAHY S.J.,
RA BOSAK S.A., MCEWAN P.J., MCKERNAN K.J., MALEK J.A., GUNARATNE P.H.,
RA RICHARDS S., WORLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W.,
RA VILLALON D.K., MUZNY D.M., SODERGREN E.J., LU X., GIBBS R.A.,
RA FAHEY J., HELTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A.,
RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BOUFFARD G.G.,
RA BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C.,
RA BUTERFIELD Y.S.N., KRZYWINSKI M.I., SKALEKA U., SMAILUS D.E.,
RA SCHNERCH A., SCHEIN J.E., JONES S.J.M., MARRA M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX SUBMITTED (MAR-2005) TO THE EMBL/GenBank/DBJ DATABASES.
RA EMBL; BC092113; AAH92113.1; -, mRNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 392
SQ SEQUENCE 392 AA; 43658 MW; AF47C05AC550C6A1 CRC64;

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RA HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F.,
RA DIATCHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L.,
RA STAPLETON M., SOARES M.B., BONALDO M.F., CASAVANT T.L., SCHEETZ T.E.,
RA BROWNSTEIN M.J., USLIN T.B., TOSHIYUKI S., CARNINCI P., PRANGE C.,
RA RAHA S.S., LOQUELLANO N.A., PETERS G.J., ABRAMSON R.D., MULLAHY S.J.,
RA BOSAK S.A., MCEWAN P.J., MCKERNAN K.J., MALEK J.A., GUNARATNE P.H.,
RA RICHARDS S., WORLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W.,
RA VILLALON D.K., MUZNY D.M., SODERGREN E.J., LU X., GIBBS R.A.,
RA FAHEY J., HELTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A.,
RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BOUFFARD G.G.,
RA BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C.,
RA RODRIGUEZ A.C., GRIMWOOD J., SCHMUTZ J., MYERS R.M.,
RA BUTERFIELD Y.S.N., KRZYWINSKI M.I., SKALEKA U., SMAILUS D.E.,
RA SCHNERCH A., SCHEIN J.E., JONES S.J.M., MARRA M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA KLEIN S.L., STRAUSBERG R.L., WAGNER L., PONTIUS J., CLIFTON S.W.,
RA RICHARDSON P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX SUBMITTED (JUN-2004) TO THE EMBL/GenBank/DBJ DATABASES.
RA EMBL; BC074228; AAH74228.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR INTERPRO; IPR001231; CD44 antigen.
DR INTERPRO; IPR00538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS00963; LINK_2; 1.
FT NON_TER 1
SQ SEQUENCE 441 AA; 49207 MW; DF9AA596D506D1A1 CRC64;

Query Match 15.3%; Score 241; DB 2; Length 441;
Best Local Similarity 34.3%; Pred. No. 5.1e-11;
Matches 57; Conservative 19; Mismatches 70; Indels 20; Gaps 3;

QY 18 VSCRIMGITLVSKKANQOLNFTFAKEACRLGLSLAGKQVETALKASFETCSYGVGDG 77
DB 32 ISCRFGVHFVEKNDYSLNQEDAVKLCGLMNTTASYAQLAIDFGFCRYGWIEDR 91
QY 78 FVVISRISPNPKCGKGVGLVWKVPVSRQFAAYCYNSSDTWTNSCIPEI----- 127
DB 92 -VLIPRIKPNPICAAANYTGITLGNESRLYDVYCNASETEKSCULPVLLNEDFSHN 150
QY 128 -ITTKDPIFNQTATQTTEFIVSDSYSVASPYSTIPAPTTTPAP 172
DB 151 TDSYDPLDTQIQNSDKSGYQGSV-----TDPAPAMITPDP 188

RESULT 10
CD44_CRIGR STANDARD; PRT; 362 AA.
AC P20944;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)

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DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS0963; LINK_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 437 AA; 49108 MW; 7088441D0E139C10 CRC64;

Query Match 14.6%; Score 229.5; DB 2; Length 437;
Best Local Similarity 26.3%; Pred. NO. 4.4e-10;
Matches 82; Conservative 34; Mismatches 111; Indels 85; Gaps 10;

QY 18 VSRIMGITLYSKANQQLNTEAKEACELLGLSLAGQDOVETALKASFETCSYGVWDG 77
DB 24 ISCRKGFVHVEKYDRYALNEDAIKLCHELNTTIANITLMEIAQDIFGFCRYGWIEDR 83
QY 78 FVVISRISPNPKCGKNGVLIWKVPVSRQAAAYCYNSSDWTNSCIP-----E 126
DB 84 -VPIRIKPNPCAANYTGIFLGNDSLRDAVCYNASETEDKSCPEVLLNETDLSHK 142
QY 127 IITTKDPIFNQTATQTTEFIVSSTYSVASPYSTIPAP-----TTTPPA-PASTS 176
DB 143 TIDSVDPLTDQNPRTQNSDKSGTVDPGPAMITPDGQDWDIDQGTDTDPHGDPSTK 202
QY 177 IPRKKLICVTEVFNETSMSTE--TEPFVENKAAPKNEAGFGVPTALLVALLPFGA 234
DB 203 -----GDGSDSTEQTNEPGIDH-----SGYQEVPG----- 227
QY 235 AAGLGFYVVKRYKAFPTTNKQKEMETKVKKEEKANDSNPEESKK----- 283
DB 228 -----HHFPGTDHEVNE-FDTEHTTENSDDGCHVEHPRHHDQDNTGRD 273
QY 284 -TDKNPESKSP 294
DB 274 YTRPDDESKEP 285

RESULT 12
CD44_PAPHA STANDARD; PRT; 362 AA.
AC P14745;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN Name=CD44;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]_
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 66-74.
RX MEDLINE=89282830; PubMed=2471974;
RA Idzerda R.L., Carter W.G., Nottenburg C., Wayner E.A., Gallatin W.M.,
RA St John T.;
RT "Isolation and DNA sequence of a cDNA clone encoding a lymphocyte
RT adhesion receptor for high endothelium."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4659-4663(1989).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Extensively modified including N- and O-linked glycosylation,
```

```
CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC of phosphate to cytoplasmic domain serine residues.
CC -!- SIMILARITY: Contains 1 Link domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M22452; AAA35385.1; -; mRNA.
DR HSSP; P98066; LTSG.
DR SWR; P14745; 20-168.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR PROSITE; PS01241; LINK_1; 1.
DR PROSITE; PS0963; LINK_2; 1.
KW Alternative splicing; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; Phosphorylation; Proteoglycan;
KW Pyrolidone carboxylic acid; Receptor; Signal; Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 362
FT TOPO_DOM 21 269
FT TRANSMEM 270 290
FT TOPO_DOM 291 362
FT DOMAIN 32 120
FT REGION 225 269
FT COMPRES 150 158
FT MOD_RES 21 21
FT MOD_RES 292 292
FT MOD_RES 326 326
FT CARBOHYD 25 25
FT CARBOHYD 57 57
FT CARBOHYD 100 100
FT CARBOHYD 110 110
FT CARBOHYD 120 120
FT CARBOHYD 256 256
FT DISULFID 53 118
FT DISULFID 77 97
FT CONFLICT 67 67
SQ SEQUENCE 362 AA; 578BFCE7C3D52FEF CRC64;

Query Match 14.1%; Score 222.5; DB 1; Length 362;
Best Local Similarity 25.5%; Pred. No. 1.3e-09;
Matches 92; Conservative 43; Mismatches 127; Indels 99; Gaps 16;

QY 4 LVQGSRLRAELSIQVSCRIMGITLVSKKANQQLNFTFAKACRLGLSLAGKQOVETALK 63
DB 14 LVQLSL--AQIDLNITCRFEGIVHVEKNGRYSISRTAEADLCRAFNSTLPTMAQMEKALS 71
QY 64 ASFETCSYGVWDGFFVVISRISPNPKCGKNGVLIWKVPVSRQAAAYCYNSSDWTNSC 123
DB 72 IGFETCRYGFI-BGHVVPIRHPNSICAANTGYILTSNTS-QYDTYCFNASAPGEDC 129
QY 124 IPEIITTKDPIFNQTATQTTEFIVSDST-YSVASPYSTIP-----APT----- 166
DB 130 -----TSVTDLPNAFDGPITITIVNRDCTRYVKKGEYRNPEDINPSPTDDDDVSSGSS 184
QY 167 -----TTTPAPASTSIPRRKKLICVTEVFMEFSTMTETETEPFVENKAAF 210
DB 185 ERSGSTLGGYIFYNHFSTSPPIPEDG-----PWITDSTDRTPATRDQCAF 229
QY 211 K-----NEAGF-----GG-----VPTALLVALLFPGAAGLFCY 242
DB 230 DPGSGSHHTGSESAGSHSGREGGANTTSGLRTPQIPWLIILASL-LALAILAVC- 287
QY 243 VKRYVKAAPFTNKNQOKMETK---VVKEEKANDSNPEESKTKDK---NPESKSPS 295
DB 288 ----IAVNSRRRCQKKLVINNGNGAVERDKSSGLN-GEASKSQEMVHLVNKESSTPD 342
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QY 296 K 296
Db 343 Q 343

RESULT 13
O70509 RAT PRELIMINARY; PRT; 364 AA.
AC O70509;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Glycoprotein CD44s (Cd44 protein).
GN Name=Cd44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
RA Stevens J.W.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney, and Pituitary gland;
RX MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalusz D.E.,
RA Schnerzh A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG NIH MGC Project;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065147; AAC17117.1; -; mRNA.
DR EMBL; BC061531; AAH61531.1; -; mRNA.
DR EMBL; BC085703; AAH85703.1; -; mRNA.
DR HSSP; P98066; 107B.
DR SMK; O70509; 24-172.
DR Ensembl; ENSRNOG0000006094; Rattus norvegicus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; P:hyaluronic acid binding; IEA.
DR GO; GO:0005515; P:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.

Query Match 14.1%; Score 222; DB 2; Length 364;
Best Local Similarity 24.4%; Pred. No. 1.4e-09;
Matches 85; Conservative 55; Mismatches 149; Indels 60; Gaps 13;

QY 4 LVQSLRAEELSIOVSCRMIGITLVSKANQOOLNFTEAKEACRLGLSLAGKQDVETALK 63
Db 15 LIQLSLAQOQIDLNITCRVAGVHVKEKGRYSISRTEAADLCEAFVTTLPMAQMLALS 74
QY 64 ASFETCSYGVGDGVFVVISRISPNPKGKNGVGLVIMKVPVSRQFAAYCVNSSDTWTNSC 123
Db 75 KGFETCRYGFI-EGHVVIPIHPNAICAAANTGVYILLASNTSHYDTYCFNASAPLEDC 133
QY 124 IPEIITKDPINFNTQTOTTEFIVSDST-YSVASPYST-----IPAPT----- 166
Db 134 -----TSVTDLPNSFDGPVTTITVNRDGRTRYKKGGEYRTHQEDIDASNIIDVSSGSTI 188
QY 167 --TTPPA-PASTSIPRRKLLICVTEVFEMETSTMST-ETEPFVENKAFFK-----NEAAGF 217
Db 189 EKSTPEGYLHTDLPTSQPTGDRDDAFPIGSTLATSDDGSSMDPRGGFDVTVTHGSELGH 248
QY 218 GG-----VPTALLVALLFFGAAGLFCVYKRYVKAFFPTNKNQOK 259
Db 249 SSGNQDSGVTTTSGPARRRQIPFWLLILASL-LALALILAVC-----IAVNSRRRCGQKK 302
QY 260 EMIEYK---VVEEKANDSNPNBESKKTDKNPEESKPSKTVRCLEAE 305
Db 303 KLVINGNGTVEDRKFSELN-GEASKSQBMVHLVKNKEPTETPDQFMAD 350

RESULT 14
CD44_RAT STANDARD; PRT; 503 AA.
AC P26051; Q99021;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1997 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (extracellular matrix receptor-III) (ECM-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
DE 24).
GN Name=Cd44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC STRAIN=BDIX; TISSUE=Pancreas;
RX MEDLINE=91191552; PubMed=1707342; DOI=10.1016/0092-8674(91)90403-L;
RA Guenther U., Hofmann M., Rudy W., Reber S., Zoeller M., Haussmann I.,
RA Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT "A new variant of glycoprotein CD44 confers metastatic potential to
RT rat carcinoma cells."
RL Cell 65:13-24 (1991).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RA Stevens J.W., Midura R.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SULFATION OF TYR-288.
RX PubMed=9692903;
RA Sleeman J.F., Rahmsdorf U., Steffen A., Ponta H., Herrlich P.;
RT "CD44 variant exon v5 encodes a tyrosine that is sulphated."
RL Eur. J. Biochem. 255:74-80(1998).

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OM protein - protein search, using sw model  
Run on: March 20, 2006, 14:17:31 ; Search time 61.3443 Seconds  
(without alignments)  
2191.725 Million cell updates/sec

Title: US-10-063-510-6\_COPY\_17\_322  
Perfect score: 1575  
Sequence: 1 TRLVQSLRAELSIQVSC.....NPEESKSPKTTVRCLEAEV 306  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description  
SUMMARIES

RESULT 1  
ID AAY13379 standard; protein; 322 AA.  
DE Amino acid sequence of protein PRO263.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 2  
ID AAY87287 standard; protein; 322 AA.  
DE Human signal peptide containing protein HSPP-64 SEQ ID NO:64.  
PN WO200006510-A2.  
PD 06-JAN-2000.  
PA (INCY-) INCYTE PHARM INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 3; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 3  
ID ADC78521 standard; protein; 322 AA.  
DE Human PRO263 protein.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 3; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 4  
ID AAB80247 standard; protein; 322 AA.  
DE Human PRO263 protein.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 4; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 5  
ID AAB87528 standard; protein; 322 AA.  
DE Human PRO263.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 4; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 6  
ID AAB88391 standard; protein; 322 AA.  
DE Human membrane or secretory protein clone PSEC0135.

PN EP1067182-A2.  
PD 10-JAN-2001.  
PA (HELI-) HELIX RES INST.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 4; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 7  
ID ABG95853 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 5; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 8  
ID ABB84832 standard; protein; 322 AA.  
DE Human PRO263 protein sequence SEQ ID NO:32.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 5; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 9  
ID ABB95438 standard; protein; 322 AA.  
DE Human angiogenesis related protein PRO263 SEQ ID NO: 32.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 5; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 10  
ID ABB71625 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 11  
ID ABU71480 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 12  
ID ABU71926 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

RESULT 13  
ID ABO01809 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2002197671-A1.  
PD 26-DEC-2002.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 14  
ID ABU90878 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 15  
ID ABO33937 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 16  
ID ABU71954 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 17  
ID ABU54382 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 18  
ID ABO47397 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO263.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 19  
ID ABU71508 standard; protein; 322 AA.  
DE Human secreted polypeptide PRO263.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 20  
ID ABU72289 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 21  
ID ABO90962 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 22  
ID ABO27283 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO263.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 23  
ID ABU64534 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #38.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 24  
ID ABU67380 standard; protein; 322 AA.  
DE Human secreted protein PRO263.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 25  
ID ABU92478 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 26  
ID ABO14900 standard; protein; 322 AA.  
DE Human secreted / transmembrane polypeptide PRO263.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 27  
ID ABU81148 standard; protein; 322 AA.  
DE Human secreted polypeptide PRO263.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 28  
ID ABO53263 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 29  
ID ABU98265 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 30  
ID ABU89270 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 31  
ID ABU82477 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.



Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 32  
ID ABU69657 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 33  
ID ABU96441 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 34  
ID ABU72111 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 35  
ID ABO14839 standard; protein; 322 AA.  
DE Human secreted / transmembrane polypeptide PRO263.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 36  
ID ADR29406 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 37  
ID ABO17063 standard; protein; 322 AA.  
DE Human transmembrane PRO polypeptide (SeqID 6).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 38  
ID ABO44241 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO 263.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 39  
ID ADA18262 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 40  
ID ABO32791 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein PRO263.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 41  
ID ADA19868 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 42  
ID ADB17251 standard; protein; 322 AA.  
DE Human transmembrane PRO polypeptide (SeqID 6).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 43  
ID ABO34851 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 44  
ID ADA16237 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 45  
ID ADA20040 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 46  
ID ABO34169 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO 263.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 47  
ID ADA42382 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 48  
ID ABO17529 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 49  
ID ADA00337 standard; protein; 322 AA.  
DE Human secreted/transmembrane polypeptide PRO 263.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 6; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 50

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ID ADA16661 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 51
ID ADA13090 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 52
ID ADA11958 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 53
ID ADA17305 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 54
ID ADA42808 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 55
ID ABO17590 standard; protein; 322 AA.
DE Human PRO polypeptide #56.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 56
ID ADB95579 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 57
ID ADB77727 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 58
ID ADB74863 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 59
ID ADB68258 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 60
ID ADB68065 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 61
ID ADB90882 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 62
ID ADC28509 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 63
ID ADC39709 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 64
ID ADC40223 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 65
ID ADC19047 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 66
ID ADC34347 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 67
ID ADC29402 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1575; DB 7; Length 322;
  Best Local Similarity 100.0%; Pred. No. 1e-140;
RESULT 68
ID ADC28933 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
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PN US2003049677-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 69  
 ID ADC40818 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003054400-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 70  
 ID ADC19475 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003054441-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 71  
 ID ADC06962 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein.  
 PN US2003060602-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 72  
 ID ADC17141 standard; protein; 322 AA.  
 DE Mammalian PRO polypeptide (SeqID 6).  
 PN US2003065143-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 73  
 ID ADC33923 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003073077-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 74  
 ID ADC12993 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003073079-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 75  
 ID ADC14839 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003073208-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 76  
 ID ADC52334 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003138882-A1.  
 PD 24-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 77  
 ID ADC12445 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003082541-A1.

PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 78  
 ID ADD10321 standard; protein; 322 AA.  
 DE Human secreted/transmembrane PRO polypeptide #16.  
 PN US2003105011-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 79  
 ID ADD05000 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003104469-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 80  
 ID ADD11281 standard; protein; 322 AA.  
 DE Human secreted/transmembrane PRO polypeptide #16.  
 PN US2003105013-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 81  
 ID ADD04006 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003104381-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 82  
 ID ADD03582 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003108983-A1.  
 PD 12-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 83  
 ID ADD37074 standard; protein; 322 AA.  
 DE Human secreted/transmembrane PRO polypeptide #16.  
 PN US2003105012-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 84  
 ID ADD36010 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003105298-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 85  
 ID ADE34834 standard; protein; 322 AA.  
 DE Human secreted/transmembrane protein, #40.  
 PN US2003077583-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1575; DB 7; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 1e-140;  
 RESULT 86  
 ID ADG01011 standard; protein; 322 AA.  
 DE Novel human secreted and transmembrane protein PRO263.  
 PN US2003078387-A1.  
 PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 87  
ID ADG08564 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 88  
ID ADG95185 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 89  
ID ADH24038 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 90  
ID ADH34064 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 91  
ID ADH29897 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 92  
ID ADH23868 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 93  
ID ADG85272 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 94  
ID ADH24548 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 95  
ID ADH37404 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
FN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 96  
ID ADH01993 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
FN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 97  
ID ADH37574 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
FN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 98  
ID ADG85612 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 99  
ID ADH24208 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 100  
ID ADH38502 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 101  
ID ADG83623 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
FN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 102  
ID ADH29431 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 103  
ID ADH27547 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 104  
ID ADH37744 standard; protein; 322 AA.  
DE Human secreted and transmembrane protein PRO263.  
FN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 105  
ID ADH37921 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 106  
ID ADH57341 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 107  
ID ADH59317 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 108  
ID ADH53483 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 109  
ID ADH53653 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 110  
ID ADH51989 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 111  
ID ADH49844 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 112  
ID ADI25354 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 113  
ID ADH90147 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 114  
ID ADI25524 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 115  
ID ADH97698 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 116  
ID ADI38096 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 117  
ID ADI03546 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 118  
ID ADI11903 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 119  
ID ADH89977 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 120  
ID ADH98378 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 121  
ID ADI11053 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 122  
ID ADI11563 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 123  
ID ADI11563 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;

ID ADH98208 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 124  
ID ADH98548 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 125  
ID ADH98038 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 126  
ID ADI05026 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 127  
ID ADI03376 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 128  
ID ADI04771 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 129  
ID ADH78225 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181688-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 130  
ID ADI19569 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 131  
ID ADH90317 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 132  
ID ADI03036 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 133  
ID ADH77885 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 134  
ID ADH97868 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 135  
ID ADI01253 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003190869-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 136  
ID ADI01948 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 137  
ID ADI03206 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 138  
ID ADI11393 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 139  
ID ADI02295 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 140  
ID ADI11733 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 7; Length 322;  
Pred. No. 1e-140;  
RESULT 141  
ID ADI05370 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.

PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 142  
ID ADH79442 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 143  
ID ADI19399 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 144  
ID ADI05200 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 145  
ID ADH79612 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 146  
ID ADI01438 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 147  
ID ADI01608 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 148  
ID ADI01778 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 149  
ID ADH79782 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 150  
ID ADI04600 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003171550-A1.

PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 151  
ID ADI02736 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 152  
ID ADH78055 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 153  
ID ADI25694 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 154  
ID ADI25864 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 155  
ID ADK65376 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 156  
ID ADH98718 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 157  
ID ADH79959 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 158  
ID ADJ26364 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 7; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 159  
ID ADL93690 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003040013-A1.  
PD 27-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 160  
ID ADC52144 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 161  
ID ADE79279 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 162  
ID ADE79703 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 163  
ID ADE73379 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 164  
ID ADE41282 standard; protein; 322 AA.  
DE Human secreted/transmembrane PRO polypeptide #16.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 165  
ID ADE71444 standard; protein; 322 AA.  
DE Human PDEBC Incyte 3044710CD1.  
PN US2003124543-A1.  
PD 03-JUL-2003.  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 166  
ID ADE73914 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 167  
ID ADE99468 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 168  
ID ADE98587 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003211569-A1.  
PD 13-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 169  
ID AD899014 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 170  
ID ADG40484 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J F.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 171  
ID ADF73878 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 172  
ID ADF73454 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 173  
ID ADH06576 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 174  
ID ADH06406 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 175  
ID ADG68827 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 176  
ID ADH27717 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 177  
ID ADH27717 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 178  
ID ADH27717 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180912-A1.  
PD 25-SEP-2003.



ID ADG85442 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003166948-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 187  
ID ADH06236 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 188  
ID ADH33066 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 189  
ID ADH24378 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 190  
ID ADG69507 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 191  
ID ADH07770 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 192  
ID ADG85782 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 193  
ID ADH39328 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
FN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 194  
ID ADH33520 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
FN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 195  
ID ADH33860 standard; protein; 322 AA.

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DE Human PRO polypeptide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 196
ID ADH01070 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 197
ID ADG69677 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 198
ID ADH02163 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 199
ID ADG69167 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 200
ID ADG85952 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 201
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 202
ID ADH39505 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 203
ID ADH02503 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 204
ID ADG68997 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 205
ID ADH07600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 206
ID ADG86122 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 207
ID ADH24718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 208
ID ADH25766 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 209
ID ADH38332 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 210
ID ADH20513 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 211
ID ADH57171 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 212
ID ADH43465 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;
RESULT 213
ID ADH07368 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004006211-A1.
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PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 214  
ID ADH52159 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 215  
ID ADH59913 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003215904-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 216  
ID ADH49525 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 217  
ID ADH06941 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 218  
ID ADH90487 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 219  
ID ADI11223 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 220  
ID ADI18683 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003152999-A1.  
PD 14-AUG-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 221  
ID ADJ99630 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003187238-A1.

ID ADH9888 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 222  
ID ADI65403 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 223  
ID ADI02118 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 224  
ID ADH90657 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 225  
ID ADI37666 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 226  
ID ADH97462 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003190610-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 227  
ID ADI65830 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003148371-A1.  
PD 07-AUG-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 228  
ID ADH60573 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004023331-A1.  
PD 05-FEB-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 100.0%; Score 1575; DB 8; Length 322;  
RESULT 229  
ID ADJ99630 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003187238-A1.

PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 230  
ID ADL08823 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein, #40.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 231  
ID ADJ98532 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 232  
ID ADJ98702 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 233  
ID ADH78861 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 234  
ID ADJ99095 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 235  
ID ADJ99265 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 236  
ID ADJ98883 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 237  
ID ADH79031 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 238  
ID ADK00891 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GERB ) GERBER H.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 239  
ID ADK14412 standard; protein; 322 AA.  
DE Novel human secreted and transmembrane protein PRO263.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 240  
ID ADM25164 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 241  
ID ADM29914 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 242  
ID ADK82810 standard; protein; 322 AA.  
DE Human PRO polypeptide #16.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 243  
ID ADM80861 standard; protein; 322 AA.  
DE Human PRO polypeptide #3.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 244  
ID ADO06236 standard; protein; 322 AA.  
DE Human PRO polypeptide #36.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 245  
ID ADL11088 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004137561-A1.  
PD 15-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1575; DB 8; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1e-140;  
RESULT 246  
ID ADL17997 standard; protein; 322 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK ) ASHKENAZI A.  
PA (BOTS ) BOTSTEIN D.  
PA (DESN ) DESNOYERS L.  
PA (EATO ) EATON D L.  
PA (FERR ) FERRARA N.  
PA (FILV ) FILVAROFF E.  
PA (FONG ) FONG S.  
PA (GAOW ) GAO W.  
PA (GERB ) GERBER H.



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DE Human NOVX polypeptide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOK/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.

Query Match
Best Local Similarity 90.1%; Score 1418.5; DB 8; Length 297;
RESULT 260
ID AAB34702 standard; protein; 250 AA.
DE Human secreted protein encoded by DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.

Query Match
Best Local Similarity 72.2%; Score 1136.5; DB 3; Length 250;
RESULT 261
ID AAE05364 standard; protein; 318 AA.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.

Query Match
Best Local Similarity 67.0%; Score 1055; DB 4; Length 318;
RESULT 262
ID ABB72376 standard; protein; 255 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 700.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.

Query Match
Best Local Similarity 49.1%; Score 773; DB 5; Length 255;
RESULT 263
ID AAV12323 standard; protein; 116 AA.
DE Human 5' EST secreted protein SEQ ID NO:354.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.

Query Match
Best Local Similarity 32.4%; Score 510; DB 2; Length 116;
RESULT 264
ID ADW24431 standard; protein; 364 AA.
DE Rat CD44.
PN WO200024869-A2.
PD 04-MAY-2000.
PA (UYVA) UNIV YALE.
PA (VIGN/) VIGNERY A.

Query Match
Best Local Similarity 14.2%; Score 224; DB 3; Length 364;
RESULT 265
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

Query Match
Best Local Similarity 14.2%; Score 224; DB 5; Length 364;
RESULT 266
ID AAR07355 standard; protein; 362 AA.
DE B7 adhesion receptor.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.

Query Match
Best Local Similarity 14.1%; Score 222.5; DB 2; Length 362;
RESULT 267
ID ABU79109 standard; protein; 365 AA.
DE CD44 protein.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.

Query Match
Best Local Similarity 14.1%; Score 222; DB 6; Length 365;
RESULT 268
ID ADF43353 standard; protein; 365 AA.
DE CD44 receptor polypeptide seq id 73.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.

Query Match
Best Local Similarity 14.1%; Score 222; DB 7; Length 365;
RESULT 269
ID AEA03024 standard; protein; 365 AA.
DE CD44 receptor amino acid sequence SEQ ID NO:50.
PN US2005112141-A1.
PD 26-MAY-2005.
PA (TERM/) TERMAN D S.

Query Match
Best Local Similarity 14.1%; Score 222; DB 9; Length 365;
RESULT 270
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.

Query Match
Best Local Similarity 13.8%; Score 217; DB 2; Length 503;
RESULT 271
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

Query Match
Best Local Similarity 13.8%; Score 217; DB 7; Length 503;
RESULT 272
ID ADZ51063 standard; protein; 778 AA.
DE Amino acid sequence of murine CD44.
PN WO2005034984-A1.
PD 21-APR-2005.
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.

Query Match
Best Local Similarity 13.3%; Score 209.5; DB 9; Length 778;
RESULT 273
ID ABU04619 standard; protein; 668 AA.
DE Human expressed protein tag (EPT) #1285.

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PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.2%; Score 208.5; DB 6; Length 668;  
Best Local Similarity 29.3%; Pred. No. 1.9e-10;  
RESULT 274  
ID ADQ39384 standard; protein; 668 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 13.2%; Score 208.5; DB 8; Length 668;  
Best Local Similarity 29.3%; Pred. No. 1.9e-10;  
RESULT 275  
ID AAR20816 standard; protein; 361 AA.  
DE Haematopoietic CD44 Antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 13.1%; Score 207; DB 2; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 276  
ID AAR91444 standard; protein; 361 AA.  
DE Human haematopoietic CD44 antigen.  
PN US5506126-A.  
PD 09-APR-1996.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 13.1%; Score 207; DB 2; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 277  
ID AAW80453 standard; protein; 361 AA.  
DE Human CD44 antigen (membrane form).  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 13.1%; Score 207; DB 2; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 278  
ID AAW86200 standard; protein; 361 AA.  
DE Human CD44 antigen (membrane form).  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 13.1%; Score 207; DB 2; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 279  
ID AAY96139 standard; protein; 361 AA.  
DE Human haematopoietic CD44.5.  
PN US6111093-A.  
PD 29-AUG-2000.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 13.1%; Score 207; DB 3; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 280  
ID AAU02448 standard; protein; 361 AA.  
DE Human haematopoietic antigen CD44 polypeptide.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GHEO) GEN HOSPITAL CORP.  
Query Match 13.1%; Score 207; DB 4; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 281  
ID ABU04632 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1298.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.1%; Score 207; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 282  
ID ABU04610 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1276.  
PN WO200278524-A2.

PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.1%; Score 207; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 283  
ID ABU04638 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1304.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.1%; Score 207; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 284  
ID ABU04634 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1300.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.1%; Score 207; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 285  
ID ASU04626 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1292.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.1%; Score 207; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 286  
ID ABU04630 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1296.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.1%; Score 207; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 287  
ID ABU04636 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1302.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.1%; Score 207; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 288  
ID ADO49373 standard; protein; 361 AA.  
DE Human CD44 #1.  
PN US2004072283-A1.  
PD 15-APR-2004.  
PA (SEED/) SEED B.  
PA (ALLE/) ALLEN J.  
PA (ARUF/) ARUFFO A.  
PA (CAME/) CAMERINI D.  
PA (LAUF/) LAUFFER L.  
PA (OQUE/) OQUENDO C.  
PA (SIMM/) SIMMONS D.  
PA (STAM/) STAMENKOVIC I.  
PA (STEN/) STENGELIN S.  
PA (AMIO/) AMIOT M.  
Query Match 13.1%; Score 207; DB 8; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.1e-10;  
RESULT 289  
ID AAY99851 standard; protein; 361 AA.  
DE Human CD44 cell surface adhesion receptor.  
PN WO200035935-A1.  
PD 22-JUN-2000.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 13.0%; Score 205; DB 3; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.8e-10;  
RESULT 290  
ID ABU04643 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1309.  
PN WO200278524-A2.

PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.0%; Score 205; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.8e-10;  
RESULT 291  
ID ABU04609 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1275.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.0%; Score 205; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.8e-10;  
RESULT 292  
ID ABU04644 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1310.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.0%; Score 205; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.8e-10;  
RESULT 293  
ID ADV70207 standard; protein; 361 AA.  
DE Tumor-associated antigenic target polypeptide TAT449.  
PN WO2004112829-A2.  
PD 29-DEC-2004.  
PA (GETH) GENENTECH INC.  
Query Match 13.0%; Score 205; DB 9; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.8e-10;  
RESULT 294  
ID ADY19504 standard; protein; 361 AA.  
DE PRO polypeptide SEQ ID NO 5310.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 13.0%; Score 205; DB 9; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.8e-10;  
RESULT 295  
ID AEA63870 standard; protein; 361 AA.  
DE Protein of human anti-CD44 antibody.  
PN JP2005154389-A.  
PD 16-JUN-2005.  
PA (UITY) UNIV TOKYO.  
PA (FUJI) FUJI PHARM IND CO LTD.  
Query Match 13.0%; Score 205; DB 9; Length 361;  
Best Local Similarity 24.4%; Pred. No. 1.8e-10;  
RESULT 296  
ID ABU04622 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1288.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 13.0%; Score 204; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
RESULT 297  
ID AAE30338 standard; protein; 361 AA.  
DE Human CD44 antigen.  
PN WO200276510-A1.  
PD 03-OCT-2002.  
PA (AGYT-) AGY THERAPEUTICS INC.  
Query Match 13.0%; Score 204; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
RESULT 298  
ID ADQ39385 standard; protein; 361 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 13.0%; Score 204; DB 8; Length 361;  
Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
RESULT 299  
ID ADY16699 standard; protein; 361 AA.  
DE PRO polypeptide SEQ ID NO 2505.  
PN WO2005016962-A2.

PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 13.0%; Score 204; DB 9; Length 361;  
Best Local Similarity 24.4%; Pred. No. 2.2e-10;  
RESULT 300  
ID ABP72424 standard; protein; 608 AA.  
DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.  
PN WO2003014160-A2.  
PD 20-FEB-2003.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.9%; Score 203.5; DB 6; Length 608;  
Best Local Similarity 21.8%; Pred. No. 5e-10;  
RESULT 301  
ID AAY97579 standard; protein; 700 AA.  
DE Human CD44 splice variant (RA-CD44) protein sequence.  
PN WO200075312-A1.  
PD 14-DEC-2000.  
PA (YISS) YISSUM RES & DEV CO.  
Query Match 12.9%; Score 203.5; DB 4; Length 700;  
Best Local Similarity 21.8%; Pred. No. 6.1e-10;  
RESULT 302  
ID ABU04640 standard; protein; 700 AA.  
DE Human expressed protein tag (EPT) #1306.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.9%; Score 203.5; DB 6; Length 700;  
Best Local Similarity 21.8%; Pred. No. 6.1e-10;  
RESULT 303  
ID ADD90594 standard; protein; 700 AA.  
DE Human CD44v glycoprotein SEQ ID NO:4.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.9%; Score 203.5; DB 7; Length 700;  
Best Local Similarity 21.8%; Pred. No. 6.1e-10;  
RESULT 304  
ID ADM43568 standard; protein; 700 AA.  
DE CD44vRA.  
PN WO2005007700-A1.  
PD 27-JAN-2005.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.9%; Score 203.5; DB 9; Length 700;  
Best Local Similarity 21.8%; Pred. No. 6.1e-10;  
RESULT 305  
ID ADD90592 standard; protein; 361 AA.  
DE Human CD44std glycoprotein SEQ ID NO:2.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.9%; Score 203; DB 7; Length 361;  
Best Local Similarity 24.4%; Pred. No. 2.7e-10;  
RESULT 306  
ID ADM43572 standard; protein; 361 AA.  
DE CD44s.  
PN WO2005007700-A1.  
PD 27-JAN-2005.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.9%; Score 203; DB 9; Length 361;  
Best Local Similarity 24.4%; Pred. No. 2.7e-10;  
RESULT 307  
ID AAY97651 standard; protein; 436 AA.  
DE CD44Hextra/tmFAScyto protein sequence.  
PN WO200100854-A2.  
PD 04-JAN-2001.  
PA (ANGI-) ANGIOGENE PHARM LTD.  
Query Match 12.9%; Score 203; DB 4; Length 436;  
Best Local Similarity 25.4%; Pred. No. 3.5e-10;  
RESULT 308  
ID ABU04642 standard; protein; 436 AA.  
DE Human expressed protein tag (EPT) #1308.



PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.9%; Score 203; DB 6; Length 436;  
Best Local Similarity 25.4%; Pred. No. 3.5e-10;  
RESULT 309  
ID ABU04653 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1319.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.9%; Score 203; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 310  
ID ABU04616 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1282.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.9%; Score 203; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 311  
ID ADP65295 standard; protein; 742 AA.  
DE Human CD44 antigen (homing function and Indian blood group system), CD44.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 12.9%; Score 203; DB 7; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 312  
ID ADJ61252 standard; protein; 742 AA.  
DE Human protein tyrosine kinase biomarker CD44 antigen protein.  
PN WO2004020583-A2.  
PD 11-MAR-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 12.9%; Score 203; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 313  
ID ADQ39391 standard; protein; 742 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.9%; Score 203; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 314  
ID ADR67253 standard; protein; 742 AA.  
DE Human bladder cancer associated amino acid sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERR/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (STAU/) STAUB E.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Query Match 12.9%; Score 203; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 315  
ID ADU06304 standard; protein; 742 AA.  
DE Novel bronchial cancer-associated human protein SeqID528.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
Query Match 12.9%; Score 203; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 316  
ID ADV15336 standard; protein; 742 AA.  
DE PRO polypeptide SEQ ID NO 1144.  
PN WO2005016962-A2.  
PD 24-FEB-2005.

PA (GETH) GENENTECH INC.  
Query Match 12.9%; Score 203; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 317  
ID ADV15338 standard; protein; 742 AA.  
DE PRO polypeptide SEQ ID NO 1144.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 12.9%; Score 203; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 7.3e-10;  
RESULT 318  
ID ADH18998 standard; protein; 330 AA.  
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 12.9%; Score 202.5; DB 8; Length 330;  
Best Local Similarity 25.1%; Pred. No. 2.7e-10;  
RESULT 319  
ID AAY97650 standard; protein; 431 AA.  
DE CD44HextraPASTm/cyto protein sequence.  
PN WO200100854-A2.  
PD 04-JAN-2001.  
PA (ANGI-) ANGIOGENE PHARM LTD.  
Query Match 12.9%; Score 202.5; DB 4; Length 431;  
Best Local Similarity 24.7%; Pred. No. 3.9e-10;  
RESULT 320  
ID ABU04641 standard; protein; 431 AA.  
DE Human expressed protein tag (EPT) #1307.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.9%; Score 202.5; DB 6; Length 431;  
Best Local Similarity 24.7%; Pred. No. 3.9e-10;  
RESULT 321  
ID ABU04607 standard; protein; 361 AA.  
DE Human expressed protein tag (EPT) #1273.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.8%; Score 202; DB 6; Length 361;  
Best Local Similarity 24.4%; Pred. No. 3.4e-10;  
RESULT 322  
ID ADL93508 standard; protein; 361 AA.  
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.  
PN WO2004024750-A2.  
PD 25-MAR-2004.  
PA (DYAX-) DYAX CORP.  
Query Match 12.8%; Score 202; DB 8; Length 361;  
Best Local Similarity 24.1%; Pred. No. 3.4e-10;  
RESULT 323  
ID ADS75483 standard; protein; 361 AA.  
DE Human cell surface glycoprotein CD44 amino acid sequence.  
PN JP2004275060-A.  
PD 07-OCT-2004.  
PA (SANY) SANKYO CO LTD.  
Query Match 12.8%; Score 202; DB 8; Length 361;  
Best Local Similarity 24.4%; Pred. No. 3.4e-10;  
RESULT 324  
ID ABU04618 standard; protein; 675 AA.  
DE Human expressed protein tag (EPT) #1284.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.8%; Score 202; DB 6; Length 675;  
Best Local Similarity 26.0%; Pred. No. 8e-10;  
RESULT 325  
ID ABU04621 standard; protein; 691 AA.  
DE Human expressed protein tag (EPT) #1287.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.

Query Match 12.8%; Score 202; DB 6; Length 691;  
Best Local Similarity 26.0%; Pred. No. 8.3e-10;  
RESULT 326  
ID ADQ39390 standard; protein; 691 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.8%; Score 202; DB 8; Length 691;  
Best Local Similarity 26.0%; Pred. No. 8.3e-10;  
RESULT 327  
ID ABU04620 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1286.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.8%; Score 202; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 328  
ID ABU04645 standard; protein; 742 AA.  
DE Human expressed protein tag (EPT) #1311.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.8%; Score 202; DB 6; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 329  
ID ADN95511 standard; protein; 742 AA.  
DE Human BEC/LEC-related protein sequence SeqID434.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN-) LICENTIA LTD.  
Query Match 12.8%; Score 202; DB 7; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 330  
ID ADL93506 standard; protein; 742 AA.  
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.  
PN WO2004024750-A2.  
PD 25-MAR-2004.  
PA (DYAX-) DYAX CORP.  
Query Match 12.8%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 331  
ID ADO35181 standard; protein; 742 AA.  
DE Protein #83 with increased gene expression in renal cell carcinoma.  
PN WO2004032842-A2.  
PD 22-APR-2004.  
PA (VAND-) VAN ANDEL INST.  
Query Match 12.8%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 332  
ID ADQ39383 standard; protein; 742 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.8%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 333  
ID ADQ39386 standard; protein; 742 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.8%; Score 202; DB 8; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 334  
ID ADW72142 standard; protein; 742 AA.  
DE Human CD44 protein as biomarker for colorectal cancer.  
PN US2005014165-A1.  
PD 20-JAN-2005.  
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.

Query Match 12.8%; Score 202; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 335  
ID ADZ51062 standard; protein; 742 AA.  
DE Amino acid sequence of human CD44.  
PN WO2005034984-A1.  
PD 21-APR-2005.  
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
Query Match 12.8%; Score 202; DB 9; Length 742;  
Best Local Similarity 26.0%; Pred. No. 9.1e-10;  
RESULT 336  
ID ABU04617 standard; protein; 425 AA.  
DE Human expressed protein tag (EPT) #1283.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.8%; Score 201; DB 6; Length 425;  
Best Local Similarity 22.0%; Pred. No. 5.3e-10;  
RESULT 337  
ID ADD90596 standard; protein; 699 AA.  
DE Human CD44v glycoprotein SEQ ID NO:6.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.7%; Score 200.5; DB 7; Length 699;  
Best Local Similarity 25.2%; Pred. No. 1.2e-09;  
RESULT 338  
ID ADW43570 standard; protein; 699 AA.  
DE CD44v3-V10.  
PN WO2005007700-A1.  
PD 27-JAN-2005.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.7%; Score 200.5; DB 9; Length 699;  
Best Local Similarity 25.2%; Pred. No. 1.2e-09;  
RESULT 339  
ID AAR20817 standard; protein; 493 AA.  
DE Epithelial CD44 Antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 12.7%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 9e-10;  
RESULT 340  
ID AAR91445 standard; protein; 493 AA.  
DE Human epithelial CD44 antigen.  
PN US5506126-A.  
PD 09-APR-1996.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 12.7%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 9e-10;  
RESULT 341  
ID AAW80454 standard; protein; 493 AA.  
DE Human CD44 antigen (epithelial form).  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 12.7%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 9e-10;  
RESULT 342  
ID AAW89151 standard; protein; 493 AA.  
DE Human CD44 antigen (epithelial form).  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GHO) GEN HOSPITAL CORP.  
Query Match 12.7%; Score 199.5; DB 2; Length 493;  
Best Local Similarity 23.6%; Pred. No. 9e-10;  
RESULT 343  
ID AAY96140 standard; protein; 493 AA.  
DE Human epithelial CD44.  
PN US6111093-A.  
PD 29-AUG-2000.  
PA (GHO) GEN HOSPITAL CORP.

Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 3; Length 493;  
RESULT 344  
ID AAU02449 standard; protein; 493 AA.  
DE Human epithelial antigen CD44 polypeptide.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 4; Length 493;  
RESULT 345  
ID AAU991123 standard; protein; 493 AA.  
DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.  
PN WO200244342-A2.  
PD 06-JUN-2002.  
PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 5; Length 493;  
RESULT 346  
ID ABU04637 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1303.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 347  
ID ABU04627 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1293.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 348  
ID ABU04639 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1305.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 349  
ID ABU04623 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1289.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 350  
ID ABU04631 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1297.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 351  
ID ABU04633 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1299.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 352  
ID ABU04612 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1278.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 353  
ID ABU04615 standard; protein; 395 AA.  
DE Human expressed protein tag (EPT) #1281.  
PN WO200278524-A2.  
PD 10-OCT-2002.

Best Local Similarity 22.2%; Pred. No. 9e-10;  
RESULT 353  
ID ABU04635 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1301.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 354  
ID ABU04613 standard; protein; 493 AA.  
DE Human expressed protein tag (EPT) #1279.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 6; Length 493;  
RESULT 355  
ID ADL93507 standard; protein; 493 AA.  
DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.  
PN WO2004024750-A2.  
PD 25-MAR-2004.  
PA (DYAX-) DYAX CORP.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 8; Length 493;  
RESULT 356  
ID ADO49375 standard; protein; 493 AA.  
DE Human CD44 #2.  
PN US2004072283-A1.  
PD 15-APR-2004.  
PA (SEED/) SEED B.  
PA (ALLE/) ALLEN J.  
PA (ARUP/) ARUPFO A.  
PA (CAVE/) CAMERINI D.  
PA (LAUF/) LAUFFER L.  
PA (OQUE/) OQUENDO C.  
PA (SIMM/) SIMMONS D.  
PA (STAM/) STAMENKOVIC I.  
PA (STEN/) STENGELIN S.  
PA (AMIO/) AMIOT M.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 8; Length 493;  
RESULT 357  
ID AEB87764 standard; protein; 493 AA.  
DE Human CD44, breast tumor marker.  
PN WO2005071419-A2.  
PD 04-AUG-2005.  
PA (IPSO-) IPSOGEN.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (PAOL-) INST PAOLI CALMETTES.  
Query Match  
Best Local Similarity 12.7%; Score 199.5; DB 9; Length 493;  
RESULT 358  
ID ABU04649 standard; protein; 338 AA.  
DE Human expressed protein tag (EPT) #1315.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.6%; Score 199; DB 6; Length 338;  
RESULT 359  
ID ABU04605 standard; protein; 338 AA.  
DE Human expressed protein tag (EPT) #1271.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match  
Best Local Similarity 12.6%; Score 199; DB 6; Length 338;  
RESULT 360  
ID ABU04615 standard; protein; 395 AA.  
DE Human expressed protein tag (EPT) #1281.  
PN WO200278524-A2.  
PD 10-OCT-2002.

PA (ZYCO-) ZYCOS INC.  
Query Match 12.6%; Score 198; DB 6; Length 395;  
Best Local Similarity 23.0%; Pred. No. 9.2e-10;  
RESULT 361  
ID ABU04604 standard; protein; 719 AA.  
DE Human expressed protein tag (EPT) #1270.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.5%; Score 197; DB 6; Length 719;  
Best Local Similarity 26.3%; Pred. No. 2.6e-09;  
RESULT 362  
ID ABU04650 standard; protein; 719 AA.  
DE Human expressed protein tag (EPT) #1316.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.5%; Score 197; DB 6; Length 719;  
Best Local Similarity 26.3%; Pred. No. 2.6e-09;  
RESULT 363  
ID ABM83594 standard; protein; 535 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3843.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.5%; Score 196.5; DB 8; Length 535;  
Best Local Similarity 25.4%; Pred. No. 1.9e-09;  
RESULT 364  
ID ADQ39381 standard; protein; 535 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.5%; Score 196.5; DB 8; Length 535;  
Best Local Similarity 25.4%; Pred. No. 1.9e-09;  
RESULT 365  
ID ABU56470 standard; protein; 699 AA.  
DE Lung cancer-associated polypeptide #63.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 12.5%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 2.8e-09;  
RESULT 366  
ID ABU04647 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1313.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.5%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 2.8e-09;  
RESULT 367  
ID ABU04614 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1280.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.5%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 2.8e-09;  
RESULT 368  
ID ABU04608 standard; protein; 699 AA.  
DE Human expressed protein tag (EPT) #1274.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.5%; Score 196.5; DB 6; Length 699;  
Best Local Similarity 25.4%; Pred. No. 2.8e-09;  
RESULT 369  
ID ADV73230 standard; protein; 699 AA.  
DE Human colon tumor cell upregulated protein SEQ ID NO 71.  
PN WO2004110345-A2.  
PD 23-DEC-2004.  
PA (PHAA ) PHARMACIA CORP.

Query Match 12.5%; Score 196.5; DB 9; Length 699;  
Best Local Similarity 25.4%; Pred. No. 2.8e-09;  
RESULT 370  
ID ADY16689 standard; protein; 699 AA.  
DE PRO polypeptide SEQ ID NO 2495.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 12.5%; Score 196.5; DB 9; Length 699;  
Best Local Similarity 25.4%; Pred. No. 2.8e-09;  
RESULT 371  
ID ADI60182 standard; protein; 261 AA.  
DE Secreted polypeptide #66.  
PN WO2003025142-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.4%; Score 196; DB 7; Length 261;  
Best Local Similarity 30.9%; Pred. No. 8.1e-10;  
RESULT 372  
ID ABU04611 standard; protein; 293 AA.  
DE Human expressed protein tag (EPT) #1277.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.4%; Score 196; DB 6; Length 293;  
Best Local Similarity 30.9%; Pred. No. 9.5e-10;  
RESULT 373  
ID ABU04624 standard; protein; 294 AA.  
DE Human expressed protein tag (EPT) #1290.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.4%; Score 196; DB 6; Length 294;  
Best Local Similarity 30.9%; Pred. No. 9.5e-10;  
RESULT 374  
ID ABU04646 standard; protein; 294 AA.  
DE Human expressed protein tag (EPT) #1312.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.4%; Score 196; DB 6; Length 294;  
Best Local Similarity 30.9%; Pred. No. 9.5e-10;  
RESULT 375  
ID ADQ39389 standard; protein; 395 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.4%; Score 196; DB 8; Length 395;  
Best Local Similarity 30.9%; Pred. No. 1.4e-09;  
RESULT 376  
ID ADQ39382 standard; protein; 425 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.4%; Score 196; DB 8; Length 425;  
Best Local Similarity 30.9%; Pred. No. 1.6e-09;  
RESULT 377  
ID ADQ39388 standard; protein; 493 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.4%; Score 196; DB 8; Length 493;  
Best Local Similarity 30.9%; Pred. No. 1.9e-09;  
RESULT 378  
ID AAY12853 standard; protein; 58 AA.  
DE Human 5' EST secreted protein SEQ ID NO:443.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 12.4%; Score 195; DB 2; Length 58;

Best Local Similarity 97.6%; Pred. No. 1.3e-10;  
RESULT 379  
ID ABG17071 standard; protein; 742 AA.  
DE Novel human diagnostic protein #17062.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.3%; Score 194.5; DB 4; Length 742;  
Best Local Similarity 25.4%; Pred. No. 4.7e-09;  
RESULT 380  
ID AAM48306 standard; protein; 194 AA.  
DE Protein R2 SEQ ID 29.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 12.3%; Score 194; DB 5; Length 194;  
Best Local Similarity 30.8%; Pred. No. 8.4e-10;  
RESULT 391  
ID AAM48307 standard; protein; 200 AA.  
DE Protein R3 SEQ ID 30.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 12.3%; Score 194; DB 5; Length 200;  
Best Local Similarity 30.8%; Pred. No. 8.7e-10;  
RESULT 382  
ID AAM48308 standard; protein; 273 AA.  
DE Protein R4 SEQ ID 31.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 12.3%; Score 194; DB 5; Length 273;  
Best Local Similarity 30.8%; Pred. No. 1.3e-09;  
RESULT 383  
ID ABU04602 standard; protein; 676 AA.  
DE Human expressed protein tag (EPT) #1268.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.2%; Score 191.5; DB 6; Length 676;  
Best Local Similarity 25.8%; Pred. No. 8e-09;  
RESULT 385  
ID ABU04648 standard; protein; 271 AA.  
DE Human expressed protein tag (EPT) #1314.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.1%; Score 191; DB 6; Length 271;  
Best Local Similarity 31.5%; Pred. No. 2.5e-09;  
RESULT 386  
ID ABU04606 standard; protein; 271 AA.  
DE Human expressed protein tag (EPT) #1272.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.1%; Score 191; DB 6; Length 271;  
Best Local Similarity 31.5%; Pred. No. 2.5e-09;  
RESULT 387  
ID ABU04651 standard; protein; 470 AA.  
DE Human expressed protein tag (EPT) #1317.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.1%; Score 191; DB 6; Length 470;  
Best Local Similarity 31.5%; Pred. No. 5.4e-09;

RESULT 388  
ID ABU04603 standard; protein; 470 AA.  
DE Human expressed protein tag (EPT) #1269.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 12.1%; Score 191; DB 6; Length 470;  
Best Local Similarity 31.5%; Pred. No. 5.4e-09;  
RESULT 389  
ID AAM48305 standard; protein; 170 AA.  
DE Protein R1 SEQ ID 28.  
PN WO200192507-A1.  
PD 06-DEC-2001.  
PA (FUJI-) FUJICHEMICO LTD.  
Query Match 11.9%; Score 188; DB 5; Length 170;  
Best Local Similarity 35.7%; Pred. No. 2.6e-09;  
RESULT 390  
ID ABP73148 standard; protein; 112 AA.  
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOGE/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.9%; Score 187; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 1.8e-09;  
RESULT 391  
ID ABP73150 standard; protein; 113 AA.  
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOGE/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.8%; Score 186.5; DB 6; Length 113;  
Best Local Similarity 36.3%; Pred. No. 2.1e-09;  
RESULT 392  
ID ABP73151 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOGE/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.7%; Score 185; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 2.8e-09;  
RESULT 393  
ID ABP73152 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOGE/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.6%; Score 183; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 4.4e-09;  
RESULT 394  
ID ABP73149 standard; protein; 112 AA.  
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOGE/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 11.6%; Score 182; DB 6; Length 112;  
Best Local Similarity 34.2%; Pred. No. 5.4e-09;  
RESULT 395  
ID ABP73153 standard; protein; 112 AA.  
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOGE/) KOGERMAN P.

PA (PAEL/) PAELL T.  
Query Match 11.5%; Score 181; DB 6; Length 112;  
Best Local Similarity 36.0%; Pred. No. 6.8e-09;  
RESULT 396  
ID AAY12170 standard; protein; 69 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 483.  
PN WO906554-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 11.4%; Score 179; DB 2; Length 69;  
Best Local Similarity 95.0%; Pred. No. 5.4e-09;  
RESULT 397  
ID ABG17067 standard; protein; 920 AA.  
DE Novel human diagnostic protein #17058.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.1%; Score 175.5; DB 4; Length 920;  
Best Local Similarity 25.9%; Pred. No. 4e-07;  
RESULT 398  
ID ADI60410 standard; protein; 920 AA.  
DE Secreted polypeptide encoded by gene splice variant #46.  
PN WO2003025142-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.1%; Score 175.5; DB 7; Length 920;  
Best Local Similarity 25.9%; Pred. No. 4e-07;  
RESULT 399  
ID AAM28056 standard; protein; 34 AA.  
DE Peptide #2093 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.8%; Score 170; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
RESULT 400  
ID ABG7308 standard; peptide; 34 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.8%; Score 170; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
RESULT 401  
ID ADB64426 standard; protein; 510 AA.  
DE Human protein encoded by clone FEBRA20038970.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.5%; Score 150; DB 7; Length 510;  
Best Local Similarity 23.6%; Pred. No. 4.8e-05;  
RESULT 402  
ID ABP73154 standard; protein; 80 AA.  
DE Deletion mutant of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 9.4%; Score 148.5; DB 6; Length 80;  
Best Local Similarity 37.0%; Pred. No. 5.2e-06;  
RESULT 403  
ID ADP07712 standard; protein; 162 AA.  
DE Human secreted protein, seq id 195.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.2%; Score 145; DB 8; Length 162;  
Best Local Similarity 33.0%; Pred. No. 3e-05;  
RESULT 404  
ID ADM80807 standard; protein; 237 AA.  
DE Human CADECW-36 protein SEQ ID NO:36.

PN WO2004015396-A2.  
PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 9.2%; Score 145; DB 8; Length 237;  
Best Local Similarity 33.0%; Pred. No. 5e-05;  
RESULT 405  
ID AAR26044 standard; protein; 277 AA.  
DE Tumour necrosis factor-induced glycoprotein TSG-6.  
PN WO9212175-A1.  
PD 23-JUL-1992.  
PA (UUNY ) UNIV NEW YORK STATE.  
Query Match 9.2%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
RESULT 406  
ID AAM13654 standard; protein; 277 AA.  
DE Tumour necrosis factor-stimulated gene-6 protein.  
PN WO9704075-A1.  
PD 06-FEB-1997.  
PA (UUNY ) UNIV NEW YORK STATE.  
Query Match 9.2%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
RESULT 407  
ID AAW84087 standard; protein; 277 AA.  
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.  
PN US846763-A.  
PD 08-DEC-1998.  
PA (UUNY ) UNIV NEW YORK STATE.  
Query Match 9.2%; Score 145; DB 2; Length 277;  
Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
RESULT 408  
ID AAE02361 standard; protein; 277 AA.  
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.  
PN US6210905-B1.  
PD 03-APR-2001.  
PA (UUNY ) UNIV NEW YORK STATE.  
Query Match 9.2%; Score 145; DB 4; Length 277;  
Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
RESULT 409  
ID ABG70870 standard; protein; 277 AA.  
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.  
PN US2002090708-A1.  
PD 11-JUL-2002.  
PA (UUNY ) UNIV NEW YORK STATE.  
Query Match 9.2%; Score 145; DB 5; Length 277;  
Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
RESULT 410  
ID ABR58556 standard; protein; 277 AA.  
DE Human cancer related protein SEQ ID NO:213.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 9.2%; Score 145; DB 6; Length 277;  
Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
RESULT 411  
ID ABU56653 standard; protein; 277 AA.  
DE Lung cancer-associated polypeptide #246.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 9.2%; Score 145; DB 6; Length 277;  
Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
RESULT 412  
ID ADE25781 standard; protein; 277 AA.  
DE Human protein differentially expressed in foam cells #58.  
PN US2003194721-A1.  
PD 16-OCT-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.2%; Score 145; DB 7; Length 277;  
Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
RESULT 413  
ID ADN39919 standard; protein; 277 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.  
PN WO2003042661-A2.

PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 9.2%; Score 145; DB 7; Length 277;  
 Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
 RESULT 414  
 ID ADN38974 standard; protein; 277 AA.  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 9.2%; Score 145; DB 7; Length 277;  
 Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
 RESULT 415  
 ID ADQ21506 standard; protein; 277 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 9.2%; Score 145; DB 8; Length 277;  
 Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
 RESULT 416  
 ID ADK51534 standard; protein; 277 AA.  
 DE Human lipopolysaccharide-sensitive polypeptide #14.  
 PN WO2004069870-A2.  
 PD 19-AUG-2004.  
 PA (UYLE-) RIJKSUNIV LEIDEN.  
 Query Match 9.2%; Score 145; DB 8; Length 277;  
 Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
 RESULT 417  
 ID ADM38508 standard; protein; 277 AA.  
 DE Immunomodulatory gene TNFA induced protein 6.  
 PN WO2005000099-A2.  
 PD 06-JAN-2005.  
 PA (GENZ-) GENZYME CORP.  
 Query Match 9.2%; Score 145; DB 9; Length 277;  
 Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
 RESULT 418  
 ID AEA23596 standard; protein; 277 AA.  
 DE Human PRO polypeptide SEQ ID NO 138.  
 PN WO2005051988-A2.  
 PD 09-JUN-2005.  
 PA (GETH-) GENENTECH INC.  
 Query Match 9.2%; Score 145; DB 9; Length 277;  
 Best Local Similarity 33.0%; Pred. No. 6.2e-05;  
 RESULT 419  
 ID ADK67822 standard; protein; 2626 AA.  
 DE Human BRCC300 polypeptide.  
 PN WO2004012755-A1.  
 PD 12-FEB-2004.  
 PA (WIST-) WISTAR INST.  
 Query Match 9.2%; Score 145; DB 8; Length 2626;  
 Best Local Similarity 33.0%; Pred. No. 0.0013;  
 RESULT 420  
 ID ADS85081 standard; protein; 275 AA.  
 DE Mouse atopic dermatitis-related protein sequence SeqID83.  
 PN WO2004031386-A1.  
 PD 15-APR-2004.  
 PA (GENO-) GENOX RES INC.  
 PA (UYJU-) UNIV JUNTENDO.  
 Query Match 9.1%; Score 144; DB 8; Length 275;  
 Best Local Similarity 33.0%; Pred. No. 7.6e-05;  
 RESULT 421  
 ID ADO09968 standard; protein; 897 AA.  
 DE Human NOV1C cDNA.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.  
 PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.

(GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERR/) ZERHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJJ/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (MILL/) MILLET I.  
 PA (ROTH/) ROTHENBERG M E.  
 Query Match 8.6%; Score 136; DB 8; Length 897;  
 Best Local Similarity 21.2%; Pred. No. 0.0022;  
 RESULT 422  
 ID ABJ10588 standard; protein; 897 AA.  
 DE Human novel protein NOV1C SEQ ID NO: 211.  
 PN WO200259315-A2.  
 PD 01-AUG-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 8.5%; Score 134; DB 5; Length 897;  
 Best Local Similarity 20.7%; Pred. No. 0.0034;  
 RESULT 423  
 ID ADH71312 standard; protein; 897 AA.  
 DE Human protein of the invention NOV9a SEQ ID NO:208.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 8.5%; Score 134; DB 8; Length 897;  
 Best Local Similarity 20.7%; Pred. No. 0.0034;  
 RESULT 424  
 ID ADH71356 standard; protein; 1502 AA.  
 DE Human protein of the invention NOV9w SEQ ID NO:252.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 8.5%; Score 134; DB 8; Length 1502;  
 Best Local Similarity 20.7%; Pred. No. 0.0069;  
 RESULT 425  
 ID ABJ10586 standard; protein; 2675 AA.  
 DE Human novel protein NOV1a SEQ ID NO: 2.  
 PN WO200259315-A2.  
 PD 01-AUG-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 8.5%; Score 134; DB 5; Length 2675;  
 Best Local Similarity 17.8%; Pred. No. 0.015;  
 RESULT 426  
 ID ADO09971 standard; protein; 2675 AA.  
 DE Human NOV1a variant.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.  
 PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERR/) ZERHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.

PA (TCHE/) TCHERNEV V T.  
PA (SIUJ/) SI J.  
PA (EDIN/) EDINGER S R.  
PA (STON/) STONE D J.  
PA (SCIO/) SCIORE P.  
PA (MILL/) MILLET I.  
PA (ROTH/) ROTHENBERG M E.  
Query Match 8.5%; Score 134; DB 8; Length 2675;  
Best Local Similarity 17.8%; Pred. No. 0.015;  
RESULT 427  
ID ADO09836 standard; protein; 2675 AA.  
DE Human NOVIa.  
PN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHIMKETS R A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (MILL/) MILLER C E.  
PA (BOLD/) BOLDOG F L.  
PA (LILL/) LI L.  
PA (TAUF/) TAUFIER R J.  
PA (KERU/) KEKUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERR/) ZERHUSEN B D.  
PA (LIUX/) LIU X.  
PA (COLM/) COLMAN S D.  
PA (TCHE/) TCHERNEV V T.  
PA (SIUJ/) SI J.  
PA (EDIN/) EDINGER S R.  
PA (STON/) STONE D J.  
PA (SCIO/) SCIORE P.  
PA (MILL/) MILLET I.  
PA (ROTH/) ROTHENBERG M E.  
Query Match 8.5%; Score 134; DB 8; Length 2675;  
Best Local Similarity 17.8%; Pred. No. 0.015;  
RESULT 428  
ID AAM47684 standard; protein; 1394 AA.  
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.  
PN WO200181544-A2.  
PD 01-NOV-2001.  
PA (WEIG/) WEIGEL P A.  
PA (ZHOU/) ZHOU B.  
PA (WEIG/) WEIGEL J A.  
Query Match 8.4%; Score 133; DB 5; Length 1394;  
Best Local Similarity 20.7%; Pred. No. 0.0078;  
RESULT 429  
ID ABG72499 standard; protein; 1416 AA.  
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #1.  
PN WO200286093-A2.  
PD 31-OCT-2002.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Query Match 8.4%; Score 133; DB 6; Length 1416;  
Best Local Similarity 20.7%; Pred. No. 0.0079;  
RESULT 430  
ID AAM47675 standard; protein; 1431 AA.  
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.  
PN WO200181544-A2.  
PD 01-NOV-2001.  
PA (WEIG/) WEIGEL P A.  
PA (ZHOU/) ZHOU B.  
PA (WEIG/) WEIGEL J A.  
Query Match 8.4%; Score 133; DB 5; Length 1431;  
Best Local Similarity 18.5%; Pred. No. 0.0081;  
RESULT 431  
ID ABG72498 standard; protein; 1431 AA.  
DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).  
PN WO200286093-A2.

PD 31-OCT-2002.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Query Match 8.4%; Score 133; DB 6; Length 1431;  
Best Local Similarity 18.5%; Pred. No. 0.0081;  
RESULT 432  
ID ADH71358 standard; protein; 1510 AA.  
DE Human protein of the invention NOV9x SEQ ID NO:254.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.4%; Score 133; DB 8; Length 1510;  
Best Local Similarity 20.7%; Pred. No. 0.0087;  
RESULT 433  
ID ABG72514 standard; protein; 1653 AA.  
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.  
PN WO200286093-A2.  
PD 31-OCT-2002.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Query Match 8.4%; Score 133; DB 6; Length 1653;  
Best Local Similarity 20.7%; Pred. No. 0.0098;  
RESULT 434  
ID ADM90835 standard; protein; 1895 AA.  
DE Human pharmacologically useful protein SeqID 228.  
PN WO2004020595-A2.  
PD 11-MAR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAF-) DNAFORM KK.  
Query Match 8.4%; Score 133; DB 8; Length 1895;  
Best Local Similarity 20.7%; Pred. No. 0.012;  
RESULT 435  
ID ADH71360 standard; protein; 2551 AA.  
DE Human protein of the invention NOV9y SEQ ID NO:256.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.4%; Score 133; DB 8; Length 2551;  
Best Local Similarity 20.7%; Pred. No. 0.018;  
RESULT 436  
ID ABM84174 standard; protein; 2285 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 8.4%; Score 132.5; DB 8; Length 2285;  
Best Local Similarity 27.4%; Pred. No. 0.017;  
RESULT 437  
ID ABM84173 standard; protein; 2384 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 8.4%; Score 132.5; DB 8; Length 2384;  
Best Local Similarity 27.4%; Pred. No. 0.018;  
RESULT 438  
ID ABP72603 standard; protein; 883 AA.  
DE Rat mutant brain-enriched hyaluronan binding protein.  
PN WO2003007880-A2.  
PD 30-JAN-2003.  
PA (UYVA) UNIV YALE.  
PA (HOCK/) HOCKFIELD S.  
PA (MATT/) MATTHEWS R T.  
Query Match 8.3%; Score 131.5; DB 6; Length 883;  
Best Local Similarity 24.3%; Pred. No. 0.0058;  
RESULT 439  
ID ADK67779 standard; protein; 883 AA.  
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYVA) UNIV YALE.  
Query Match 8.3%; Score 131.5; DB 8; Length 883;



Best Local Similarity 24.3%; Pred. No. 0.0058;  
RESULT 440  
ID ABB34752 standard; protein; 883 AA.  
DE Mammalian mutant BEHAB protein.  
PN WO2005069852-A2.  
PD 04-AUG-2005.  
PA (UTYA ) UNIV YALE.  
Query Match 8.3%; Score 131.5; DB 9; Length 883;  
Best Local Similarity 24.3%; Pred. No. 0.0058;  
RESULT 441  
ID AAB61236 standard; protein; 649 AA.  
DE Mature human TANGO 332 protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 131; DB 4; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0042;  
RESULT 442  
ID ABO32673 standard; protein; 649 AA.  
DE Secreted polypeptide-related protein #74.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 8.3%; Score 131; DB 6; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0042;  
RESULT 443  
ID ADB90778 standard; protein; 649 AA.  
DE Human TANGO 332 mature protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 131; DB 7; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0042;  
RESULT 444  
ID ADF71513 standard; protein; 649 AA.  
DE Human TANGO 332 mature protein.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 131; DB 7; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0042;  
RESULT 445  
ID ADQ10331 standard; protein; 649 AA.  
DE Human polypeptide #167.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 131; DB 8; Length 649;  
Best Local Similarity 20.4%; Pred. No. 0.0042;  
RESULT 446  
ID AAB61234 standard; protein; 671 AA.  
DE Human TANGO 332 protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 131; DB 4; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0044;  
RESULT 447  
ID ABO32671 standard; protein; 671 AA.  
DE Secreted polypeptide-related protein #73.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.

PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 8.3%; Score 131; DB 6; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0044;  
RESULT 448  
ID ADB90776 standard; protein; 671 AA.  
DE Human TANGO 332 protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 131; DB 7; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0044;  
RESULT 449  
ID ADF71511 standard; protein; 671 AA.  
DE Human TANGO 332.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 131; DB 7; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0044;  
RESULT 450  
ID ADQ10329 standard; protein; 671 AA.  
DE Human polypeptide #165.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 8.3%; Score 131; DB 8; Length 671;  
Best Local Similarity 20.4%; Pred. No. 0.0044;  
RESULT 451  
ID ADH18892 standard; protein; 806 AA.  
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 8.3%; Score 131; DB 8; Length 806;  
Best Local Similarity 20.4%; Pred. No. 0.0057;  
RESULT 452  
ID AAY97583 standard; protein; 911 AA.  
DE Human secreted protein PRO6018.  
PN WO200075317-A2.  
PD 14-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 4; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 453  
ID ABG34055 standard; protein; 911 AA.  
DE Human Pro peptide #26.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 5; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 454  
ID ADI28032 standard; protein; 911 AA.  
DE ECMCAD protein 6755002CD1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 8.3%; Score 131; DB 5; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 455  
ID ADA01320 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003068779-A1.  
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 456
ID ADA43749 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 457
ID ADA43517 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 458
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 459
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 460
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 461
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 462
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 463
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 464
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 465
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 466
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 467
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 468
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 469
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 470
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 471
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 472
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.3%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0067;
RESULT 473
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 483		
ID ADG82450 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US200307744-A1.		
PD 24-APR-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 7; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 484		
ID ADE51703 standard; protein; 911 AA.		
DE Human secreted/transmembrane polypeptide PRO6018.		
PN US2003104560-A1.		
PD 05-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 485		
ID ADE51819 standard; protein; 911 AA.		
DE Human secreted/transmembrane polypeptide PRO6018.		
PN US2003104561-A1.		
PD 05-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 486		
ID ADE37677 standard; protein; 911 AA.		
DE Human secreted/transmembrane polypeptide PRO6018.		
PN US2003104564-A1.		
PD 05-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 487		
ID ADE37561 standard; protein; 911 AA.		
DE Human secreted/transmembrane polypeptide PRO6018.		
PN US2003104565-A1.		
PD 05-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 488		
ID ADU95332 standard; protein; 911 AA.		
DE Human secreted/transmembrane polypeptide PRO6018.		
PN US2003138901-A1.		
PD 24-JUL-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 489		
ID ADE38032 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003104566-A1.		
PD 05-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 490		
ID ADE76121 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003124665-A1.		
PD 03-JUL-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 491		
ID ADE39444 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003119117-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 492		
ID ADE39444 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003119117-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 493		
ID ADE39444 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003119117-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 494		
ID ADE39444 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003119117-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 495		
ID ADE39444 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003119117-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 496		
ID ADE39444 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003119117-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 497		
ID ADE39444 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003119117-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	8.3%;	Score 131; DB 8; Length 911;
Best Local Similarity	20.4%;	Pred. No. 0.0067;
RESULT 498		
ID ADE39444 standard; protein; 911 AA.		
DE Human PRO polypeptide #26.		
PN US2003119		

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RESULT 492
ID ADE04248 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 493
ID ADE39845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 494
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 495
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 496
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 497
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 498
ID ADE37916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 499
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 500
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 501
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 502
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 503
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 504
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 505
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 506
ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 507
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 508
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 509
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 131; DB 8; Length 911;
Pred. No. 0.0067;
RESULT 510
ID ADD88932 standard; protein; 911 AA.
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DE Human PRO polypeptide #26.  
PN US200313889-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 511  
ID AD19826 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US200313890-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 512  
ID AD877404 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 513  
ID AD865280 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 514  
ID AD839328 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 515  
ID AD838513 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 516  
ID AD81066 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 517  
ID ADQ10950 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 518  
ID ADH31478 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 519  
ID ADH38726 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.

PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 520  
ID ADH29361 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 521  
ID ADH23664 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 522  
ID ADH26994 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 523  
ID ADH38262 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 524  
ID ADH26878 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 525  
ID ADH38146 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 526  
ID ADH38842 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 527  
ID ADH23780 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 528  
ID ADH40156 standard; protein; 911 AA.  
DE Human PRO6018 protein.  
PN US2003119132-A1.

PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 529  
ID ADH40040 standard; protein; 911 AA.  
DE Human PRO6018 protein.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 530  
ID ADH31362 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 531  
ID ADH29240 standard; protein; 911 AA.  
DE Human secreted and transmembrane polypeptide PRO6018.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 532  
ID ADH49455 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 533  
ID ADH51919 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 534  
ID ADH49774 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 535  
ID ADH52375 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 536  
ID ADH52491 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 537  
ID ADH58488 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119121-A1.  
PD 26-JUN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 538  
ID ADH51803 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 539  
ID ADH58364 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 540  
ID ADI13561 standard; protein; 911 AA.  
DE Novel human secreted and transmembrane protein PRO6018.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 541  
ID ADK00817 standard; protein; 911 AA.  
DE Human PRO polypeptide #26.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 542  
ID ADL08558 standard; protein; 911 AA.  
DE Human secreted/transmembrane polypeptide PRO6018.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 543  
ID ABM80156 standard; protein; 911 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 8; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 544  
ID AEA00137 standard; protein; 911 AA.  
DE Human TAT145 protein SEQ ID NO:89.  
PN US2005106644-A1.  
PD 19-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 9; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 545  
ID AEA00657 standard; protein; 911 AA.  
DE Human TAT145 protein sequence SeqID89.  
PN US2005107595-A1.  
PD 19-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 8.3%; Score 131; DB 9; Length 911;  
Best Local Similarity 20.4%; Pred. No. 0.0067;  
RESULT 546  
ID AAB61242 standard; protein; 883 AA.  
DE Murine brevudin protein.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 8.3%; Score 130.5; DB 4; Length 883;  
 Best Local Similarity 24.4%; Pred. No. 0.0072;  
 RESULT 547  
 ID ABO32678 standard; protein; 883 AA.  
 DE Secreted polypeptide-related protein #119.  
 PN US2003022279-A1.  
 PD 30-JAN-2003.  
 PA (FRAS/) FRASER C C.  
 PA (BARN/) BARNES T M.  
 PA (SHAR/) SHARP J D.  
 PA (KIRS/) KIRST S J.  
 PA (MYER/) MYERS P S.  
 PA (LEIB/) LEIBY K R.  
 PA (HOLT/) HOLTZMAN D A.  
 PA (MCCA/) MCCARTHY S A.  
 PA (WRIG/) WRIGHTON N.  
 PA (MACK/) MACKAY C R.  
 PA (GOOD/) GOODEARL A D J.  
 Query Match 8.3%; Score 130.5; DB 6; Length 883;  
 Best Local Similarity 24.4%; Pred. No. 0.0072;  
 RESULT 548  
 ID ABP72604 standard; protein; 883 AA.  
 DE Rat brain-enriched hyaluronan binding protein.  
 PN WO2003007880-A2.  
 PD 30-JAN-2003.  
 PA (UYIA/) UNIV YALE.  
 PA (HOCK/) HOCKFIELD S.  
 PA (MATT/) MATTHEWS R T.  
 Query Match 8.3%; Score 130.5; DB 6; Length 883;  
 Best Local Similarity 23.3%; Pred. No. 0.0072;  
 RESULT 549  
 ID ADB90787 standard; protein; 883 AA.  
 DE Mouse brevicain protein.  
 PN US2003082586-A1.  
 PD 01-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 8.3%; Score 130.5; DB 7; Length 883;  
 Best Local Similarity 24.4%; Pred. No. 0.0072;  
 RESULT 550  
 ID AD62581 standard; protein; 883 AA.  
 DE Rat Protein P55068, SEQ ID NO 8512.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO/) GEN HOSPITAL CORP.  
 PA (FARB/) BAYER AG.  
 Query Match 8.3%; Score 130.5; DB 7; Length 883;  
 Best Local Similarity 23.3%; Pred. No. 0.0072;  
 RESULT 551  
 ID ADP71522 standard; protein; 883 AA.  
 DE Murine brevidin protein.  
 PN US2003175733-A1.  
 PD 18-SEP-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 8.3%; Score 130.5; DB 7; Length 883;  
 Best Local Similarity 24.4%; Pred. No. 0.0072;  
 RESULT 552  
 ID ADK67782 standard; protein; 883 AA.  
 DE Rat glycosylation-variant BEHAB isoform.  
 PN WO2004013356-A1.  
 PD 12-FEB-2004.  
 PA (UYIA/) UNIV YALE.  
 Query Match 8.3%; Score 130.5; DB 8; Length 883;  
 Best Local Similarity 23.3%; Pred. No. 0.0072;  
 RESULT 553  
 ID ADQ10338 standard; protein; 883 AA.  
 DE Human polypeptide #172.  
 PN US2004121396-A1.  
 PD 24-JUN-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 8.3%; Score 130.5; DB 8; Length 883;  
 Best Local Similarity 24.4%; Pred. No. 0.0072;  
 RESULT 554  
 ID ABB34755 standard; protein; 883 AA.

DE Rat poly-sialylated brain-enriched hyaluronan binding protein.  
 PN WO2005069852-A2.  
 PD 04-AUG-2005.  
 PA (UYIA/) UNIV YALE.  
 Query Match 8.3%; Score 130.5; DB 9; Length 883;  
 Best Local Similarity 23.3%; Pred. No. 0.0072;  
 RESULT 555  
 ID ABB90349 standard; protein; 1082 AA.  
 DE Human polypeptide SEQ ID NO 2725.  
 PN WO200190304-A2.  
 PD 29-NOV-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 8.3%; Score 130.5; DB 5; Length 1082;  
 Best Local Similarity 20.6%; Pred. No. 0.0095;  
 RESULT 556  
 ID ADX15811 standard; protein; 2316 AA.  
 DE Human aggrecan.  
 PN WO2005012512-A1.  
 PD 10-FEB-2005.  
 PA (NAKA/) NAKAMURA N.  
 Query Match 8.3%; Score 130.5; DB 9; Length 2316;  
 Best Local Similarity 27.4%; Pred. No. 0.027;  
 RESULT 557  
 ID AEM80463 standard; protein; 2570 AA.  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH/) GENENTECH INC.  
 Query Match 8.3%; Score 130.5; DB 8; Length 2570;  
 Best Local Similarity 20.6%; Pred. No. 0.031;  
 RESULT 558  
 ID AAY93911 standard; protein; 457 AA.  
 DE A human hyaluronan-binding protein, designated WF-HABP.  
 PN WO200039166-A1.  
 PD 06-JUL-2000.  
 PA (AMNA-) AMERICAN NAT RED CROSS.  
 Query Match 8.2%; Score 129.5; DB 3; Length 457;  
 Best Local Similarity 20.9%; Pred. No. 0.0036;  
 RESULT 559  
 ID ABM83434 standard; protein; 761 AA.  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 8.2%; Score 129.5; DB 8; Length 761;  
 Best Local Similarity 22.8%; Pred. No. 0.0073;  
 RESULT 560  
 ID AAY93910 standard; protein; 2157 AA.  
 DE A human hyaluronan-binding protein, designated WF-HABP.  
 PN WO200039166-A1.  
 PD 06-JUL-2000.  
 PA (AMNA-) AMERICAN NAT RED CROSS.  
 Query Match 8.2%; Score 129.5; DB 3; Length 2157;  
 Best Local Similarity 20.9%; Pred. No. 0.03;  
 RESULT 561  
 ID ABR82200 standard; protein; 2570 AA.  
 DE Human CLEVER-1 protein SEQ ID NO:1.  
 PN WO2003057130-A2.  
 PD 17-JUL-2003.  
 PA (JALK/) JALKANEN S.  
 PA (IRJA/) IRJALA H.  
 PA (SALM/) SALMI M.  
 Query Match 8.2%; Score 129.5; DB 6; Length 2570;  
 Best Local Similarity 20.9%; Pred. No. 0.039;  
 RESULT 562  
 ID AAB08023 standard; protein; 95 AA.  
 DE The domain of hyaluronic acid which interacts with CD44.  
 PN WO200047163-A2.  
 PD 17-AUG-2000.  
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 Query Match 8.2%; Score 128.5; DB 3; Length 95;

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Best Local Similarity 28.7%; Pred. No. 0.00053;
RESULT 563
ID ABU04625 standard; protein; 95 AA.
DE Human expressed protein tag (EPT) #1291.
FN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 8.2%; Score 128.5; DB 6; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00053;
RESULT 564
ID AAR85442 standard; protein; 912 AA.
DE Bovine brevican core protein.
FN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 8.2%; Score 128.5; DB 2; Length 912;
Best Local Similarity 22.0%; Pred. No. 0.012;
RESULT 565
ID ADV70173 standard; protein; 671 AA.
DE Tumor-associated antigenic target polypeptide TAT152.
FN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0095;
RESULT 566
ID AEA00138 standard; protein; 671 AA.
DE Human TAT152 protein SEQ ID NO:90.
FN US2005106644-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0095;
RESULT 567
ID AEA00658 standard; protein; 671 AA.
DE Human TAT152 protein sequence SeqID90.
FN US2005107595-A1.
PD 19-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 127.5; DB 9; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0095;
RESULT 568
ID ABM83431 standard; protein; 825 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3680.
FN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.1%; Score 127.5; DB 8; Length 825;
Best Local Similarity 24.7%; Pred. No. 0.013;
RESULT 569
ID ABM83430 standard; protein; 863 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3679.
FN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.1%; Score 127.5; DB 8; Length 863;
Best Local Similarity 24.7%; Pred. No. 0.013;
RESULT 570
ID AAE30340 standard; protein; 911 AA.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.
FN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 8.1%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.014;
RESULT 571
ID ADN38942 standard; protein; 911 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.014;
RESULT 572
ID ADR67784 standard; protein; 911 AA.
DE Human glycosylation-variant BEHAB isoform.
FN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match 8.1%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.014;
RESULT 573
ID AEB34757 standard; protein; 911 AA.
DE Human poly-sialylated brain-enriched hyaluronan binding protein.
FN WO2005069852-A2.
PD 04-AUG-2005.
PA (UYVA) UNIV YALE.
Query Match 8.1%; Score 127.5; DB 9; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.014;
RESULT 574
ID ABE58557 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:214.
FN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 575
ID ABU56654 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #247.
FN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 576
ID ADN38976 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 127; DB 7; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 577
ID ADO24439 standard; protein; 277 AA.
DE Human PR087335 protein SEQ ID NO:78.
FN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 578
ID ADRI4117 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID118.
FN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 8.1%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.0032;
RESULT 579
ID ADB47827 standard; protein; 457 AA.
DE Novel human secreted protein #3.
FN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
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PA (BIRS/) BIRSE C E. 8.0%; Score 126.5; DB 7; Length 457;  
Query Match  
Best Local Similarity 20.6%; Pred. No. 0.007;  
RESULT 580  
ID ADJ55382 standard; protein; 457 AA.  
DE Novel human secreted protein #3.  
FN US2004023283-A1.  
PD 05-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 8.0%; Score 126.5; DB 8; Length 457;  
RESULT 581  
ID ADO24485 standard; protein; 277 AA.  
DE Human PRO87343 protein SEQ ID NO:124.  
FN WO2004043397-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 8.0%; Score 126; DB 8; Length 277;  
RESULT 582  
ID ADB65640 standard; protein; 482 AA.  
DE Human protein encoded by clone THYMU20143230.  
FN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 7.9%; Score 124.5; DB 7; Length 482;  
RESULT 583  
ID ADM80804 standard; protein; 259 AA.  
DE Human CADSCM-33 protein SEQ ID NO:33.  
FN WO2004015396-A2.  
PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 259;  
RESULT 584  
ID AAY13381 standard; protein; 360 AA.  
DE Amino acid sequence of protein PRO271.  
FN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 2; Length 360;  
RESULT 585  
ID ADC78533 standard; protein; 360 AA.  
DE Human PRO271 protein.  
FN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 3; Length 360;  
RESULT 586  
ID AAB80249 standard; protein; 360 AA.  
DE Human PRO271 protein.  
FN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 4; Length 360;  
RESULT 587  
ID AAU29037 standard; protein; 360 AA.  
DE Human PRO polypeptide sequence #14.  
FN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 4; Length 360;  
RESULT 588  
ID AAM38965 standard; protein; 360 AA.  
DE Human polypeptide SEQ ID NO 2110.  
FN WO200153312-A1.  
PD 26-JUL-2001.

PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 4; Length 360;  
RESULT 589  
ID ABUS8413 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003027272-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 590  
ID ABU71627 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
FN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 591  
ID ABU87961 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
FN US2003032127-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 592  
ID ABU84276 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003032112-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 593  
ID ABR66150 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027278-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 594  
ID ABR65540 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003036159-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 595  
ID ABU99480 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003040070-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 596  
ID ABU82719 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003032113-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 597  
ID ABU89840 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
FN US2003036147-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 598  
ID ABU71482 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
FN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.

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Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 599
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 600
ID ABU96142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 601
ID ABU92573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 602
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 603
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 604
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 605
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 606
ID ABU85591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 607
ID ABU98751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 608
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 609
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 610
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 611
ID ABU89365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 612
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 613
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 614
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 615
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 616
ID ABR99365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 617
ID ABR98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match          7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 618
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.
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Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 619  
ID ABO06162 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 620  
ID ABO18819 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 621  
ID ABR78240 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 622  
ID ABU84976 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 623  
ID ABO00115 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 624  
ID ABO11447 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 625  
ID ABO02092 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 626  
ID ABU54384 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein PRO271.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 627  
ID ABU88666 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 628  
ID ABU83361 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 629  
ID ABO06162 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 630  
ID ABR59198 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 631  
ID ABO09260 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 632  
ID ABO19124 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 633  
ID ABO11142 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 634  
ID ABR66760 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 635  
ID ABO15973 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 636  
ID ABO13679 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 637  
ID ABO47399 standard; protein; 360 AA.  
DE Human secreted/transmembrane polypeptide PRO271.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 638  
ID ABU65582 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, SEQ ID 28.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;

RESULT 639  
ID ABO07430 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 640  
ID ABO03617 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 641  
ID ABR67065 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 642  
ID ABO15668 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 643  
ID ABU55949 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, PRO271.  
FN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 644  
ID ABU65277 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 645  
ID ABU95222 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
FN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 646  
ID ABO07125 standard; protein; 360 AA.  
DE Human PRO271 protein.  
FN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 647  
ID ABO07735 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 648  
ID ABR69976 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 649  
ID ABU83056 standard; protein; 360 AA.

ID ABR69309 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 650  
ID ABO01450 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 651  
ID ABU81252 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 652  
ID ABR60049 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 653  
ID ABR67784 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 654  
ID ABR65172 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 655  
ID ABR68394 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 656  
ID ABR71806 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 657  
ID ABU85286 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 658  
ID ABU88976 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 659  
ID ABU83056 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 660  
ID ABU94912 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 661  
ID ABU90460 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 662  
ID ABU83971 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 663  
ID ABU93622 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 664  
ID ABR64867 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 665  
ID ABR68699 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 666  
ID ABO06515 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 667  
ID ABR99060 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 668  
ID ABU56944 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 669  
ID ABR64536 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #40.  
PN US2002160374-A1.

PD 31-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 670  
ID ABU5896 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 671  
ID ABU67382 standard; protein; 360 AA.  
DE Human secreted protein PRO271.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 672  
ID ASU82183 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 673  
ID ABU87194 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 674  
ID ABU83666 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 675  
ID ABO08040 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 676  
ID ABO14902 standard; protein; 360 AA.  
DE Human secreted / transmembrane polypeptide PRO271.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 677  
ID ABU81751 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 678  
ID ABU65915 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 679  
ID ABR59744 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032120-A1.

PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 680  
ID ABU93932 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 681  
ID ABU99785 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US200302296-A1.  
PD 30-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 682  
ID ABG66455 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 683  
ID ABR90873 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 684  
ID ABU94300 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 685  
ID ABU79182 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 686  
ID ABU86511 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 687  
ID ABU86816 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 688  
ID ABU94605 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 689  
ID ABO04532 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 690  
ID ABR70281 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 691  
ID ABU98446 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 692  
ID ABR65845 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 693  
ID ABR64562 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 694  
ID ABU79487 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 695  
ID ABU92878 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 696  
ID ABU95837 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 697  
ID ABU91057 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 698  
ID ABU90150 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 699  
ID ABO09565 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 700

ID ABO10837 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 701  
ID ABR70891 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 702  
ID ABU87499 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 703  
ID ABU91367 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 704  
ID ABU84581 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 705  
ID ABR69671 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 706  
ID ABU80048 standard; protein; 360 AA.  
DE Human PRO protein #14.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 707  
ID ABU69659 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 708  
ID ABU93317 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 709  
ID ABO09870 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 710  
ID ABO08955 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.

PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 711  
ID ABU10523 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein #14.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 712  
ID ABU95532 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 713  
ID ABU96741 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 714  
ID ABR70586 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 715  
ID ABO04937 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 716  
ID ABO08345 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 717  
ID ABO14841 standard; protein; 360 AA.  
DE Human secreted / transmembrane polypeptide PRO271.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 718  
ID ABO05552 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 719  
ID ABR73941 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 720  
ID ABR95533 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 721  
ID ABR80830 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 722  
ID ABR81135 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 723  
ID ABR80831 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 724  
ID ABR88433 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 725  
ID ABR77254 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 726  
ID ABO28738 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 727  
ID ABO31483 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 728  
ID ABR07900 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 729  
ID ABO40380 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.

PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 730  
ID ABO35805 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 731  
ID ABO43944 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 732  
ID ADA77780 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 733  
ID ABR24739 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 734  
ID ABR29418 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 735  
ID ABO03007 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 736  
ID ABR90263 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 737  
ID ABR17177 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 738  
ID ABR94923 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;



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RESULT 739
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 27-FEB-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 740
ID ABO21466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 20-MAR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 741
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 03-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 742
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 10-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 743
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 20-MAR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 744
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 03-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 745
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 10-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 746
ID ABM03576 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 10-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 747
ID ABM35027 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 17-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 748
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 27-FEB-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 749
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 13-MAR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 750
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 03-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 751
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 03-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 752
ID ABM11560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 03-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 753
ID ABM02661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 17-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 754
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 03-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 755
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 03-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 756
ID ABM29009 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 10-APR-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
RESULT 757
ID ABM06985 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;
PD 27-FEB-2003. Pred. No. 0.015;
PA (GETH ) GENENTECH INC.
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PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 758  
ID ABM21079 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 759  
ID ABM09425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 760  
ID ABO41295 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 761  
ID ABO36110 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 762  
ID ABO43639 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 763  
ID ABM76339 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 764  
ID ABM76035 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 765  
ID ABM25654 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 766  
ID ABM25959 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 767  
ID ABM25959 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;

Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 767			
ID ABO03312 standard; protein; 360 AA.			
DE Human secreted/transmembrane protein (PRO) #14.			
FN US2003036127-A1.			
PD 20-FEB-2003.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 768			
ID ABO02397 standard; protein; 360 AA.			
DE Human secreted/transmembrane protein (PRO) #14.			
FN US2003040061-A1.			
PD 27-FEB-2003.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 769			
ID ABR90568 standard; protein; 360 AA.			
DE Human secreted polypeptide PRO271, SEQ ID NO:28.			
FN US2003036130-A1.			
PD 20-FEB-2003.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 770			
ID ABR73636 standard; protein; 360 AA.			
DE Human secreted polypeptide PRO271, SEQ ID NO:28.			
FN US2003054468-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 771			
ID ABO16888 standard; protein; 360 AA.			
DE Human secreted/transmembrane protein (PRO) #14.			
FN US2003054470-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 772			
ID ABR94313 standard; protein; 360 AA.			
DE Human secreted polypeptide PRO271, SEQ ID NO:28.			
FN US2003044917-A1.			
PD 06-MAR-2003.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 773			
ID ABR75820 standard; protein; 360 AA.			
DE Human secreted polypeptide PRO271, SEQ ID NO:28.			
FN US2003044929-A1.			
PD 06-MAR-2003.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 774			
ID ADA18274 standard; protein; 360 AA.			
DE Human secreted/transmembrane protein, #42.			
FN US2003039971-A1.			
PD 27-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 775			
ID ABO32793 standard; protein; 360 AA.			
DE Human secreted/transmembrane protein PRO271.			
FN US2003045893-A1.			
PD 06-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 776			
ID ABO32793 standard; protein; 360 AA.			
DE Human secreted/transmembrane protein PRO271.			
FN US2003045893-A1.			
PD 06-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	7.7%;	Score 121.5; DB 6;	Length 360;
Best Local Similarity	34.9%;	Pred. No. 0.015;	
RESULT 777			
ID ABR71136 standard; protein; 360 AA.			
DE Human secreted polypeptide PRO271, SEQ ID NO:28.			
FN US2003059880-A1.			
PD 27-MAR-2003.			

PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 777  
ID ABR93093 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 778  
ID ABR93398 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 779  
ID ABR87823 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 780  
ID ABO27823 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 781  
ID ABO29958 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 782  
ID ABO33167 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 783  
ID ABM04855 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 784  
ID ABM08815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 785  
ID ABO36415 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 786  
ID ABO35500 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 787  
ID ABO39465 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 788  
ID ABM10340 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 789  
ID ABM11865 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 790  
ID ABO52011 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 791  
ID ABO52316 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
FN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 792  
ID ABO23634 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 793  
ID ABR97120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 794  
ID ABR86908 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
FN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 795  
ID ABO36415 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
FN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

RESULT 795  
ID ABM10950 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 796  
ID ABM28094 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 797  
ID ABO32093 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 798  
ID ABM15220 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 799  
ID ABM06375 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 800  
ID ABM04186 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 801  
ID ABM2299 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 802  
ID ABM07595 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 803  
ID ABO40685 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 804  
ID ABM35332 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 805  
ID ABM33095 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 806  
ID ABO52621 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 807  
ID ABO50181 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 808  
ID ABU99175 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 809  
ID ABO04227 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 810  
ID ABO05857 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 811  
ID ABO34853 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 812  
ID ABM18397 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 813  
ID ADA16249 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 814  
ID ABR97425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 815  
ID ABR90525 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 816  
ID ABM01136 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 817  
ID ABR88738 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 818  
ID ABM13390 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 819  
ID ABM20774 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 820  
ID AB041905 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 821  
ID AB042515 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 822  
ID ABM10035 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 823  
ID ABM16567 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064448-A1.  
PD 03-APR-2003.

RESULT 823  
ID AB038550 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 824  
ID ABM32790 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 825  
ID ABM22604 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 826  
ID ABM74815 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 827  
ID ADA79572 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 828  
ID ABR96205 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 829  
ID ABM02356 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 830  
ID ABR86298 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 831  
ID ABR86603 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 832  
ID ABM16567 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064448-A1.  
PD 03-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 833
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 834
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 835
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 836
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 837
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 838
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 839
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 840
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 841
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 842
ID ABM75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 843
ID ABM34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 844
ID ABM34315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100661-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 845
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 846
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 847
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 848
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 849
ID ABR85688 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 850
ID ABR99670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.7%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 851
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
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PN US2003073172-A1.  
 PD 17-APR-2003.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 852  
 ID ABO16583 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003027276-A1.  
 PD 06-FEB-2003.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 853  
 ID ABO29653 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003068700-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 854  
 ID ABO22636 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003027265-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 855  
 ID ABO22941 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003054461-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 856  
 ID ABR92483 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003064446-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 857  
 ID ABO4545 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003073182-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 858  
 ID ABO17531 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003049783-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 859  
 ID ADA42394 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein, #42.  
 PN US2003054401-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 860  
 ID ADA81299 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003092121-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.

Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 861  
 ID ABO16583 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003027276-A1.  
 PD 06-FEB-2003.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 862  
 ID ABO18209 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003044920-A1.  
 PD 06-MAR-2003.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 863  
 ID ABO22636 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003027265-A1.  
 PD 06-FEB-2003.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 864  
 ID ABO22941 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003054461-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 865  
 ID ABR92483 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003064446-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 866  
 ID ABR81440 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003049744-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 867  
 ID ABO17531 standard; protein; 360 AA.  
 DE Human secreted polypeptide #38.  
 PN US2003064367-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 868  
 ID ABO17531 standard; protein; 360 AA.  
 DE Human secreted polypeptide #38.  
 PN US2003064367-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 869  
 ID ABR89653 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003073171-A1.  
 PD 17-APR-2003.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 870  
 ID ABR26569 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 871  
ID ABM13695 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 872  
ID ABO28433 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 873  
ID ABO30263 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 874  
ID ABO7290 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 875  
ID ABO37025 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 876  
ID ABO37025 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 877  
ID ABO41600 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 878  
ID ABO35195 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 879  
ID ABM25044 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104540-A1.  
PD 05-JUN-2003.

Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 880  
ID ABO47436 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 881  
ID ABO47741 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 882  
ID ABO48351 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 883  
ID ABO51401 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 884  
ID ABO51706 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 885  
ID ABO50486 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 886  
ID ABR79610 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 887  
ID ABM16872 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 888  
ID ABO17904 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 889



ID ABO20856 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003032132-A1.  
 PD 13-FEB-2003.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 890  
 ID ABR96815 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003054462-A1.  
 PD 20-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 891  
 ID ABM12170 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003064445-A1.  
 PD 03-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 892  
 ID ABM16262 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003064449-A1.  
 PD 03-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 893  
 ID ABM24129 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003064441-A1.  
 PD 03-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 894  
 ID ABM14610 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003068696-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 895  
 ID ABM04491 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003068712-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 896  
 ID ABM06680 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003068730-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 897  
 ID ABM09120 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003073174-A1.  
 PD 17-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 898  
 ID ABO39160 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003068775-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 899  
 ID ABM75425 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003104545-A1.  
 PD 05-JUN-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 900  
 ID ABM25349 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003104541-A1.  
 PD 05-JUN-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 901  
 ID ABM19859 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003104554-A1.  
 PD 05-JUN-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 902  
 ID ABO46765 standard; protein; 360 AA.  
 DE Human PRO polypeptide #14.  
 PN US2003049762-A1.  
 PD 13-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 903  
 ID ABO47070 standard; protein; 360 AA.  
 DE Human PRO polypeptide #14.  
 PN US2003049765-A1.  
 PD 13-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 904  
 ID ADA83097 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein (PRO) #14.  
 PN US2003049752-A1.  
 PD 13-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 905  
 ID ABR71501 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003032133-A1.  
 PD 13-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 906  
 ID ABR72111 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003032136-A1.  
 PD 13-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 907  
 ID ABR98450 standard; protein; 360 AA.  
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
 PN US2003036129-A1.  
 PD 20-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
 RESULT 908  
 ID ABO06820 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 909  
ID ABR84773 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 910  
ID ABR73331 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 911  
ID ABR76425 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 912  
ID ABR73026 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 913  
ID ABM18092 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 914  
ID ABO20551 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 915  
ID ABO25294 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 916  
ID ABO25599 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 917  
ID ABR94008 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 918  
ID ABR79915 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 919  
ID ABM11255 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 920  
ID ABO32862 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 921  
ID ABO30568 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 922  
ID ABO30873 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 923  
ID ABM27179 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 924  
ID ABM29924 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 925  
ID ABM05460 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 926  
ID ABM15255 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 6; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 927  
ID ABM08510 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 928  
ID ABO42210 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 929  
ID ABO37940 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 930  
ID ABO45850 standard; protein; 360 AA.  
DE Human secreted polypeptide #14.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 931  
ID ARM66653 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 932  
ID ADR20140 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 933  
ID ABM19554 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 934  
ID ABO49266 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 935  
ID ABO49571 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 936  
ID ADA78392 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073181-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 937  
ID ABR88128 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 938  
ID ABM26874 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 939  
ID ABM03271 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 940  
ID ABO39770 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 6; Length 360;  
RESULT 941  
ID ABO49876 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 7; Length 360;  
RESULT 942  
ID ABO50791 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 7; Length 360;  
RESULT 943  
ID ABO5247 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 7; Length 360;  
RESULT 944  
ID ABR74551 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 7; Length 360;  
RESULT 945  
ID ABR77030 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.7%; Score 121.5; DB 7; Length 360;  
RESULT 946  
ID ADA78392 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003073181-A1.

RESULT 946  
ID ADA16673 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 947  
ID ABM17787 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 948  
ID ABR95838 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 949  
ID ADA13102 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 950  
ID ABO21771 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 951  
ID ABO19941 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 952  
ID ABO24244 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064487-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 953  
ID ABR85993 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 954  
ID ABM10645 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 955  
ID ABM76644 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054485-A1.

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PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 956  
ID ABR89348 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 957  
ID ABM12475 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 958  
ID ABM05765 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 959  
ID ABO34890 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 960  
ID ABM02966 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 961  
ID ABM18944 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 962  
ID ABM19249 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 963  
ID ABO46460 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 964  
ID ABO48961 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;

Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 965  
ID ADA41970 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 966  
ID ABR9004 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 967  
ID ABR9043 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 968  
ID ABR72416 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 969  
ID ABR74246 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 970  
ID ABO18514 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 971  
ID ADAL17317 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 972  
ID ABR80220 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 973  
ID ABW01441 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 974  
ID ABW02051 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 975  
ID ABR87213 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 976  
ID ABW12780 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 977  
ID ABW30534 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 978  
ID ABM24434 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 979  
ID ABO29348 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 980  
ID ABO31178 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 981  
ID ABM14305 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 982  
ID ABM09730 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 983  
ID ABO38855 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003069774-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 984  
ID ABM34620 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 985  
ID ABO51096 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 986  
ID ADA42820 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 987  
ID ABO03922 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 988  
ID ABO10392 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 989  
ID ABR77635 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 990  
ID ABR78845 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 991  
ID ABO23939 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 992  
ID ABR93703 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 993  
ID ABM01746 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 994  
ID ABM78169 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 995  
ID ABR89958 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 996  
ID ABM27484 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 997  
ID ABM13085 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 998  
ID ABO31788 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 999  
ID ABM14000 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1000  
ID ABM08205 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1001  
ID ABO40075 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1002  
ID ABM74510 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096351-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1003  
ID ABM33705 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1004  
ID ABM20164 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1005  
ID ABO48656 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1006  
ID ABR72721 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1007  
ID ABO15363 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1008  
ID ABR85078 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1009  
ID ABO15058 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1010  
ID ABO17193 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1011  
ID ABM17482 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1012  
ID ABR85383 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1013  
ID ABO17592 standard; protein; 360 AA.  
DE Human PRO polypeptide #38.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1014  
ID ABM76949 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1015  
ID ABO28128 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1016  
ID ABM22909 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1017  
ID ABM30229 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1018  
ID ABM21689 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1019  
ID ABM21384 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1020  
ID ABM14915 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1021  
ID ABO40990 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068694-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1022  
ID ABO36720 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1023  
ID ABO37330 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1024  
ID ABM75120 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1025  
ID ABM33400 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003093537-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1026  
ID ABO46155 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1027  
ID ADA82463 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1028  
ID AEM31754 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1029  
ID ABM31144 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1030  
ID ADB77739 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1031  
ID ADB74875 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1032  
ID ADB85771 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1033  
ID ABM32059 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1034  
ID ABM32364 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1035  
ID ABM31449 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1036  
ID ABM30839 standard; protein; 360 AA.  
DE Human secreted polypeptide PRO271, SEQ ID NO:28.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1037  
ID ADC28521 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1038  
ID ADC39721 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1039  
ID ADC40235 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;  
Query Match  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1040  
ID ADB77739 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 7; Length 360;



Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1040  
ID ADC19059 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1041  
ID ADC34359 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1042  
ID ADC29414 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1043  
ID ADC28945 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1044  
ID ADC40830 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1045  
ID ADC19487 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1046  
ID ADC33935 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1047  
ID ADC13005 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1048  
ID ADC12457 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1049  
ID ADD0501 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1050  
ID ADD05012 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1051  
ID ADD04018 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1052  
ID ADD03594 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1053  
ID ADE34846 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1054  
ID ADG02496 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1055  
ID ADG01203 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1056  
ID ADF95378 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1057  
ID ADG12193 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1058  
ID ADH08853 standard; protein; 360 AA.

DE Human PRO polypeptide #14.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1059  
ID ADH59329 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1060  
ID ADI38108 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1061  
ID ADJ26376 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1062  
ID ADL32634 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1063  
ID ADM30168 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 7; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1064  
ID ADE79291 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1065  
ID ADE79715 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1066  
ID ADE73391 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1067  
ID ADE74165 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.

PN US2003211572-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1068  
ID ADE73926 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1069  
ID ADE74777 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein (PRO) #14.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1070  
ID ADE99480 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1071  
ID ADE98599 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1072  
ID ADE99026 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1073  
ID ADG40496 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1074  
ID ADF73890 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1075  
ID ADF59590 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.7%; Score 121.5; DB 8; Length 360;  
Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1076

ID ADF73466 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1077  
ID ADG04261 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1078  
ID ADG00421 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1079  
ID ADG82677 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1080  
ID ADG92309 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1081  
ID ADG92736 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1082  
ID ADH25958 standard; protein; 360 AA.  
DE Novel human secreted and transmembrane protein PRO271.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1083  
ID ADH32927 standard; protein; 360 AA.  
DE Human PRO polypeptide #14.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1084  
ID ADH20525 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1085  
ID ADH07380 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.  
PN US2004006211-A1.  
PD 08-JAN-2004.  
PA (DESN ) DESNOYERS L.  
PA (GODO ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (MATH ) MATHUR J P.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1086  
ID ADH59925 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003215904-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1087  
ID ADH06953 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN ) DESNOYERS L.  
PA (GODO ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (MATH ) MATHUR J P.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1088  
ID ADI18695 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003152999-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1089  
ID ADI65415 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1090  
ID ADI37678 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1091  
ID ADH97474 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003190610-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;  
Query Match Best Local Similarity 34.9%; Pred. No. 0.015;  
RESULT 1092  
ID ADI65842 standard; protein; 360 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2003148371-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC. 7.7%; Score 121.5; DB 8; Length 360;

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Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1093
ID ADH60585 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1094
ID ADJ99642 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1095
ID ADL08835 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1096
ID ADJ54666 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1097
ID ADM25176 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1098
ID ADM29926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1099
ID ADJ64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1100
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1101
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1102
ID ADM40185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1103
ID ADL91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1104
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1105
ID ADN37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1106
ID ADRI1100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.7%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1107
ID ADRI8009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK//) ASHKENAZI A.
PA (BOTS//) BOTSTEIN D.
PA (DESN//) DESNOYERS L.
PA (EATO//) EATON D L.
PA (FERR//) FERRARA N.
PA (FILV//) FILVAROFF E.
PA (FONG//) FONG S.
PA (GAOW//) GAO W.
PA (GERB//) GERBER H.
PA (GERR//) GERRITSEN M E.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GRIM//) GRIMALDI C J.
PA (GURN//) GURNEY A L.
PA (HILL//) HILLAN K J.
PA (KLJA//) KLJAVIN I J.
PA (MATH//) MATHER J P.
PA (PANJ//) PAN J.
PA (PAON//) PAONI N F.
PA (ROYM//) ROY M A.
PA (STEW//) STEWART T A.
PA (TUMA//) TUMAS D.
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PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 7.7%; Score 121.5; DB 8; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 1108  
 ID ADS74648 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein #42.  
 PN US2004185531-A1.  
 PD 23-SEP-2004.  
 PA (ASHK/) ASHKENAZI A.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 7.7%; Score 121.5; DB 8; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 1109  
 ID ADT03685 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein, #42.  
 PN US2003152922-A1.  
 PD 14-AUG-2003.  
 PA (GETH/) GENENTECH INC.  
 Query Match 7.7%; Score 121.5; DB 8; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 1110  
 ID AEA37923 standard; protein; 360 AA.  
 DE Human secreted/transmembrane protein, #42.  
 PN US2005112725-A1.  
 PD 26-MAY-2005.  
 PA (GETH/) GENENTECH INC.  
 Query Match 7.7%; Score 121.5; DB 9; Length 360;  
 Best Local Similarity 34.9%; Pred. No. 0.015;  
 RESULT 1111  
 ID AEA20028 standard; protein; 422 AA.  
 DE Novel human polypeptide SEQ ID NO 722.  
 PN WO2005049806-A2.  
 PD 02-JUN-2005.  
 PA (NUVE-) NUVELO INC.  
 Query Match 7.7%; Score 121.5; DB 9; Length 422;  
 Best Local Similarity 34.9%; Pred. No. 0.019;  
 RESULT 1112  
 ID AAW59882 standard; protein; 528 AA.  
 DE Amino acid sequence of the cDNA clone BEF (HSXCK41).  
 PN WO9831800-A2.  
 PD 23-JUL-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AUCC-) AUCKLAND UNISERVICES LTD.  
 Query Match 7.7%; Score 121; DB 2; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.028;  
 RESULT 1113  
 ID AAB61241 standard; protein; 528 AA.  
 DE Human BEF protein.  
 PN WO200100638-A2.  
 PD 04-JAN-2001.

PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 7.7%; Score 121; DB 4; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.028;  
 RESULT 1114  
 ID ABO32677 standard; protein; 528 AA.  
 DE Secreted polypeptide-related protein #75.  
 PN US2003022279-A1.  
 PD 30-JAN-2003.  
 PA (FRAS/) FRASER C C.  
 PA (BARN/) BARNES T M.  
 PA (SHAR/) SHARP J D.  
 PA (KIRS/) KIRST S J.  
 PA (MYER/) MYERS P S.  
 PA (LEIB/) LEIBY K R.  
 PA (HOLT/) HOLTZMAN D A.  
 PA (MCCA/) MCCARTHY S A.  
 PA (WRIG/) WRIGHTON N.  
 PA (WACK/) WACKAY C R.  
 PA (GOOD/) GOODEARL A D J.  
 Query Match 7.7%; Score 121; DB 6; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.028;  
 RESULT 1115  
 ID ADB90786 standard; protein; 528 AA.  
 DE Human BEF protein.  
 PN US2003082586-A1.  
 PD 01-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 7.7%; Score 121; DB 7; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.028;  
 RESULT 1116  
 ID ADF71521 standard; protein; 528 AA.  
 DE Human BEF protein.  
 PN US2003175733-A1.  
 PD 18-SEP-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 7.7%; Score 121; DB 7; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.028;  
 RESULT 1117  
 ID ADQ10337 standard; protein; 528 AA.  
 DE Human polypeptide #171.  
 PN US2004121396-A1.  
 PD 24-JUN-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 7.7%; Score 121; DB 8; Length 528;  
 Best Local Similarity 24.1%; Pred. No. 0.028;  
 RESULT 1118  
 ID AAR46627 standard; protein; 1257 AA.  
 DE Neurocan core protein.  
 PN WO9403601-A2.  
 PD 17-FEB-1994.  
 PA (UUNY-) UNIV NEW YORK STATE.  
 Query Match 7.7%; Score 120.5; DB 2; Length 1257;  
 Best Local Similarity 23.6%; Pred. No. 0.1;  
 RESULT 1119  
 ID ADQ39513 standard; protein; 1642 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 7.5%; Score 118.5; DB 8; Length 1642;  
 Best Local Similarity 25.5%; Pred. No. 0.23;  
 RESULT 1120  
 ID ADQ39515 standard; protein; 1642 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 7.5%; Score 118.5; DB 8; Length 1642;  
 Best Local Similarity 25.5%; Pred. No. 0.23;  
 RESULT 1121  
 ID ADN04531 standard; protein; 2000 AA.  
 DE Antipsoriatic protein sequence #458.  
 PN WO2004028479-A2.

PD 08-APR-2004.  
PA (GETH ) GENENTECH INC. 7.5%; Score 118.5; DB 8; Length 2000;  
Query Match 25.5%; Pred. No. 0.3;  
Best Local Similarity 25.5%; Pred. No. 0.3;  
RESULT 1122  
ID ADP23738 standard; protein; 2000 AA.  
DE PRO polypeptide SEQ ID NO:916.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC. 7.5%; Score 118.5; DB 8; Length 2000;  
Query Match 25.5%; Pred. No. 0.3;  
Best Local Similarity 25.5%; Pred. No. 0.3;  
RESULT 1123  
ID ADD48597 standard; protein; 3396 AA.  
DE Human Protein P13611, SEQ ID NO 14303.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG. 7.5%; Score 118.5; DB 7; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1124  
ID ADN95526 standard; protein; 3396 AA.  
DE Human BEC/LEC-related protein sequence SeqID449.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN-) LICENTIA LTD. 7.5%; Score 118.5; DB 7; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1125  
ID ADJ75521 standard; protein; 3396 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:773.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC. 7.5%; Score 118.5; DB 8; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1126  
ID ADQ39509 standard; protein; 3396 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 7.5%; Score 118.5; DB 8; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1127  
ID ADQ39510 standard; protein; 3396 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 7.5%; Score 118.5; DB 8; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1128  
ID ADR99164 standard; protein; 3396 AA.  
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB ) BAYER PHARM CORP.  
Query Match 7.5%; Score 118.5; DB 8; Length 3396;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1129  
ID ADZ09841 standard; protein; 3396 AA.  
DE Human breast cancer marker CSPG2 protein.  
PN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB ) BAYER HEALTHCARE AG. 7.5%; Score 118.5; DB 9; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1130  
ID ADZ70548 standard; protein; 3396 AA.  
DE Human protein from lung cancer marker gene CSPG2.  
PN WO2005032495-A2.  
PD 14-APR-2005.  
PA (FARB ) BAYER PHARM CORP. 7.5%; Score 118.5; DB 9; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1131  
ID AEA04473 standard; protein; 3396 AA.  
DE Human protein from gene overexpressed in cancer, CSPG2.  
PN WO2005044990-A2.  
PD 19-MAY-2005.  
PA (FARB ) BAYER HEALTHCARE LLC. 7.5%; Score 118.5; DB 9; Length 3396;  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES. 7.5%; Score 118.5; DB 9; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1132  
ID AEB17604 standard; protein; 3396 AA.  
DE Human CSPG2 protein SeqID18.  
PN JP2005110602-A.  
PD 28-APR-2005.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
PA (SUMO ) SUMITOMO CHEM CO LTD. 7.5%; Score 118.5; DB 9; Length 3396;  
Query Match 25.5%; Pred. No. 0.63;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
RESULT 1133  
ID ADZ09886 standard; protein; 6792 AA.  
DE Human breast cancer marker CSPG2 protein.  
PN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB ) BAYER HEALTHCARE AG. 7.5%; Score 118.5; DB 9; Length 6792;  
Query Match 25.5%; Pred. No. 1.6;  
Best Local Similarity 25.5%; Pred. No. 1.6;  
RESULT 1134  
ID ADJ76266 standard; protein; 2397 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1518.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC. 7.4%; Score 116; DB 8; Length 2397;  
Query Match 28.4%; Pred. No. 0.67;  
Best Local Similarity 28.4%; Pred. No. 0.67;  
RESULT 1135  
ID AAR85443 standard; protein; 908 AA.  
DE Rat brevican core protein.  
PN WO9526201-A1.  
PD 05-OCT-1995.  
PA (LJOL-) LA JOLLA CANCER RES FOUND. 7.3%; Score 115; DB 2; Length 908;  
Query Match 22.2%; Pred. No. 0.22;  
Best Local Similarity 22.2%; Pred. No. 0.22;  
RESULT 1136  
ID ADQ31200 standard; protein; 1257 AA.  
DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.  
PN WO2004041197-A2.  
PD 21-MAY-2004.  
PA (UYCA-) UNIV CASE WESTERN RESERVE. 7.3%; Score 114.5; DB 8; Length 1257;  
Query Match 23.1%; Pred. No. 0.39;  
Best Local Similarity 23.1%; Pred. No. 0.39;  
RESULT 1137  
ID ADD48595 standard; protein; 656 AA.  
DE Rat Protein AF072892, SEQ ID NO 14301.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG. 7.2%; Score 114; DB 7; Length 656;  
Query Match 28.4%; Pred. No. 0.18;  
Best Local Similarity 28.4%; Pred. No. 0.18;  
RESULT 1138  
ID ADP71273 standard; protein; 191 AA.  
DE Human LP2 protein B-B' domain SeqID8.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEBK ) SEIKAGAKU KOGYO CO LTD. 7.1%; Score 112.5; DB 8; Length 191;  
Query Match 26.6%; Pred. No. 0.045;  
Best Local Similarity 26.6%; Pred. No. 0.045;  
RESULT 1139

ID ABB10268 standard; protein; 287 AA.  
DE Human cDNA SEQ ID NO: 576.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.1%; Score 112.5; DB 4; Length 287;  
Best Local Similarity 25.7%; Pred. No. 0.079;  
RESULT 1140  
ID ABP66855 standard; protein; 287 AA.  
DE Human polypeptide SEQ ID NO: 576.  
PN US2002090472-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 7.1%; Score 112.5; DB 5; Length 287;  
Best Local Similarity 25.7%; Pred. No. 0.079;  
RESULT 1141  
ID ADM67304 standard; protein; 340 AA.  
DE Human protein SEQ ID NO: 397.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 7.1%; Score 112.5; DB 8; Length 340;  
Best Local Similarity 26.6%; Pred. No. 0.1;  
RESULT 1142  
ID ABU11635 standard; protein; 343 AA.  
DE Human MDDT polypeptide SEQ ID 582.  
PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.1%; Score 112.5; DB 6; Length 343;  
Best Local Similarity 26.6%; Pred. No. 0.1;  
RESULT 1143  
ID ABU36285 standard; protein; 402 AA.  
DE Protein encoded by Prokaryotic essential gene #21812.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.1%; Score 111.5; DB 6; Length 402;  
Best Local Similarity 22.5%; Pred. No. 0.16;  
RESULT 1144  
ID ADP71271 standard; protein; 200 AA.  
DE Human aggregan protein B-B' domain SeqID6.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG) SEIKAGAKU KOGYO CO LTD.  
Query Match 7.0%; Score 111; DB 8; Length 200;  
Best Local Similarity 37.4%; Pred. No. 0.067;  
RESULT 1145  
ID AAM52242 standard; protein; 655 AA.  
DE Human versican isoform V3 SEQ ID NO 2.  
PN WO200179384-A2.  
PD 25-OCT-2001.  
PA (WIGH/) WIGHT T N.  
PA (MERR/) MERRILLEES M.  
Query Match 7.0%; Score 111; DB 5; Length 655;  
Best Local Similarity 29.4%; Pred. No. 0.34;  
RESULT 1146  
ID ADQ39511 standard; protein; 655 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.0%; Score 111; DB 8; Length 655;  
Best Local Similarity 29.4%; Pred. No. 0.34;  
RESULT 1147  
ID AAR12609 standard; protein; 2409 AA.  
DE Versican.  
PN W09108230-A.  
PD 13-JUN-1991.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.

Query Match 7.0%; Score 111; DB 2; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2;  
RESULT 1148  
ID ABR47429 standard; protein; 2409 AA.  
DE Breast cancer associated protein sequence SEQ ID NO: 90.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 7.0%; Score 111; DB 6; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2;  
RESULT 1149  
ID ADQ39514 standard; protein; 2409 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.0%; Score 111; DB 8; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2;  
RESULT 1150  
ID ADQ39512 standard; protein; 2409 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.0%; Score 111; DB 8; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2;  
RESULT 1151  
ID ADV70260 standard; protein; 2409 AA.  
DE Tumor-associated antigenic target polypeptide TAT498.  
PN WO2004112829-A2.  
PD 29-DEC-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.0%; Score 111; DB 9; Length 2409;  
Best Local Similarity 29.4%; Pred. No. 2;  
RESULT 1152  
ID AAY93913 standard; protein; 353 AA.  
DE A human hyaluronan-binding protein, designated BM-HABP.  
PN WO200039166-A1.  
PD 08-JUL-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (AMNA-) AMERICAN NAT RED CROSS.  
Query Match 6.9%; Score 109; DB 3; Length 353;  
Best Local Similarity 24.3%; Pred. No. 0.23;  
RESULT 1153  
ID ABP97200 standard; protein; 1321 AA.  
DE Tumor-associated antigenic target protein TAT185 SEQ ID NO: 82.  
PN WO2003024392-A2.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.9%; Score 109; DB 6; Length 1321;  
Best Local Similarity 21.4%; Pred. No. 1.4;  
RESULT 1154  
ID ADJ69615 standard; protein; 1321 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1421.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 6.9%; Score 109; DB 7; Length 1321;  
Best Local Similarity 21.4%; Pred. No. 1.4;  
RESULT 1155  
ID ADN38944 standard; protein; 1321 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: 262.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.9%; Score 109; DB 7; Length 1321;  
Best Local Similarity 21.4%; Pred. No. 1.4;  
RESULT 1156  
ID ADO31196 standard; protein; 1321 AA.  
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.  
PN WO2004041197-A2.  
PD 21-MAY-2004.

PA (UYCA-) UNIV CASE WESTERN RESERVE.  
Query Match 6.9%; Score 109; DB 8; Length 1321;  
Best Local Similarity 21.4%; Pred. No. 1.4;  
RESULT 1157  
ID ABJ56909 standard; protein; 322 AA.  
DE 151P3D4 v-2 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 322;  
Best Local Similarity 28.6%; Pred. No. 0.25;  
RESULT 1158  
ID ABJ56908 standard; protein; 322 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 322;  
Best Local Similarity 28.6%; Pred. No. 0.25;  
RESULT 1159  
ID ABJ56918 standard; protein; 353 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 353;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1160  
ID AAY57081 standard; protein; 354 AA.  
DE Human proteoglycan link protein precursor amino acid sequence.  
PN WO9556763-A1.  
PD 11-NOV-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 6.9%; Score 108; DB 3; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1161  
ID AAY57084 standard; protein; 354 AA.  
DE Human proteoglycan link protein precursor #2.  
PN WO9556763-A1.  
PD 11-NOV-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 6.9%; Score 108; DB 3; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1162  
ID ABJ56902 standard; protein; 354 AA.  
DE 151P3D4 v-1 354aa protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1163  
ID ABJ56906 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1164  
ID ABJ56914 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1165  
ID ABJ56898 standard; protein; 354 AA.  
DE 151P3D4 v-8 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.

Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1166  
ID ABJ56895 standard; protein; 354 AA.  
DE 151P3D4 v-5 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1167  
ID ABJ56897 standard; protein; 354 AA.  
DE 151P3D4 v-7 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1168  
ID ABJ56901 standard; protein; 354 AA.  
DE 151P3D4 v-11 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1169  
ID ABJ56894 standard; protein; 354 AA.  
DE 151P3D4 v-4 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1170  
ID ABJ56905 standard; protein; 354 AA.  
DE Human cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1171  
ID ABJ56899 standard; protein; 354 AA.  
DE 151P3D4 v-9 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1172  
ID ABJ56912 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1173  
ID ABJ56893 standard; protein; 354 AA.  
DE 151P3D4 v-3 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1174  
ID ABJ56891 standard; protein; 354 AA.  
DE 151P3D4 v-1 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.9%; Score 108; DB 6; Length 354;  
Best Local Similarity 28.6%; Pred. No. 0.28;  
RESULT 1175  
ID ABJ56896 standard; protein; 354 AA.  
DE 151P3D4 v-6 protein clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.



Best Local Similarity 28.6%; Pred. No. 0.28;  
 RESULT 1175  
 ID ABJ56896 standard; protein; 354 AA.  
 DE 151P3D4 v-6 protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.9%; Score 108; DB 6; Length 354;  
 Best Local Similarity 28.6%; Pred. No. 0.28;  
 RESULT 1176  
 ID ABJ56900 standard; protein; 354 AA.  
 DE 151P3D4 v-10 protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.9%; Score 108; DB 6; Length 354;  
 Best Local Similarity 28.6%; Pred. No. 0.28;  
 RESULT 1177  
 ID ABJ56899 standard; protein; 354 AA.  
 DE Transcript variant 121P1 v-1.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.9%; Score 108; DB 6; Length 354;  
 Best Local Similarity 28.6%; Pred. No. 0.28;  
 RESULT 1178  
 ID ABJ56904 standard; protein; 354 AA.  
 DE 151P3D4 v-1 protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.9%; Score 108; DB 6; Length 354;  
 Best Local Similarity 28.6%; Pred. No. 0.28;  
 RESULT 1179  
 ID ADP07795 standard; protein; 354 AA.  
 DE Human secreted protein, seq id 278.  
 PN WO2004042000-A2.  
 PD 21-MAY-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 6.9%; Score 108; DB 8; Length 354;  
 Best Local Similarity 28.6%; Pred. No. 0.28;  
 RESULT 1180  
 ID AAR77034 standard; protein; 355 AA.  
 DE Rat brain-enriched hyaluronan binding protein.  
 PN WO9527785-A1.  
 PD 19-OCT-1995.  
 PA (UYVA) UNIV YALE.  
 Query Match 6.9%; Score 108; DB 2; Length 355;  
 Best Local Similarity 28.9%; Pred. No. 0.28;  
 RESULT 1181  
 ID ADH71348 standard; protein; 552 AA.  
 DE Human protein of the invention NOV9s SEQ ID NO:244.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 6.9%; Score 108; DB 8; Length 552;  
 Best Local Similarity 29.2%; Pred. No. 0.52;  
 RESULT 1182  
 ID ABJ56890 standard; protein; 721 AA.  
 DE Transcript variant 151P3D4 v-2.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.9%; Score 108; DB 6; Length 721;  
 Best Local Similarity 28.6%; Pred. No. 0.75;  
 RESULT 1183  
 ID ABJ56892 standard; protein; 721 AA.  
 DE 151P3D4 v-2 protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.9%; Score 108; DB 6; Length 721;  
 Best Local Similarity 28.6%; Pred. No. 0.75;

RESULT 1184  
 ID ABJ56903 standard; protein; 721 AA.  
 DE 151P3D4 v-1 721aa protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.9%; Score 108; DB 6; Length 721;  
 Best Local Similarity 28.6%; Pred. No. 0.75;  
 RESULT 1185  
 ID ABG72500 standard; protein; 93 AA.  
 DE Human 190KDa Hyaluronan receptor for endocytosis (HARE) LINK domain.  
 PN WO200286093-A2.  
 PD 31-OCT-2002.  
 PA (WEIG/) WEIGEL P H.  
 PA (WEIG/) WEIGEL J A.  
 Query Match 6.8%; Score 107; DB 6; Length 93;  
 Best Local Similarity 29.2%; Pred. No. 0.056;  
 RESULT 1186  
 ID AAB83358 standard; protein; 315 AA.  
 DE NOV2 protein sequence.  
 PN WO200136638-A2.  
 PD 25-MAY-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 6.8%; Score 107; DB 4; Length 315;  
 Best Local Similarity 29.2%; Pred. No. 0.3;  
 RESULT 1187  
 ID ADH71316 standard; protein; 315 AA.  
 DE Human protein of the invention NOV9c SEQ ID NO:212.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 6.8%; Score 107; DB 8; Length 315;  
 Best Local Similarity 29.2%; Pred. No. 0.3;  
 RESULT 1188  
 ID AAY57083 standard; protein; 339 AA.  
 DE Rat proteoglycan link protein precursor.  
 PN WO9956763-A1.  
 PD 11-NOV-1999.  
 PA (REGC) UNIV CALIFORNIA.  
 Query Match 6.8%; Score 107; DB 3; Length 339;  
 Best Local Similarity 28.6%; Pred. No. 0.33;  
 RESULT 1189  
 ID ABJ56915 standard; protein; 354 AA.  
 DE Rat cartilage link protein.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.8%; Score 107; DB 6; Length 354;  
 Best Local Similarity 28.6%; Pred. No. 0.35;  
 RESULT 1190  
 ID AAY57082 standard; protein; 355 AA.  
 DE Chicken proteoglycan link protein precursor.  
 PN WO9956763-A1.  
 PD 11-NOV-1999.  
 PA (REGC) UNIV CALIFORNIA.  
 Query Match 6.8%; Score 107; DB 3; Length 355;  
 Best Local Similarity 34.9%; Pred. No. 0.35;  
 RESULT 1191  
 ID ABJ56907 standard; protein; 355 AA.  
 DE Mouse cartilage link protein.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 6.8%; Score 107; DB 6; Length 355;  
 Best Local Similarity 28.6%; Pred. No. 0.35;  
 RESULT 1192  
 ID ADH71336 standard; protein; 533 AA.  
 DE Human protein of the invention NOV9m SEQ ID NO:232.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 6.8%; Score 107; DB 8; Length 533;  
 Best Local Similarity 29.2%; Pred. No. 0.62;

RESULT 1193  
ID ADH71334 standard; protein; 533 AA.  
DE Human protein of the invention NOV91 SEQ ID NO:230.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 533;  
Best Local Similarity 29.2%; Pred. No. 0.62;  
RESULT 1194  
ID ADH71340 standard; protein; 552 AA.  
DE Human protein of the invention NOV90 SEQ ID NO:236.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.65;  
RESULT 1195  
ID ADH71346 standard; protein; 552 AA.  
DE Human protein of the invention NOV9r SEQ ID NO:242.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.65;  
RESULT 1196  
ID ADH71354 standard; protein; 552 AA.  
DE Human protein of the invention NOV9v SEQ ID NO:250.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.65;  
RESULT 1197  
ID ADH71344 standard; protein; 552 AA.  
DE Human protein of the invention NOV9q SEQ ID NO:240.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.65;  
RESULT 1198  
ID ADH71342 standard; protein; 552 AA.  
DE Human protein of the invention NOV9p SEQ ID NO:238.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.65;  
RESULT 1199  
ID ADH71350 standard; protein; 552 AA.  
DE Human protein of the invention NOV9t SEQ ID NO:246.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.65;  
RESULT 1200  
ID ADH71314 standard; protein; 556 AA.  
DE Human protein of the invention NOV9b SEQ ID NO:210.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 556;  
Best Local Similarity 29.2%; Pred. No. 0.65;  
RESULT 1201  
ID ABM83433 standard; protein; 774 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.  
FN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.8%; Score 107; DB 8; Length 774;  
Best Local Similarity 21.5%; Pred. No. 1;  
RESULT 1202  
ID ABM83432 standard; protein; 822 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.  
FN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.8%; Score 107; DB 8; Length 822;  
Best Local Similarity 21.5%; Pred. No. 1.1;  
RESULT 1203  
ID ADO31202 standard; protein; 1268 AA.  
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.  
FN WO2004041197-A2.  
PD 21-MAY-2004.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
Query Match 6.8%; Score 107; DB 8; Length 1268;  
Best Local Similarity 26.2%; Pred. No. 2;  
RESULT 1204  
ID ABB69806 standard; protein; 1795 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 6.8%; Score 107; DB 4; Length 1795;  
Best Local Similarity 24.1%; Pred. No. 3.2;  
RESULT 1205  
ID ADH71332 standard; protein; 2417 AA.  
DE Human protein of the invention NOV9K SEQ ID NO:228.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 8; Length 2417;  
Best Local Similarity 29.2%; Pred. No. 4.9;  
RESULT 1206  
ID ABJ10587 standard; protein; 2420 AA.  
DE Human novel protein NOV1b SEQ ID NO: 4.  
FN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.8%; Score 107; DB 5; Length 2420;  
Best Local Similarity 29.2%; Pred. No. 4.9;  
RESULT 1207  
ID ADO09838 standard; protein; 2420 AA.  
DE Human NOV1b.  
FN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHIMKETS R A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (MILL/) MILLER C E.  
PA (BOLD/) BOLDOG F L.  
PA (LILL/) LI L.  
PA (TAUP/) TAUPIER R J.  
PA (KEKU/) KEKUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERH/) ZERHUSEN B D.  
PA (LIUX/) LIU X.  
PA (COLM/) COLMAN S D.  
PA (TCHE/) TCHERNEV V T.  
PA (SIJJ/) SI J.  
PA (EDIN/) EDINGER S R.  
PA (STON/) STONE D J.  
PA (SCIO/) SCIORE P.  
PA (MILL/) MILLET I.  
PA (ROTH/) ROTHENBERG M E.  
Query Match 6.8%; Score 107; DB 8; Length 2420;  
Best Local Similarity 29.2%; Pred. No. 4.9;  
RESULT 1208  
ID ADH71338 standard; protein; 552 AA.  
DE Human protein of the invention NOV9n SEQ ID NO:234.

PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.7%; Score 106; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 0.8;  
RESULT 1209  
ID AAB12304 standard; protein; 341 AA.  
DE Human secreted protein encoded by gene 4 clone HFHC41.  
PN WO200029422-A1.  
PD 25-MAY-2000.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 105.5; DB 3; Length 341;  
Best Local Similarity 28.9%; Pred. No. 0.46;  
RESULT 1210  
ID AAY57080 standard; protein; 354 AA.  
DE Human link protein precursor amino acid sequence.  
PN WO9956763-A1.  
PD 11-NOV-1999.  
PA (REOC) UNIV CALIFORNIA.  
Query Match 6.7%; Score 105; DB 3; Length 354;  
Best Local Similarity 33.7%; Pred. No. 0.54;  
RESULT 1211  
ID ABJ56913 standard; protein; 354 AA.  
DE Bovine cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 6.7%; Score 105; DB 6; Length 354;  
Best Local Similarity 33.7%; Pred. No. 0.54;  
RESULT 1212  
ID AAB42164 standard; protein; 330 AA.  
DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.6%; Score 104.5; DB 3; Length 330;  
Best Local Similarity 18.7%; Pred. No. 0.55;  
RESULT 1213  
ID ABU07339 standard; protein; 139 AA.  
DE Human expressed protein tag (BPT) #2040.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCO INC.  
Query Match 6.6%; Score 104; DB 6; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.19;  
RESULT 1214  
ID ABU07336 standard; protein; 139 AA.  
DE Human expressed protein tag (BPT) #2037.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCO INC.  
Query Match 6.6%; Score 104; DB 6; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.19;  
RESULT 1215  
ID ADQ39387 standard; protein; 139 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.6%; Score 104; DB 8; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.19;  
RESULT 1216  
ID ADY16502 standard; protein; 139 AA.  
DE PRO polypeptide SEQ ID NO 2308.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 6.6%; Score 104; DB 9; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.19;  
RESULT 1217  
ID AEB29759 standard; protein; 139 AA.  
DE Human CD44 isoform RC.  
PN WO2005067667-A2.

PD 28-JUL-2005.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 6.6%; Score 104; DB 9; Length 139;  
Best Local Similarity 20.7%; Pred. No. 0.19;  
RESULT 1218  
ID ADF71269 standard; protein; 195 AA.  
DE Human LPI protein B-B' domain SeqID4.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG) SEIKAGAKU KOGYO CO LTD.  
Query Match 6.6%; Score 104; DB 8; Length 195;  
Best Local Similarity 33.7%; Pred. No. 0.3;  
RESULT 1219  
ID ADF71267 standard; protein; 200 AA.  
DE Human versican protein B-B' domain SeqID2.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG) SEIKAGAKU KOGYO CO LTD.  
Query Match 6.6%; Score 104; DB 8; Length 200;  
Best Local Similarity 32.5%; Pred. No. 0.31;  
RESULT 1220  
ID ADH71352 standard; protein; 552 AA.  
DE Human protein of the invention NOV9u SEQ ID NO:248.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.6%; Score 104; DB 8; Length 552;  
Best Local Similarity 29.2%; Pred. No. 1.2;  
RESULT 1221  
ID ABB60536 standard; protein; 1712 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 8400.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.6%; Score 104; DB 4; Length 1712;  
Best Local Similarity 22.7%; Pred. No. 5.9;  
RESULT 1222  
ID ABB65987 standard; protein; 183 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.5%; Score 102.5; DB 4; Length 183;  
Best Local Similarity 29.7%; Pred. No. 0.38;  
RESULT 1223  
ID ADX72128 standard; protein; 309 AA.  
DE Plant full length insert polypeptide seqid 41494.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ) LIU J.  
PA (ZHOU) ZHOU Y.  
PA (KOVA) KOVALIC D K.  
PA (SCRE) SCREEN S E.  
PA (TAB) TABASKA J E.  
PA (CAOV) CAO Y.  
Query Match 6.5%; Score 102; DB 8; Length 309;  
Best Local Similarity 24.6%; Pred. No. 0.87;  
RESULT 1224  
ID ADN23553 standard; protein; 380 AA.  
DE Bacterial polypeptide #6206.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 6.4%; Score 101.5; DB 8; Length 380;  
Best Local Similarity 25.5%; Pred. No. 1.3;  
RESULT 1225  
ID AAB23034 standard; protein; 590 AA.  
DE Human SLIT protein-like splice variant, SECK 3352358-2.  
PN WO200053742-A2.

PD 14-SEP-2000.  
 PA (CURA-) CURAGEN CORP. 6.4%; Score 101.5; DB 3; Length 590;  
 Query Match Best Local Similarity 20.6%; Pred. No. 2.4;  
 RESULT 1226  
 ID ADA23289 standard; protein; 590 AA.  
 DE Human SECX polypeptide, SEC6.  
 PN US2003054514-A1.  
 PD 20-MAR-2003.  
 PA (SHIM/) SHIMKETS R A.  
 PA (LARO/) LAROCHELLE W J.  
 Query Match Best Local Similarity 20.6%; Pred. No. 2.4;  
 RESULT 1227  
 ID AAU76528 standard; protein; 402 AA.  
 DE Human LP polypeptide #1.  
 PN WO200216578-A2.  
 PD 28-FEB-2002.  
 PA (ELL) LILLY & CO ELI.  
 Query Match Best Local Similarity 30.9%; Pred. No. 1.7;  
 RESULT 1228  
 ID AAU09883 standard; protein; 402 AA.  
 DE Novel human secreted protein #23.  
 PN WO200179454-A1.  
 PD 25-OCT-2001.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 PA (SMIK) SMITHKLINE BEECHAM PLC.  
 Query Match Best Local Similarity 30.9%; Pred. No. 1.7;  
 RESULT 1229  
 ID ADF59259 standard; protein; 402 AA.  
 DE Human polypeptide sequence SEQ ID NO:1667.  
 PN WO2003080795-A2.  
 PD 02-OCT-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match Best Local Similarity 30.9%; Pred. No. 1.7;  
 RESULT 1230  
 ID ADF74155 standard; protein; 412 AA.  
 DE Human novel brain/hippocampus protein #43.  
 PN JP2003009886-A.  
 PD 14-JAN-2003.  
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
 PA (PROT-) PROTEIN EXPRESS KK.  
 Query Match Best Local Similarity 30.9%; Pred. No. 1.8;  
 RESULT 1231  
 ID ABB68940 standard; protein; 1379 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 33612.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match Best Local Similarity 20.2%; Pred. No. 9.4;  
 RESULT 1232  
 ID AAR77035 standard; protein; 378 AA.  
 DE Cat brain-enriched hyaluronan binding protein.  
 PN WO9527785-A1.  
 PD 19-OCT-1995.  
 PA (UYVA) UNIV VALE.  
 Query Match Best Local Similarity 24.1%; Pred. No. 1.8;  
 RESULT 1233  
 ID ABP57346 standard; protein; 402 AA.  
 DE Human secreted protein SECP-17 SEQ ID NO:17.  
 PN WO2003004615-A2.  
 PD 16-JAN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 PA (LUYU/) LU Y.  
 Query Match Best Local Similarity 30.9%; Pred. No. 2.2;  
 RESULT 1234  
 ID AAY95556 standard; protein; 3178 AA.  
 ID ABJ56917 standard; protein; 201 AA.  
 DE Human cartilage link protein.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match Best Local Similarity 28.0%; Pred. No. 0.93;  
 RESULT 1235  
 ID ABJ56916 standard; protein; 201 AA.  
 DE 151P3D4 v-1 protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match Best Local Similarity 28.0%; Pred. No. 0.93;  
 RESULT 1236  
 ID ABJ56919 standard; protein; 600 AA.  
 DE 151P3D4 v-2 protein clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match Best Local Similarity 28.0%; Pred. No. 4.2;  
 RESULT 1237  
 ID ABB70377 standard; protein; 1428 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 37923.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match Best Local Similarity 28.4%; Pred. No. 14;  
 RESULT 1238  
 ID ABB69720 standard; protein; 1126 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 35952.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match Best Local Similarity 25.0%; Pred. No. 11;  
 RESULT 1239  
 ID ABB60403 standard; protein; 2112 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 8001.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match Best Local Similarity 6.2%; Score 98; DB 4; Length 2112;  
 RESULT 1240  
 ID AAY95559 standard; protein; 2870 AA.  
 DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).  
 PN WO200040711-A2.  
 PD 13-JUL-2000.  
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
 Query Match Best Local Similarity 6.1%; Score 96; DB 3; Length 2870;  
 RESULT 1241  
 ID ADN07634 standard; protein; 2870 AA.  
 DE Caenorhabditis elegans LOV -1 deletion mutant protein.  
 PN US6723557-B1.  
 PD 20-APR-2004.  
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
 Query Match Best Local Similarity 22.4%; Pred. No. 68;  
 RESULT 1242  
 ID ADW79951 standard; protein; 2870 AA.  
 DE Nematode location of vulva (lov-1) mutant protein.  
 PN US6849717-B1.  
 PD 01-FEB-2005.  
 PA (CALY) CALIFORNIA INST OF TECHNOLOGY.  
 Query Match Best Local Similarity 6.1%; Score 96; DB 9; Length 2870;  
 RESULT 1243  
 ID AAY95556 standard; protein; 3178 AA.

DE Caenorhabditis elegans LOV-1 (location of vulva) protein.  
 PN WO20040711-A2.  
 PD 13-JUL-2000.  
 PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 Query Match 6.1%; Score 96; DB 3; Length 3178;  
 Best Local Similarity 22.4%; Pred. No. 79;  
 RESULT 1244  
 ID ADN07623 standard; protein; 3178 AA.  
 DE Caenorhabditis elegans location of vulva (LOV) -1 protein.  
 PN US6723557-B1.  
 PD 20-APR-2004.  
 PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 Query Match 6.1%; Score 96; DB 8; Length 3178;  
 Best Local Similarity 22.4%; Pred. No. 79;  
 RESULT 1245  
 ID ADM79940 standard; protein; 3178 AA.  
 DE Nematode location of vulva (lov-1) protein.  
 PN US6849717-B1.  
 PD 01-FEB-2005.  
 PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 Query Match 6.1%; Score 96; DB 9; Length 3178;  
 Best Local Similarity 22.4%; Pred. No. 79;  
 RESULT 1246  
 ID ADO41972 standard; protein; 231 AA.  
 DE Human cell adhesion and extracellular matrix protein 1 SeqID1.  
 PN WO2004048529-A2.  
 PD 10-JUN-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 6.1%; Score 95.5; DB 8; Length 231;  
 Best Local Similarity 30.2%; Pred. No. 2.4;  
 RESULT 1247  
 ID ADG67145 standard; protein; 803 AA.  
 DE Novel human protein sequence #2118.  
 PN EP1440981-A2.  
 PD 28-JUL-2004.  
 PA (RRAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 6.0%; Score 94; DB 8; Length 803;  
 Best Local Similarity 21.9%; Pred. No. 19;  
 RESULT 1248  
 ID AAU18060 standard; protein; 258 AA.  
 DE Human immunoglobulin polypeptide SEQ ID NO 205.  
 PN WO200155315-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.9%; Score 93.5; DB 4; Length 258;  
 Best Local Similarity 24.6%; Pred. No. 4.4;  
 RESULT 1249  
 ID ABB10532 standard; protein; 258 AA.  
 DE Human CDNA SEQ ID NO: 840.  
 PN WO200154474-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.9%; Score 93.5; DB 4; Length 258;  
 Best Local Similarity 24.6%; Pred. No. 4.4;  
 RESULT 1250  
 ID ABP67119 standard; protein; 258 AA.  
 DE Human polypeptide SEQ ID NO 840.  
 PN US2002090672-A1.  
 PD 11-JUL-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 5.9%; Score 93.5; DB 5; Length 258;  
 Best Local Similarity 24.6%; Pred. No. 4.4;  
 RESULT 1251  
 ID ADB31684 standard; protein; 258 AA.  
 DE Human novel protein SEQ ID NO 205.  
 PN US2003077606-A1.  
 PD 24-APR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.9%; Score 93.5; DB 7; Length 258;  
 Best Local Similarity 24.6%; Pred. No. 4.4;  
 RESULT 1252

ID AAU17999 standard; protein; 261 AA.  
 DE Human immunoglobulin polypeptide SEQ ID NO 144.  
 PN WO200155315-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.9%; Score 93.5; DB 4; Length 261;  
 Best Local Similarity 24.6%; Pred. No. 4.4;  
 RESULT 1253  
 ID ABB10361 standard; protein; 261 AA.  
 DE Human CDNA SEQ ID NO: 669.  
 PN WO200154474-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.9%; Score 93.5; DB 4; Length 261;  
 Best Local Similarity 24.6%; Pred. No. 4.4;  
 RESULT 1254  
 ID ABP6948 standard; protein; 261 AA.  
 DE Human polypeptide SEQ ID NO 669.  
 PN US2002090672-A1.  
 PD 11-JUL-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 5.9%; Score 93.5; DB 5; Length 261;  
 Best Local Similarity 24.6%; Pred. No. 4.4;  
 RESULT 1255  
 ID ADB31623 standard; protein; 261 AA.  
 DE Human novel protein SEQ ID NO 144.  
 PN US2003077606-A1.  
 PD 24-APR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.9%; Score 93.5; DB 7; Length 261;  
 Best Local Similarity 24.6%; Pred. No. 4.4;  
 RESULT 1256  
 ID ABG01510 standard; protein; 320 AA.  
 DE Novel human diagnostic protein #1501.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HVSE-) HVSEQ INC.  
 Query Match 5.9%; Score 93.5; DB 4; Length 320;  
 Best Local Similarity 23.2%; Pred. No. 5.9;  
 RESULT 1257  
 ID ADE36618 standard; protein; 339 AA.  
 DE Plasmid PCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.  
 PN WO2003080856-A2.  
 PD 02-OCT-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 5.9%; Score 93.5; DB 7; Length 339;  
 Best Local Similarity 23.1%; Pred. No. 6.3;  
 RESULT 1258  
 ID ADE36592 standard; protein; 339 AA.  
 DE Human NOVla protein SEQ ID NO:2.  
 PN WO2003080856-A2.  
 PD 02-OCT-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 5.9%; Score 93.5; DB 7; Length 339;  
 Best Local Similarity 23.1%; Pred. No. 6.3;  
 RESULT 1259  
 ID ABR58582 standard; protein; 359 AA.  
 DE Human cancer related protein SEQ ID NO:239.  
 PN WO2003025138-A2.  
 PD 27-MAR-2003.  
 PA (FOSB-) BOS BIOTECHNOLOGY INC.  
 Query Match 5.9%; Score 93.5; DB 6; Length 359;  
 Best Local Similarity 23.1%; Pred. No. 6.9;  
 RESULT 1260  
 ID ABP70439 standard; protein; 359 AA.  
 DE Amino acid sequence of human TIM-1 allele 1.  
 PN WO2003002722-A2.  
 PD 09-JAN-2003.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Query Match 5.9%; Score 93.5; DB 6; Length 359;  
 Best Local Similarity 23.1%; Pred. No. 6.9;

RESULT 1261  
ID ABP70441 standard; protein; 359 AA.  
DE Amino acid sequence of human TIM-1 allele 4.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.9%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1262  
ID ABP70438 standard; protein; 359 AA.  
DE Amino acid sequence of human TIM-1 allele 1.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.9%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1263  
ID ABR48174 standard; protein; 359 AA.  
DE Human bladder cancer associated protein sequence SEQ ID NO:64.  
PN WO2003003906-A2.  
PD 16-JAN-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 5.9%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1264  
ID AAO26680 standard; protein; 359 AA.  
DE KIM-1 related protein, SEQ ID No 8.  
PN WO200298920-A1.  
PD 12-DEC-2002.  
PA (BIOI ) BIOGEN INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 5.9%; Score 93.5; DB 6; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1265  
ID ADE36594 standard; protein; 359 AA.  
DE Human NOV1b protein SEQ ID NO:4.  
PN WO2003008056-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.9%; Score 93.5; DB 7; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1266  
ID ADN38984 standard; protein; 359 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 5.9%; Score 93.5; DB 7; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1267  
ID ADQ76690 standard; protein; 359 AA.  
DE Human kidney injury molecule-1 (KIM-1).  
PN WO2004060041-A2.  
PD 22-JUL-2004.  
PA (BIOG-) BIOGEN IDEC MA INC.  
Query Match 5.9%; Score 93.5; DB 8; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1268  
ID ABR99971 standard; protein; 359 AA.  
DE HAVCR1 protein, SEQ ID 25.  
PN WO2005001092-A2.  
PD 06-JAN-2005.  
PA (AMHP ) WYETH.  
Query Match 5.9%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1269  
ID ADY98071 standard; protein; 359 AA.  
DE Human TIM-1 allele 1-encoded protein.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Query Match 5.9%; Score 93.5; DB 9; Length 359;

Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1270  
ID ADY98077 standard; protein; 359 AA.  
DE Human TIM-1 allele 4-encoded protein.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Query Match 5.9%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1271  
ID ADY98073 standard; protein; 359 AA.  
DE Human TIM-1 allele 2-encoded protein.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Query Match 5.9%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1272  
ID AD279370 standard; protein; 359 AA.  
DE Human kidney injury molecule-1(b) complete protein.  
PN US2005112117-A1.  
PD 26-MAY-2005.  
PA (BAIL/) BAILLY V.  
PA (BONV/) BONVENTRE J.  
Query Match 5.9%; Score 93.5; DB 9; Length 359;  
Best Local Similarity 23.1%; Pred. No. 6.9;  
RESULT 1273  
ID ABG07923 standard; protein; 366 AA.  
DE Novel human diagnostic protein #7914.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 93.5; DB 4; Length 366;  
Best Local Similarity 23.2%; Pred. No. 7.1;  
RESULT 1274  
ID ADP04445 standard; protein; 1381 AA.  
DE Sea squirt protein with tissue specific expression in development Seq40.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 5.9%; Score 93.5; DB 8; Length 1381;  
Best Local Similarity 22.9%; Pred. No. 43;  
RESULT 1275  
ID ABR63235 standard; protein; 2055 AA.  
DE Glucanase sequence from strain KG15.  
PN WO2003008618-A2.  
PD 30-JAN-2003.  
PA (NEDE ) NEDERLANDSE ORG TORGEPAST.  
Query Match 5.9%; Score 93.5; DB 6; Length 2055;  
Best Local Similarity 23.3%; Pred. No. 75;  
RESULT 1276  
ID AAR88466 standard; protein; 629 AA.  
DE Drosophila scavenger receptor class CI.  
PN WO9600288-A2.  
PD 04-JAN-1996.  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
Query Match 5.9%; Score 93; DB 2; Length 629;  
Best Local Similarity 19.9%; Pred. No. 17;  
RESULT 1277  
ID ABG33057 standard; protein; 629 AA.  
DE Fruit fly scavenger receptor type CI (dSR-CI).  
PN US6429289-B1.  
PD 06-AUG-2002.  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
Query Match 5.9%; Score 93; DB 5; Length 629;  
Best Local Similarity 19.9%; Pred. No. 17;  
RESULT 1278  
ID AAE21524 standard; protein; 629 AA.  
DE Drosophila melanogaster scavenger receptor class CI (dSR-CI).  
PN US6350859-B1.  
PD 26-FEB-2002.

PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 Query Match 5.9%; Score 93; DB 5; Length 629;  
 Best Local Similarity 19.9%; Pred. No. 17;  
 RESULT 1279  
 ID ABP73157 standard; protein; 40 AA.  
 DE Deletion mutant of a CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO/) STROENBLAD S.  
 PA (KOG/) KOGERMAN P.  
 PA (PAEL/) PAELL T.  
 Query Match 5.9%; Score 92.5; DB 6; Length 40;  
 Best Local Similarity 54.1%; Pred. No. 0.42;  
 RESULT 1280  
 ID AAW61380 standard; protein; 300 AA.  
 DE Mouse junctional adhesion molecule protein.  
 PN WO9824897-A1.  
 PD 11-JUN-1998.  
 PA (HOPF) HOFFMANN LA ROCHE & CO AG F.  
 Query Match 5.9%; Score 92.5; DB 2; Length 300;  
 Best Local Similarity 23.4%; Pred. No. 6.7;  
 RESULT 1281  
 ID AAY23325 standard; protein; 300 AA.  
 DE A33 related antigen JAM.  
 PN WO9927098-A2.  
 PD 03-JUN-1999.  
 PA (GETH) GENENTECH INC.  
 Query Match 5.9%; Score 92.5; DB 2; Length 300;  
 Best Local Similarity 23.4%; Pred. No. 6.7;  
 RESULT 1282  
 ID ADH62537 standard; protein; 300 AA.  
 DE Murine JAM protein used in the exemplification of the invention.  
 PN US2003171568-A1.  
 PD 11-SEP-2003.  
 PA (ASHK/) ASHKENAZI A.  
 PA (FONG/) FONG S.  
 PA (GODD/) GODDARD A.  
 PA (GURN/) GURNEY A L.  
 PA (NAPI/) NAPIER M A.  
 PA (TUMA/) TUMAS D.  
 PA (WOOD/) WOOD W I.  
 Query Match 5.9%; Score 92.5; DB 7; Length 300;  
 Best Local Similarity 23.4%; Pred. No. 6.7;  
 RESULT 1283  
 ID ADK40853 standard; protein; 300 AA.  
 DE Mouse junction adhesion molecule (JAM).  
 PN US669688-B1.  
 PD 02-MAR-2004.  
 PA (UINY) UNIV NEW YORK STATE RES FOUND.  
 Query Match 5.9%; Score 92.5; DB 8; Length 300;  
 Best Local Similarity 23.4%; Pred. No. 6.7;  
 RESULT 1284  
 ID ADN35293 standard; protein; 300 AA.  
 DE Human JAM protein.  
 PN WO2004031105-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 5.9%; Score 92.5; DB 8; Length 300;  
 Best Local Similarity 23.4%; Pred. No. 6.7;  
 RESULT 1285  
 ID ADU66693 standard; protein; 300 AA.  
 DE Mouse junctional adhesion molecule (JAM).  
 PN US2004235768-A1.  
 PD 25-NOV-2004.  
 PA (KORN/) KORNECKI E.  
 PA (SOBO/) SOBOCKA M B.  
 Query Match 5.9%; Score 92.5; DB 8; Length 300;  
 Best Local Similarity 23.4%; Pred. No. 6.7;  
 RESULT 1286  
 ID ABP70440 standard; protein; 365 AA.  
 DE Amino acid sequence of human TIM-1 allele 3.  
 PN WO2003002722-A2.  
 PD 09-JAN-2003.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Query Match 5.9%; Score 92.5; DB 6; Length 365;  
 Best Local Similarity 22.6%; Pred. No. 8.7;  
 RESULT 1287  
 ID ADY98075 standard; protein; 365 AA.  
 DE Human TIM-1 allele 3-encoded protein.  
 PN WO2005027854-A2.  
 PD 31-MAR-2005.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 Query Match 5.9%; Score 92.5; DB 9; Length 365;  
 Best Local Similarity 22.6%; Pred. No. 8.7;  
 RESULT 1288  
 ID ABB50001 standard; protein; 569 AA.  
 DE Listeria monocytogenes protein #2705.  
 PN WO200177335-A2.  
 PD 18-OCT-2001.  
 PA (INSP) INST PASTEUR.  
 Query Match 5.9%; Score 92.5; DB 5; Length 569;  
 Best Local Similarity 21.4%; Pred. No. 16;  
 RESULT 1289  
 ID ABU2518 standard; protein; 569 AA.  
 DE Protein encoded by Prokaryotic essential gene #18045.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.9%; Score 92.5; DB 6; Length 569;  
 Best Local Similarity 21.4%; Pred. No. 16;  
 RESULT 1290  
 ID AAU48553 standard; protein; 706 AA.  
 DE Propionibacterium acnes immunogenic protein #9449.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.9%; Score 92.5; DB 4; Length 706;  
 Best Local Similarity 25.4%; Pred. No. 22;  
 RESULT 1291  
 ID ABM45072 standard; protein; 706 AA.  
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #9748.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.9%; Score 92.5; DB 6; Length 706;  
 Best Local Similarity 25.4%; Pred. No. 22;  
 RESULT 1292  
 ID ADN18863 standard; protein; 994 AA.  
 DE Bacterial polypeptide #1516.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOV/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.9%; Score 92.5; DB 8; Length 994;  
 Best Local Similarity 19.7%; Pred. No. 34;  
 RESULT 1293  
 ID ABR53566 standard; protein; 1636 AA.  
 DE Protein sequence #SEQ ID 1997.  
 PN EPI258494-A1.  
 PD 20-NOV-2002.  
 PA (CELL-) CELLZOME AG.  
 Query Match 5.9%; Score 92.5; DB 6; Length 1636;  
 Best Local Similarity 19.7%; Pred. No. 68;  
 RESULT 1294  
 ID ADK64364 standard; protein; 1636 AA.  
 DE Disease treating protein complex-derived protein #1193.  
 PN EPI338608-A2.  
 PD 27-AUG-2003.  
 PA (CELL-) CELLZOME AG.  
 Query Match 5.9%; Score 92.5; DB 7; Length 1636;  
 Best Local Similarity 19.7%; Pred. No. 68;  
 RESULT 1295

ID ABP70442 standard; protein; 364 AA.  
 DE Amino acid sequence of human TIM-1 allele 5.  
 PN WO2003002722-A2.  
 PD 09-JAN-2003.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Query Match 5.8%; Score 92; DB 6; Length 364;  
 Best Local Similarity 21.6%; Pred. No. 9.7;  
 RESULT 1296  
 ID ADY98079 standard; protein; 364 AA.  
 DE Human TIM-1 allele 5-encoded protein.  
 PN WO2005027854-A2.  
 PD 31-MAR-2005.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA (DAND ) DANA FARBEN CANCER INST INC.  
 Query Match 5.8%; Score 92; DB 9; Length 364;  
 Best Local Similarity 21.6%; Pred. No. 9.7;  
 RESULT 1297  
 ID ABG93047 standard; protein; 966 AA.  
 DE S. cerevisiae BAX-associated protein fragment SEQ ID 52.  
 PN WO200264766-A2.  
 PD 22-AUG-2002.  
 PA (JANC ) JANSSEN PHARM NV.  
 Query Match 5.8%; Score 92; DB 5; Length 966;  
 Best Local Similarity 20.3%; Pred. No. 3.7;  
 RESULT 1298  
 ID ADI87298 standard; protein; 966 AA.  
 DE Yeast Stress-related protein from gene YBR112C.  
 PN WO2004092398-A2.  
 PD 28-OCT-2004.  
 PA (BADI ) BASF PLANT SCI GMBH.  
 Query Match 5.8%; Score 92; DB 8; Length 966;  
 Best Local Similarity 20.3%; Pred. No. 3.7;  
 RESULT 1299  
 ID AAU18036 standard; protein; 166 AA.  
 DE Human immunoglobulin polypeptide SEQ ID NO 181.  
 PN WO200155315-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.8%; Score 91.5; DB 4; Length 166;  
 Best Local Similarity 31.9%; Pred. No. 3.7;  
 RESULT 1300  
 ID ABB10469 standard; protein; 166 AA.  
 DE Human cDNA SEQ ID NO: 777.  
 PN WO200154474-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.8%; Score 91.5; DB 4; Length 166;  
 Best Local Similarity 31.9%; Pred. No. 3.7;  
 RESULT 1301  
 ID ABP67056 standard; protein; 166 AA.  
 DE Human polypeptide SEQ ID NO 777.  
 PN US2002090672-A1.  
 PD 11-JUL-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 5.8%; Score 91.5; DB 5; Length 166;  
 Best Local Similarity 31.9%; Pred. No. 3.7;  
 RESULT 1302  
 ID ADB31660 standard; protein; 166 AA.  
 DE Human novel protein SEQ ID NO 181.  
 PN US2003077606-A1.  
 PD 24-APR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.8%; Score 91.5; DB 7; Length 166;  
 Best Local Similarity 31.9%; Pred. No. 3.7;  
 RESULT 1303  
 ID AAB75555 standard; protein; 298 AA.  
 DE Gene 1 human secreted protein homologous amino acid sequence #109.  
 PN WO2000077026-A1.  
 PD 21-DEC-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 Query Match 5.8%; Score 91.5; DB 4; Length 639;  
 Best Local Similarity 22.0%; Pred. No. 2.3;  
 RESULT 1304  
 ID ADR46581 standard; protein; 300 AA.  
 DE Mouse junctional adhesion molecule-1, SEQ ID 12.  
 PN JP2004242513-A.  
 PD 02-SEP-2004.  
 PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.  
 Query Match 5.8%; Score 91.5; DB 8; Length 300;  
 Best Local Similarity 23.4%; Pred. No. 8.3;  
 RESULT 1305  
 ID AAM52302 standard; protein; 350 AA.  
 DE ActA protein fragment #2.  
 PN WO200171356-A2.  
 PD 27-SEP-2001.  
 PA (CNRS ) CENT NAT RECH SCI.  
 PA (CUR1-) INST CURIE.  
 Query Match 5.8%; Score 91.5; DB 4; Length 350;  
 Best Local Similarity 22.0%; Pred. No. 10;  
 RESULT 1306  
 ID AAM52301 standard; protein; 376 AA.  
 DE ActA protein fragment #1.  
 PN WO200171356-A2.  
 PD 27-SEP-2001.  
 PA (CNRS ) CENT NAT RECH SCI.  
 PA (CUR1-) INST CURIE.  
 Query Match 5.8%; Score 91.5; DB 4; Length 376;  
 Best Local Similarity 22.0%; Pred. No. 11;  
 RESULT 1307  
 ID AAM52300 standard; protein; 610 AA.  
 DE ActA protein.  
 PN WO200171356-A2.  
 PD 27-SEP-2001.  
 PA (CNRS ) CENT NAT RECH SCI.  
 PA (CUR1-) INST CURIE.  
 Query Match 5.8%; Score 91.5; DB 4; Length 610;  
 Best Local Similarity 22.0%; Pred. No. 22;  
 RESULT 1308  
 ID AAG79171 standard; protein; 639 AA.  
 DE Amino acid sequence of an ActA fragment.  
 PN WO200174858-A2.  
 PD 11-OCT-2001.  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Query Match 5.8%; Score 91.5; DB 4; Length 639;  
 Best Local Similarity 22.0%; Pred. No. 23;  
 RESULT 1309  
 ID AAU09142 standard; protein; 639 AA.  
 DE Lyseteria monocytogenes ActA.  
 PN WO200174853-A2.  
 PD 11-OCT-2001.  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Query Match 5.8%; Score 91.5; DB 4; Length 639;  
 Best Local Similarity 22.0%; Pred. No. 23;  
 RESULT 1310  
 ID ABB47677 standard; protein; 639 AA.  
 DE Listeria monocytogenes protein #381.  
 PN WO200177335-A2.  
 PD 18-OCT-2001.  
 PA (INSP ) INST PASTEUR.  
 Query Match 5.8%; Score 91.5; DB 5; Length 639;  
 Best Local Similarity 22.0%; Pred. No. 23;  
 RESULT 1311  
 ID ADN20575 standard; protein; 1103 AA.  
 DE Bacterial polypeptide #3228.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.



Query Match  
Best Local Similarity 5.8%; Score 91.5; DB 8; Length 1103;  
RESULT 1312  
ID ABP60839 standard; protein; 246 AA.  
DE Caenorhabditis elegans thioredoxin-like protein SEQ ID NO:188.  
FN WO200250289-A1.  
PD 27-JUN-2002.  
PA (SENB-) SEMBIOSYS GENETICS INC.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Query Match  
Best Local Similarity 5.8%; Score 91; DB 5; Length 246;  
RESULT 1313  
ID AEA08149 standard; protein; 4262 AA.  
DE Human mucin 17 (MUC17SEC) protein - SEQ ID 4.  
FN US2005100925-A1.  
PD 12-MAY-2005.  
PA (BATR/) BATRA S.  
PA (MONI/) MONIAUX N.  
Query Match  
Best Local Similarity 5.8%; Score 91; DB 9; Length 4262;  
RESULT 1314  
ID AEA08148 standard; protein; 4493 AA.  
DE Human mucin 17 protein - SEQ ID 3.  
FN US2005100925-A1.  
PD 12-MAY-2005.  
PA (BATR/) BATRA S.  
PA (MONI/) MONIAUX N.  
Query Match  
Best Local Similarity 5.8%; Score 91; DB 9; Length 4493;  
RESULT 1315  
ID ADV11098 standard; protein; 463 AA.  
DE Plant full length insert polypeptide seqid 66913.  
FN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match  
Best Local Similarity 5.7%; Score 90.5; DB 8; Length 463;  
RESULT 1316  
ID ADG73740 standard; protein; 505 AA.  
DE Aspergillus niger Brea-109.  
FN US2003215950-A1.  
PD 20-NOV-2003.  
PA (LASU/) LASURE L L.  
PA (DAIZ/) DAI Z.  
Query Match  
Best Local Similarity 5.7%; Score 90.5; DB 8; Length 505;  
RESULT 1317  
ID AB860186 standard; protein; 1714 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7350.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 5.7%; Score 90.5; DB 4; Length 1714;  
RESULT 1318  
ID AB869419 standard; protein; 1976 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35049.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 5.7%; Score 90.5; DB 4; Length 1976;  
RESULT 1319  
ID ABP70443 standard; protein; 364 AA.  
DE Amino acid sequence of human TIM-1 allele 6.  
FN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.

Query Match  
Best Local Similarity 5.7%; Score 90; DB 6; Length 364;  
RESULT 1320  
ID ADY98081 standard; protein; 364 AA.  
DE Human TIM-1 allele 5-encoded protein.  
FN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PA (DAND) DANA FARRER CANCER INST INC.  
Query Match  
Best Local Similarity 5.7%; Score 90; DB 9; Length 364;  
RESULT 1321  
ID ABB59507 standard; protein; 629 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 5313.  
FN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 5.7%; Score 90; DB 4; Length 629;  
RESULT 1322  
ID ADD47260 standard; protein; 957 AA.  
DE Human Protein AAC02272, SEQ ID NO 12954.  
FN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 5.7%; Score 90; DB 7; Length 957;  
RESULT 1323  
ID ADE58049 standard; protein; 957 AA.  
DE Human Protein AAC02272, SEQ ID NO 3917.  
FN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 5.7%; Score 90; DB 7; Length 957;  
RESULT 1324  
ID ADD47264 standard; protein; 957 AA.  
DE Human Protein AAC02272, SEQ ID NO 12958.  
FN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 5.7%; Score 90; DB 7; Length 957;  
RESULT 1325  
ID ADE58045 standard; protein; 957 AA.  
DE Human Protein AAC02272, SEQ ID NO 3913.  
FN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 5.7%; Score 90; DB 7; Length 957;  
RESULT 1326  
ID ADQ29696 standard; protein; 1217 AA.  
DE Human colorectal cancer-associated protein #51.  
FN EPI439393-A2.  
PD 21-JUL-2004.  
PA (FARB) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match  
Best Local Similarity 5.7%; Score 90; DB 8; Length 1217;  
RESULT 1327  
ID ABG66756 standard; protein; 1296 AA.  
DE Human novel polypeptide #91.  
FN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 5.7%; Score 90; DB 5; Length 1296;  
RESULT 1328

ID ABG66702 standard; protein; 1296 AA.  
DE Human novel polypeptide #37.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.7%; Score 90; DB 5; Length 1296;  
Best Local Similarity 18.3%; Pred. No. 86;  
RESULT 1329  
ID ABP70432 standard; protein; 305 AA.  
DE Amino acid sequence of murine TIM-2 BALB/c allele.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.7%; Score 89.5; DB 6; Length 305;  
Best Local Similarity 24.3%; Pred. No. 13;  
RESULT 1330  
ID ABP70433 standard; protein; 305 AA.  
DE Amino acid sequence of murine TIM-2 ES-HBA and DBA/2J allele.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Query Match 5.7%; Score 89.5; DB 6; Length 305;  
Best Local Similarity 24.3%; Pred. No. 13;  
RESULT 1331  
ID ADY98061 standard; protein; 305 AA.  
DE Mouse TIM-2 variant.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBEN CANCER INST INC.  
Query Match 5.7%; Score 89.5; DB 9; Length 305;  
Best Local Similarity 24.3%; Pred. No. 13;  
RESULT 1332  
ID ADY98059 standard; protein; 305 AA.  
DE Mouse TIM-2.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBEN CANCER INST INC.  
Query Match 5.7%; Score 89.5; DB 9; Length 305;  
Best Local Similarity 24.3%; Pred. No. 13;  
RESULT 1333  
ID AAR5213 standard; protein; 480 AA.  
DE Blowfly larvae PM95 antigen.  
PN AU9517609-A.  
PD 02-NOV-1995.  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
Query Match 5.7%; Score 89.5; DB 2; Length 480;  
Best Local Similarity 22.1%; Pred. No. 25;  
RESULT 1334  
ID AB084994 standard; protein; 917 AA.  
DE Murine cancer-associated protein (CAP) MP07-101.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 5.7%; Score 89.5; DB 8; Length 917;  
Best Local Similarity 21.4%; Pred. No. 59;  
RESULT 1335  
ID ABG65879 standard; protein; 307 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.7%; Score 89; DB 4; Length 307;  
Best Local Similarity 31.6%; Pred. No. 15;  
RESULT 1336  
ID ABP69313 standard; protein; 343 AA.  
DE Human polypeptide SEQ ID NO 1360.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.7%; Score 89; DB 5; Length 343;  
Best Local Similarity 27.7%; Pred. No. 17;

RESULT 1337  
ID AAR69554 standard; protein; 416 AA.  
DE Human lysosomal membrane sialoglycoprotein lamp-1.  
PN WO9429342-A1.  
PD 22-DEC-1994.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
PA (UNMI ) UNIV MICHIGAN.  
Query Match 5.7%; Score 89; DB 2; Length 416;  
Best Local Similarity 23.6%; Pred. No. 22;  
RESULT 1338  
ID AAY52550 standard; protein; 416 AA.  
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).  
PN WO958658-A2.  
PD 18-NOV-1999.  
PA (EPIM-) EPIMUNE INC.  
Query Match 5.7%; Score 89; DB 3; Length 416;  
Best Local Similarity 23.6%; Pred. No. 22;  
RESULT 1339  
ID ADP65283 standard; protein; 416 AA.  
DE Human lysosomal-associated membrane protein 1.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 5.7%; Score 89; DB 7; Length 416;  
Best Local Similarity 23.6%; Pred. No. 22;  
RESULT 1340  
ID ADN03755 standard; protein; 416 AA.  
DE Antipsoriatic protein sequence #74.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 5.7%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 22;  
RESULT 1341  
ID ADP49321 standard; protein; 416 AA.  
DE Human lysosomal associated membrane protein LAMP #1.  
PN WO2004048337-A2.  
PD 10-JUN-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.7%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 22;  
RESULT 1342  
ID ADP23231 standard; protein; 416 AA.  
DE PRO polypeptide SEQ ID NO:325.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 5.7%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 22;  
RESULT 1343  
ID ADU60107 standard; protein; 416 AA.  
DE Housekeeping gene protein, SEQ ID 68.  
PN US2004229233-A1.  
PD 18-NOV-2004.  
PA (NIGA ) NGK INSULATORS LTD.  
Query Match 5.7%; Score 89; DB 8; Length 416;  
Best Local Similarity 23.6%; Pred. No. 22;  
RESULT 1344  
ID ADW85920 standard; protein; 416 AA.  
DE Human lysosomal-associated membrane protein-1.  
PN WO2005012912-A2.  
PD 10-FEB-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 5.7%; Score 89; DB 9; Length 416;  
Best Local Similarity 23.6%; Pred. No. 22;  
RESULT 1345  
ID ADR66408 standard; protein; 832 AA.  
DE Aspergillus fumigatus essential gene protein #458.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Query Match 5.7%; Score 89; DB 8; Length 832;

Best Local Similarity 19.8%; Pred. No. 58;  
 RESULT 1346  
 ID ABB70039 standard; protein; 846 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 36909.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 5.7%; Score 89; DB 4; Length 846;  
 Best Local Similarity 22.5%; Pred. No. 59;  
 RESULT 1347  
 ID ABB67102 standard; protein; 882 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 28098.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 5.7%; Score 89; DB 4; Length 882;  
 Best Local Similarity 22.5%; Pred. No. 63;  
 RESULT 1348  
 ID ADQ7103 standard; protein; 951 AA.  
 DE Cell proliferation-related polypeptide #118.  
 PN WO2004061122-A2.  
 PD 22-JUL-2004.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.7%; Score 89; DB 8; Length 951;  
 Best Local Similarity 22.1%; Pred. No. 70;  
 RESULT 1349  
 ID ADM19804 standard; protein; 1076 AA.  
 DE Protein encoded by novel human channel/transporter gene #122.  
 PN WO200154472-A2.  
 PD 02-AUG-2001.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Query Match 5.7%; Score 89; DB 4; Length 1076;  
 Best Local Similarity 21.1%; Pred. No. 83;  
 RESULT 1350  
 ID ADX97567 standard; protein; 2624 AA.  
 DE Pancreatic cancer associated human protein, SEQ ID 115.  
 PN EP1471075-A2.  
 PD 27-OCT-2004.  
 PA (HINZ/) HINZMANN B.  
 PA (ROSE/) ROSENTHAL A.  
 PA (PILA/) PILARSKY C.  
 PA (DAHL/) DAHL E.  
 PA (SPEC/) SPECHT T.  
 PA (LICH/) LICHTNER R.  
 Query Match 5.7%; Score 89; DB 8; Length 2624;  
 Best Local Similarity 27.7%; Pred. No. 2.8e+02;  
 RESULT 1351  
 ID AAG39194 standard; protein; 193 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48458.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 5.6%; Score 88.5; DB 3; Length 193;  
 Best Local Similarity 21.4%; Pred. No. 8.8;  
 RESULT 1352  
 ID AAG39193 standard; protein; 199 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48457.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 5.6%; Score 88.5; DB 3; Length 199;  
 Best Local Similarity 21.4%; Pred. No. 9.1;  
 RESULT 1353  
 ID ABG15314 standard; protein; 358 AA.  
 DE Novel human diagnostic protein #15305.  
 PN WO200175057-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.6%; Score 88.5; DB 4; Length 358;  
 Best Local Similarity 20.2%; Pred. No. 20;  
 RESULT 1354  
 ID AAR11605 standard; protein; 392 AA.  
 DE Human 75KD TNF-binding protein.  
 PN EP417563-A.  
 PD 20-MAR-1991.

PA (HOFF) HOFFMANN-LA ROCHE AG.  
 Query Match 5.6%; Score 88.5; DB 2; Length 392;  
 Best Local Similarity 21.8%; Pred. No. 23;  
 RESULT 1355  
 ID AAY30935 standard; protein; 392 AA.  
 DE Human tumour necrosis factor binding protein fragment.  
 PN EP939121-A2.  
 PD 01-SEP-1999.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 Query Match 5.6%; Score 88.5; DB 2; Length 392;  
 Best Local Similarity 21.8%; Pred. No. 23;  
 RESULT 1356  
 ID AAB86818 standard; protein; 392 AA.  
 DE Human TNFPP-associated protein #2.  
 PN EP1132471-A2.  
 PD 12-SEP-2001.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 Query Match 5.6%; Score 88.5; DB 4; Length 392;  
 Best Local Similarity 21.8%; Pred. No. 23;  
 RESULT 1357  
 ID ABO68455 standard; protein; 451 AA.  
 DE Pseudomonas aeruginosa polypeptide #630.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.6%; Score 88.5; DB 7; Length 451;  
 Best Local Similarity 20.7%; Pred. No. 28;  
 RESULT 1358  
 ID ABB63417 standard; protein; 481 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 17043.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 5.6%; Score 88.5; DB 4; Length 481;  
 Best Local Similarity 21.2%; Pred. No. 31;  
 RESULT 1359  
 ID AAG64210 standard; protein; 596 AA.  
 DE Murine HSP47 interacting protein, M4.  
 PN JP2001145493-A.  
 PD 29-MAY-2001.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Query Match 5.6%; Score 88.5; DB 4; Length 596;  
 Best Local Similarity 21.3%; Pred. No. 41;  
 RESULT 1360  
 ID AAY37234 standard; protein; 708 AA.  
 DE Chlamydia trachomatis cellular envelope protein.  
 PN WO9928475-A2.  
 PD 10-JUN-1999.  
 PA (GEST) GENSET.  
 Query Match 5.6%; Score 88.5; DB 2; Length 708;  
 Best Local Similarity 23.6%; Pred. No. 52;  
 RESULT 1361  
 ID ADE86597 standard; protein; 995 AA.  
 DE Frog tail resorption protein.  
 PN US2003129685-A1.  
 PD 10-JUL-2003.  
 PA (NIJU/) NI J.  
 PA (YOUN/) YOUNG P E.  
 PA (KENN/) KENNY J J.  
 PA (OLSE/) OLSEN H S.  
 PA (MOOR/) MOORE P A.  
 PA (WEIY/) WEI Y.  
 PA (GREE/) GREENE J M.  
 PA (RUBE/) RUBEN S M.  
 Query Match 5.6%; Score 88; DB 8; Length 995;  
 Best Local Similarity 19.9%; Pred. No. 92;  
 RESULT 1362  
 ID ADN23131 standard; protein; 3507 AA.  
 DE Bacterial polypeptide #5784.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.6%; Score 88; DB 8; Length 3507;  
Best Local Similarity 20.1%; Pred. No. 5.2e+02;  
RESULT 1363  
ID ABP43908 standard; protein; 4315 AA.  
DE MUC5B partial gene protein.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.6%; Score 88; DB 5; Length 4315;  
Best Local Similarity 23.8%; Pred. No. 6.9e+02;  
RESULT 1364  
ID ADL23265 standard; protein; 5703 AA.  
DE Human MUC5B.  
PN WO2004019041-A1.  
PD 04-NAR-2004.  
PA (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.  
PA (PACK/) PACKER N H.  
PA (KARL/) KARLSSON N.  
PA (SCHU/) SCHULZ B L.  
Query Match 5.6%; Score 88; DB 8; Length 5703;  
Best Local Similarity 23.8%; Pred. No. 1e+03;  
RESULT 1365  
ID AEB56507 standard; protein; 5858 AA.  
DE Radiochemotherapy response detection associated protein SEQ ID NO 82.  
PN WO2005073411-A1.  
PD 11-AUG-2005.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 5.6%; Score 88; DB 9; Length 5858;  
Best Local Similarity 23.8%; Pred. No. 1e+03;  
RESULT 1366  
ID AAG13468 standard; protein; 310 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12974.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.6%; Score 87.5; DB 3; Length 310;  
Best Local Similarity 23.2%; Pred. No. 21;  
RESULT 1367  
ID AAG13467 standard; protein; 331 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12973.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.6%; Score 87.5; DB 3; Length 331;  
Best Local Similarity 23.2%; Pred. No. 23;  
RESULT 1368  
ID AAY52525 standard; protein; 536 AA.  
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP.  
Query Match 5.6%; Score 87.5; DB 3; Length 536;  
Best Local Similarity 23.9%; Pred. No. 44;  
RESULT 1369  
ID AAU96329 standard; protein; 536 AA.  
DE Der HMW-map polypeptide #16.  
PN WO200222807-A2.  
PD 21-NAR-2002.  
PA (HESK-) HESKA CORP.  
Query Match 5.6%; Score 87.5; DB 5; Length 536;  
Best Local Similarity 23.9%; Pred. No. 44;  
RESULT 1370  
ID AAY52523 standard; protein; 555 AA.  
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP.  
Query Match 5.6%; Score 87.5; DB 3; Length 555;  
Best Local Similarity 23.9%; Pred. No. 46;  
RESULT 1371  
ID AAU96327 standard; protein; 555 AA.  
DE Der HMW-map polypeptide #14.

PN WO200222807-A2.  
PD 21-MAR-2002.  
PA (HESK-) HESKA CORP.  
Query Match 5.6%; Score 87.5; DB 5; Length 555;  
Best Local Similarity 23.9%; Pred. No. 46;  
RESULT 1372  
ID AAU96328 standard; protein; 555 AA.  
DE Der HMW-map polypeptide #15.  
PN WO200222807-A2.  
PD 21-MAR-2002.  
PA (HESK-) HESKA CORP.  
Query Match 5.6%; Score 87.5; DB 5; Length 555;  
Best Local Similarity 23.9%; Pred. No. 46;  
RESULT 1373  
ID ADB64946 standard; protein; 717 AA.  
DE Human protein encoded by clone PROST20036350.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.6%; Score 87.5; DB 7; Length 717;  
Best Local Similarity 17.8%; Pred. No. 66;  
RESULT 1374  
ID ADH71768 standard; protein; 904 AA.  
DE Human protein of the invention NOV28n SEQ ID NO:664.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.6%; Score 87.5; DB 8; Length 904;  
Best Local Similarity 23.8%; Pred. No. 90;  
RESULT 1375  
ID AAM16313 standard; protein; 906 AA.  
DE Yeast alpha factor-G-alpha protein fusion.  
PN WO9711159-A1.  
PD 27-MAR-1997.  
PA (HEAR-) HEARTLAND BIOTECHNOLOGIES LLC.  
Query Match 5.6%; Score 87.5; DB 2; Length 906;  
Best Local Similarity 19.7%; Pred. No. 91;  
RESULT 1376  
ID ADZ03664 standard; protein; 981 AA.  
DE PRG4-Lub:1 protein.  
PN WO2005016130-A2.  
PD 24-FEB-2005.  
PA (AMHP) WYETH.  
Query Match 5.6%; Score 87.5; DB 9; Length 981;  
Best Local Similarity 20.2%; Pred. No. 1e+02;  
RESULT 1377  
ID ADZ03672 standard; protein; 1038 AA.  
DE PRG4-Lub:3 protein.  
PN WO2005016130-A2.  
PD 24-FEB-2005.  
PA (AMHP) WYETH.  
Query Match 5.6%; Score 87.5; DB 9; Length 1038;  
Best Local Similarity 22.3%; Pred. No. 1.1e+02;  
RESULT 1378  
ID ADZ03676 standard; protein; 1069 AA.  
DE PRG4-Lub:4 protein.  
PN WO2005016130-A2.  
PD 24-FEB-2005.  
PA (AMHP) WYETH.  
Query Match 5.6%; Score 87.5; DB 9; Length 1069;  
Best Local Similarity 22.3%; Pred. No. 1.1e+02;  
RESULT 1379  
ID AAM54844 standard; protein; 1085 AA.  
DE Bovine parathyroid calcium receptor 1 protein 5Kb fragment.  
PN US5763569-A.  
PD 09-JUN-1998.  
PA (NPSF-) NPS PHARM INC.  
PA (BGHM) BRIGHAM & WOMEN'S HOSPITAL.  
Query Match 5.6%; Score 87.5; DB 2; Length 1085;  
Best Local Similarity 22.7%; Pred. No. 1.2e+02;  
RESULT 1380  
ID AAY41778 standard; protein; 1085 AA.

DE Bovine parathyroid calcium receptor 1 protein sequence.  
 PN US5962314-A.  
 PD 05-OCT-1999.  
 PA (NPSF-) NPS PHARM INC.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 5.6%; Score 87.5; DB 2; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.2e+02;  
 RESULT 1381  
 ID AAM9563 standard; protein; 1085 AA.  
 DE Bovine parathyroid calcium receptor BoPCar 1.  
 PN US5858684-A.  
 PD 12-JAN-1999.  
 PA (NPSF-) NPS PHARM INC.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 5.6%; Score 87.5; DB 2; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.2e+02;  
 RESULT 1382  
 ID AAY51825 standard; protein; 1085 AA.  
 DE Bovine calcium receptor BoPCar1 protein.  
 PN US6031003-A.  
 PD 29-FEB-2000.  
 PA (NPSF-) NPS PHARM INC.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 5.6%; Score 87.5; DB 3; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.2e+02;  
 RESULT 1383  
 ID AAB47820 standard; protein; 1085 AA.  
 DE BoPCar1.  
 PN US6313146-B1.  
 PD 06-NOV-2001.  
 PA (NPSF-) NPS PHARM INC.  
 Query Match 5.6%; Score 87.5; DB 5; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.2e+02;  
 RESULT 1384  
 ID ADJ93194 standard; protein; 1085 AA.  
 DE Bovine extracellular Ca-sensing receptor.  
 PN WO200296946-A1.  
 PD 05-DEC-2002.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 Query Match 5.6%; Score 87.5; DB 7; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.2e+02;  
 RESULT 1385  
 ID ADI40961 standard; protein; 1085 AA.  
 DE Bovine GPCR CASR.  
 PN US2004018976-A1.  
 PD 29-JAN-2004.  
 PA (FEDE/) FEDER J N.  
 PA (MINT/) MINTIER G.  
 PA (RAMA/) RAMANATHAN C S.  
 Query Match 5.6%; Score 87.5; DB 8; Length 1085;  
 Best Local Similarity 22.7%; Pred. No. 1.2e+02;  
 RESULT 1386  
 ID ADI41015 standard; protein; 1085 AA.  
 DE Bovine GPCR CASR #2.  
 PN US2004018976-A1.  
 PD 29-JAN-2004.  
 PA (FEDE/) FEDER J N.  
 PA (MINT/) MINTIER G.  
 PA (RAMA/) RAMANATHAN C S.  
 Query Match 5.6%; Score 87.5; DB 9; Length 1100;  
 Best Local Similarity 22.3%; Pred. No. 1.2e+02;  
 RESULT 1387  
 ID AD203680 standard; protein; 1100 AA.  
 DE PRG4-Lub-5 protein.  
 PN WO2005016130-A2.  
 PD 24-FEB-2005.  
 PA (AMHP ) WYETH.  
 Query Match 5.6%; Score 87.5; DB 9; Length 1100;  
 Best Local Similarity 22.3%; Pred. No. 1.2e+02;  
 RESULT 1388  
 ID ADS24007 standard; protein; 1322 AA.  
 DE Bacterial polypeptide #13040.  
 PN US2003233675-A1.

PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.6%; Score 87.5; DB 8; Length 1322;  
 Best Local Similarity 22.9%; Pred. No. 1.5e+02;  
 RESULT 1389  
 ID ADI72180 standard; protein; 2829 AA.  
 DE X. laevis mutated adenomatous polyposis coli (APC) protein.  
 PN WO2004018677-A1.  
 PD 04-MAR-2004.  
 PA (EISA ) EISAI CO LTD.  
 Query Match 5.6%; Score 87.5; DB 8; Length 2829;  
 Best Local Similarity 21.2%; Pred. No. 4.3e+02;  
 RESULT 1390  
 ID ADP44997 standard; protein; 235 AA.  
 DE Rat Protein CAA82313, SEQ ID NO 10428.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 Query Match 5.5%; Score 87; DB 7; Length 235;  
 Best Local Similarity 27.8%; Pred. No. 16;  
 RESULT 1391  
 ID AAY29082 standard; protein; 288 AA.  
 DE T. gondii immunogenic protein.  
 PN WO9932633-A1.  
 PD 01-JUL-1999.  
 PA (HESK-) HESKA CORP.  
 Query Match 5.5%; Score 87; DB 2; Length 288;  
 Best Local Similarity 29.7%; Pred. No. 21;  
 RESULT 1392  
 ID AAY29081 standard; protein; 288 AA.  
 DE T. gondii immunogenic protein.  
 PN WO9932633-A1.  
 PD 01-JUL-1999.  
 PA (HESK-) HESKA CORP.  
 Query Match 5.5%; Score 87; DB 2; Length 288;  
 Best Local Similarity 29.7%; Pred. No. 21;  
 RESULT 1393  
 ID AAU25553 standard; protein; 288 AA.  
 DE T. gondii immunogenic protein Ptg1397.  
 PN US2001014447-A1.  
 PD 16-AUG-2001.  
 PA (MILH/) MILHAUSEN M J.  
 Query Match 5.5%; Score 87; DB 4; Length 288;  
 Best Local Similarity 29.7%; Pred. No. 21;  
 RESULT 1394  
 ID AAU25552 standard; protein; 288 AA.  
 DE T. gondii immunogenic protein Ptg288.  
 PN US2001014447-A1.  
 PD 16-AUG-2001.  
 PA (MILH/) MILHAUSEN M J.  
 Query Match 5.5%; Score 87; DB 4; Length 288;  
 Best Local Similarity 29.7%; Pred. No. 21;  
 RESULT 1395  
 ID ADG17391 standard; protein; 288 AA.  
 DE T. gondii protein #79.  
 PN US2003194393-A1.  
 PD 16-OCT-2003.  
 PA (MILH/) MILHAUSEN M J.  
 Query Match 5.5%; Score 87; DB 7; Length 288;  
 Best Local Similarity 29.7%; Pred. No. 21;  
 RESULT 1396  
 ID ADG17394 standard; protein; 288 AA.  
 DE T. gondii protein #82.  
 PN US2003194393-A1.  
 PD 16-OCT-2003.  
 PA (MILH/) MILHAUSEN M J.  
 Query Match 5.5%; Score 87; DB 7; Length 288;  
 Best Local Similarity 29.7%; Pred. No. 21;  
 RESULT 1397  
 ID ADG17394 standard; protein; 288 AA.  
 DE T. gondii protein #82.  
 PN US2003194393-A1.  
 PD 16-OCT-2003.  
 PA (MILH/) MILHAUSEN M J.  
 Query Match 5.5%; Score 87; DB 7; Length 288;  
 Best Local Similarity 29.7%; Pred. No. 21;  
 RESULT 1398  
 ID ADS24007 standard; protein; 1322 AA.  
 DE Bacterial polypeptide #13040.  
 PN US2003233675-A1.

RESULT 1397  
ID ADJ76313 standard; protein; 363 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1565.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 5.5%; Score 87; DB 8; Length 363;  
Best Local Similarity 25.3%; Pred. No. 29;  
RESULT 1398  
ID ADY37611 standard; protein; 363 AA.  
DE Lung cancer related protein, SEQ ID 87.  
PN US2005048589-A1.  
PD 03-MAR-2005.  
PA (JEND/) JENDOUBI M.  
Query Match 5.5%; Score 87; DB 9; Length 363;  
Best Local Similarity 25.3%; Pred. No. 29;  
RESULT 1399  
ID AAR01940 standard; protein; 417 AA.  
DE Tumour necrosis factor.  
PN JP01285191-A.  
PD 16-NOV-1989.  
PA (GREC) GREEN CROSS CORP.  
Query Match 5.5%; Score 87; DB 2; Length 417;  
Best Local Similarity 23.6%; Pred. No. 35;  
RESULT 1400  
ID ADX91714 standard; protein; 611 AA.  
DE Plant full length insert polypeptide seqid 54378.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 5.5%; Score 87; DB 8; Length 611;  
Best Local Similarity 21.8%; Pred. No. 59;  
RESULT 1401  
ID AAG83274 standard; protein; 631 AA.  
DE Chlamydia trachomatis PmpH(N-term) fusion protein.  
PN WO200140474-A2.  
PD 07-JUN-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.5%; Score 87; DB 4; Length 631;  
Best Local Similarity 28.1%; Pred. No. 62;  
RESULT 1402  
ID ABB94245 standard; protein; 631 AA.  
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.  
PN WO200208267-A2.  
PD 31-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 5.5%; Score 87; DB 5; Length 631;  
Best Local Similarity 28.1%; Pred. No. 62;  
RESULT 1403  
ID ADD2755 standard; protein; 664 AA.  
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.  
PN WO2003041560-A2.  
PD 22-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.5%; Score 87; DB 7; Length 664;  
Best Local Similarity 28.1%; Pred. No. 66;  
RESULT 1404  
ID AAR60563 standard; protein; 862 AA.  
DE Yeast 2.6 kD agglutination gene FLO1S.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SABP) SAPPORO BREWERIES.  
PA (PANI-) PANIMOLABORATORIO BRYGERILABORATORIUM.  
Query Match 5.5%; Score 87; DB 2; Length 862;  
Best Local Similarity 19.1%; Pred. No. 94;  
RESULT 1405  
ID AAR58754 standard; protein; 894 AA.  
DE S. cerevisiae FLO1.  
Query Match 5.5%; Score 87; DB 2; Length 1537;  
Best Local Similarity 19.1%; Pred. No. 2.1e+02;  
PN WO9418330-A1.  
PD 18-AUG-1994.  
PA (UNIL) UNILEVER PLC.  
PA (UNIL) UNILEVER NV.  
Query Match 5.5%; Score 87; DB 2; Length 894;  
Best Local Similarity 19.1%; Pred. No. 99;  
RESULT 1406  
ID AAR47578 standard; protein; 894 AA.  
DE Flocculation protein of Saccharomyces cerevisiae.  
PN WO9401567-A1.  
PD 20-JAN-1994.  
PA (UNIL) UNILEVER PLC.  
PA (UNIL) UNILEVER NV.  
Query Match 5.5%; Score 87; DB 2; Length 894;  
Best Local Similarity 19.1%; Pred. No. 99;  
RESULT 1407  
ID AAU38901 standard; protein; 1016 AA.  
DE C. trachomatis CT872 protein.  
PN WO200181379-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.5%; Score 87; DB 4; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.2e+02;  
RESULT 1408  
ID ABG91037 standard; protein; 1016 AA.  
DE Chlamydia trachomatis outer membrane protein H protein.  
PN WO200262380-A2.  
PD 15-AUG-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 5.5%; Score 87; DB 5; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.2e+02;  
RESULT 1409  
ID ADD42682 standard; protein; 1016 AA.  
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.  
PN WO2003041560-A2.  
PD 22-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.5%; Score 87; DB 7; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.2e+02;  
RESULT 1410  
ID ADD43800 standard; protein; 1016 AA.  
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 95.  
PN WO2003049762-A2.  
PD 19-JUN-2003.  
PA (CHIR-) CHIRON SPA.  
Query Match 5.5%; Score 87; DB 7; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.2e+02;  
RESULT 1411  
ID ADW29028 standard; protein; 1016 AA.  
DE C trachomatis polymorphic membrane protein (PmpH) Seq 22.  
PN WO2005002619-A2.  
PD 13-JAN-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 5.5%; Score 87; DB 9; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.2e+02;  
RESULT 1412  
ID AEA19092 standard; protein; 1016 AA.  
DE Chlamydia trachomatis protein - SEQ ID 95.  
PN US2005106162-A1.  
PD 19-MAY-2005.  
PA (GRAN/) GRANDI G.  
PA (RATT/) RATTI G.  
Query Match 5.5%; Score 87; DB 9; Length 1016;  
Best Local Similarity 28.1%; Pred. No. 1.2e+02;  
RESULT 1413  
ID AAR60562 standard; protein; 1537 AA.  
DE Yeast 4.7 kD agglutination gene FLO1L.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SABP) SAPPORO BREWERIES.  
PA (PANI-) PANIMOLABORATORIO BRYGERILABORATORIUM.  
Query Match 5.5%; Score 87; DB 2; Length 1537;  
Best Local Similarity 19.1%; Pred. No. 2.1e+02;

RESULT 1414  
ID ADP87475 standard; protein; 1537 AA.  
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.  
PN WO2004057033-A1.  
PD 08-JUL-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
Query Match 5.5%; Score 87; DB 8; Length 1537;  
Best Local Similarity 19.1%; Pred. No. 2.1e+02;  
RESULT 1415  
ID ADN18745 standard; protein; 1537 AA.  
DE Bacterial polypeptide #1398.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.5%; Score 87; DB 8; Length 1537;  
Best Local Similarity 19.1%; Pred. No. 2.1e+02;  
RESULT 1416  
ID ABB67362 standard; protein; 1575 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28878.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 5.5%; Score 87; DB 4; Length 1575;  
Best Local Similarity 20.5%; Pred. No. 2.2e+02;  
RESULT 1417  
ID AAU39177 standard; protein; 238 AA.  
DE Propionibacterium acnes immunogenic protein #73.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.5%; Score 86.5; DB 4; Length 238;  
Best Local Similarity 22.7%; Pred. No. 18;  
RESULT 1418  
ID ABM35696 standard; protein; 238 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #372.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.5%; Score 86.5; DB 6; Length 238;  
Best Local Similarity 22.7%; Pred. No. 18;  
RESULT 1419  
ID AAP91941 standard; peptide; 400 AA.  
DE Sequence of preprospasmolysin.  
PN DE3808456-A.  
PD 28-SEP-1989.  
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
Query Match 5.5%; Score 86.5; DB 1; Length 400;  
Best Local Similarity 30.8%; Pred. No. 37;  
RESULT 1420  
ID AAR69555 standard; protein; 410 AA.  
DE Human lysosomal membrane sialoglycoprotein lamp-2.  
PN WO9429342-A1.  
PD 22-DEC-1994.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 5.5%; Score 86.5; DB 2; Length 410;  
Best Local Similarity 20.7%; Pred. No. 38;  
RESULT 1421  
ID ADN19290 standard; protein; 503 AA.  
DE Bacterial polypeptide #1943.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.5%; Score 86.5; DB 8; Length 503;  
Best Local Similarity 22.1%; Pred. No. 50;  
RESULT 1422  
ID ADM48341 standard; protein; 681 AA.  
DE Marburg virus glycoprotein, GP.  
PN US2003215794-A1.  
PD 20-NOV-2003.  
PA (KAWA/) KAWAOKA Y.  
PA (JASE/) JASENOSKY L D.  
PA (NEUM/) NEUMANN G.  
Query Match 5.5%; Score 86.5; DB 8; Length 681;  
Best Local Similarity 19.2%; Pred. No. 76;  
RESULT 1423  
ID ABU25742 standard; protein; 687 AA.  
DE Protein encoded by Prokaryotic essential gene #11269.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.5%; Score 86.5; DB 6; Length 687;  
Best Local Similarity 23.2%; Pred. No. 77;  
RESULT 1424  
ID ABG15647 standard; protein; 714 AA.  
DE Novel human diagnostic protein #15638.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.5%; Score 86.5; DB 4; Length 714;  
Best Local Similarity 18.2%; Pred. No. 81;  
RESULT 1425  
ID ABG15147 standard; protein; 714 AA.  
DE Novel human diagnostic protein #15138.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.5%; Score 86.5; DB 4; Length 714;  
Best Local Similarity 18.2%; Pred. No. 81;  
RESULT 1426  
ID AAY54466 standard; protein; 788 AA.  
DE Amino acid sequence of intestinal insect mucin isoform IIM14.  
PN WO9967373-A2.  
PD 29-DEC-1999.  
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.  
Query Match 5.5%; Score 86.5; DB 3; Length 788;  
Best Local Similarity 27.2%; Pred. No. 93;  
RESULT 1427  
ID AAY54467 standard; protein; 807 AA.  
DE Amino acid sequence of intestinal insect mucin isoform IIM22.  
PN WO9967373-A2.  
PD 29-DEC-1999.  
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.  
Query Match 5.5%; Score 86.5; DB 3; Length 807;  
Best Local Similarity 27.2%; Pred. No. 96;  
RESULT 1428  
ID ADA14416 standard; protein; 1579 AA.  
DE Mouse spermatogenesis related protein sequence SEQ ID NO:158.  
PN WO2003068969-A1.  
PD 21-AUG-2003.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 5.5%; Score 86.5; DB 6; Length 1579;  
Best Local Similarity 21.1%; Pred. No. 2.4e+02;  
RESULT 1429  
ID ADT07505 standard; protein; 2109 AA.  
DE Human colon-specific polypeptide (CSP) #22.  
PN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 5.5%; Score 86.5; DB 8; Length 2109;  
Best Local Similarity 26.1%; Pred. No. 3.6e+02;  
RESULT 1430  
ID ADT07506 standard; protein; 2254 AA.  
DE Human colon-specific polypeptide (CSP) #23.  
PN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 5.5%; Score 86.5; DB 8; Length 2254;

Best Local Similarity 26.1%; Pred. No. 3.9e+02;  
RESULT 1431  
ID ADT07507 standard; protein; 2401 AA.  
DE Human colon-specific polypeptide (CSP) #24.  
PN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 5.5%; Score 86.5; DB 8; Length 2401;  
Best Local Similarity 26.1%; Pred. No. 4.3e+02;  
RESULT 1432  
ID AAY57453 standard; protein; 2781 AA.  
DE Human transcriptional regulatory factor SEQ ID NO:10.  
PN WO957143-A1.  
PD 11-NOV-1999.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.5%; Score 86.5; DB 3; Length 2781;  
Best Local Similarity 20.8%; Pred. No. 5.2e+02;  
RESULT 1433  
ID ADF42724 standard; protein; 2781 AA.  
DE Human BTF amino acid sequence SEQ ID NO:30.  
PN WO2003102163-A2.  
PD 11-DEC-2003.  
PA (META-) METABOLEX INC.  
Query Match 5.5%; Score 86.5; DB 8; Length 2781;  
Best Local Similarity 20.8%; Pred. No. 5.2e+02;  
RESULT 1434  
ID ADO00984 standard; protein; 2781 AA.  
DE Human homologue of Fruit fly AD-related protein CG171135.  
PN US2004067535-A1.  
PD 08-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Query Match 5.5%; Score 86.5; DB 8; Length 2781;  
Best Local Similarity 20.8%; Pred. No. 5.2e+02;  
RESULT 1435  
ID ADQ18653 standard; protein; 2781 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1472.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.5%; Score 86.5; DB 8; Length 2781;  
Best Local Similarity 20.8%; Pred. No. 5.2e+02;  
RESULT 1436  
ID AAY57452 standard; protein; 2907 AA.  
DE Human transcriptional regulatory factor SEQ ID NO:1.  
PN WO957143-A1.  
PD 11-NOV-1999.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.5%; Score 86.5; DB 3; Length 2907;  
Best Local Similarity 20.8%; Pred. No. 5.6e+02;  
RESULT 1437  
ID ABM82857 standard; protein; 476 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3106.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 5.5%; Score 86; DB 8; Length 476;  
Best Local Similarity 32.1%; Pred. No. 52;  
RESULT 1438  
ID ABM83144 standard; protein; 476 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3393.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 5.5%; Score 86; DB 8; Length 476;  
Best Local Similarity 32.1%; Pred. No. 52;  
RESULT 1439  
ID AAB98978 standard; protein; 551 AA.  
DE Rabbit FCLPL.  
PN WO200134797-A1.  
PD 17-MAY-2001.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 5.5%; Score 86; DB 4; Length 551;  
Best Local Similarity 26.4%; Pred. No. 64;

RESULT 1440  
ID ADD18594 standard; protein; 601 AA.  
DE Human disease related protein SeqID25.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 5.5%; Score 86; DB 7; Length 601;  
Best Local Similarity 22.0%; Pred. No. 72;  
RESULT 1441  
ID AAY05477 standard; protein; 750 AA.  
DE C. albicans Rbt1 protein sequence.  
PN WO9918115-A1.  
PD 15-APR-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 5.5%; Score 86; DB 2; Length 750;  
Best Local Similarity 23.4%; Pred. No. 97;  
RESULT 1442  
ID ADX76173 standard; protein; 857 AA.  
DE Plant full length insert polypeptide seqid 45539.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOV/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TAB/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 5.5%; Score 86; DB 8; Length 857;  
Best Local Similarity 22.1%; Pred. No. 1.2e+02;  
RESULT 1443  
ID ADB79822 standard; protein; 1080 AA.  
DE Mouse putative deubiquitinating enzyme 8, SEQ ID 62.  
PN EPI279744-A2.  
PD 29-JAN-2003.  
PA (WARN) WARNER LAMBERT CO.  
Query Match 5.5%; Score 86; DB 7; Length 1080;  
Best Local Similarity 20.2%; Pred. No. 1.6e+02;  
RESULT 1444  
ID ABG28388 standard; protein; 1086 AA.  
DE Novel human diagnostic protein #28379.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.5%; Score 86; DB 4; Length 1086;  
Best Local Similarity 19.8%; Pred. No. 1.6e+02;  
RESULT 1445  
ID ABG05675 standard; protein; 1190 AA.  
DE Novel human diagnostic protein #5666.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.5%; Score 86; DB 4; Length 1190;  
Best Local Similarity 19.8%; Pred. No. 1.8e+02;  
RESULT 1446  
ID AAG23116 standard; protein; 193 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26303.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 5.4%; Score 85.5; DB 3; Length 193;  
Best Local Similarity 20.9%; Pred. No. 17;  
RESULT 1447  
ID AAG23115 standard; protein; 199 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26302.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 5.4%; Score 85.5; DB 3; Length 199;  
Best Local Similarity 20.9%; Pred. No. 18;  
RESULT 1448  
ID AAB09826 standard; protein; 346 AA.  
DE Endoglucanase protein sequence 6.  
PN WO200024879-A1.  
PD 04-MAY-2000.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.



Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 3; Length 346;  
RESULT 1449  
ID AAOI5057 standard; protein; 346 AA.  
DE Phycomyces nitens endoglucanase-related protein.  
PN WO200242474-A1.  
PD 30-MAY-2002.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 5; Length 346;  
RESULT 1450  
ID ABB08065 standard; protein; 346 AA.  
DE P. nitens CP99002 PCEI protein.  
PN WO200238754-A1.  
PD 16-MAY-2002.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 5; Length 346;  
RESULT 1451  
ID ADA37114 standard; protein; 346 AA.  
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.  
PN WO2003052105-A1.  
PD 26-JUN-2003.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 6; Length 346;  
RESULT 1452  
ID AAR57350 standard; protein; 354 AA.  
DE Human cartilage link protein.  
PN WO9415627-A1.  
PD 21-JUL-1994.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 2; Length 354;  
RESULT 1453  
ID AB93134 standard; protein; 649 AA.  
DE Herbicidally active polypeptide SEQ ID NO 2345.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 5; Length 649;  
RESULT 1454  
ID ABB78250 standard; protein; 652 AA.  
DE Amino acid sequence of a human heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 5; Length 652;  
RESULT 1455  
ID ABU15839 standard; protein; 686 AA.  
DE Protein encoded by Prokaryotic essential gene #1366.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 6; Length 686;  
RESULT 1456  
ID ADN47243 standard; protein; 695 AA.  
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1121.  
PN WO2004022736-A1.  
PD 18-MAR-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 8; Length 695;  
RESULT 1457  
ID ADD47689 standard; protein; 780 AA.  
DE Human Protein XP\_027074, SEQ ID NO 13385.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.

Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 7; Length 780;  
RESULT 1458  
ID ADD47692 standard; protein; 780 AA.  
DE Human Protein XP\_027074, SEQ ID NO 13388.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 7; Length 780;  
RESULT 1459  
ID AAB07743 standard; protein; 781 AA.  
DE A snake venom protease (SVPH-4) polypeptide variant SVPH-4b.  
PN WO200403525-A2.  
PD 27-JUL-2000.  
PA (IMNV) IMMUNEX CORP.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 3; Length 781;  
RESULT 1460  
ID ADE71292 standard; protein; 781 AA.  
DE Novel human protein #46.  
PN JP2002345493-A.  
PD 03-DEC-2002.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 7; Length 781;  
RESULT 1461  
ID ABB78248 standard; protein; 841 AA.  
DE Amino acid sequence of a zebrafish heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 5; Length 841;  
RESULT 1462  
ID ABB71012 standard; protein; 843 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 4; Length 843;  
RESULT 1463  
ID ABB78249 standard; protein; 977 AA.  
DE Amino acid sequence of a zebrafish heart of glass polypeptide.  
PN WO200262205-A2.  
PD 15-AUG-2002.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 5; Length 977;  
RESULT 1464  
ID ABU54710 standard; protein; 1784 AA.  
DE Human CA125 protein amino terminal sequence.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 6; Length 1784;  
RESULT 1465  
ID ABU54858 standard; protein; 1794 AA.  
DE Human CA125 amino terminal domain.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match  
Best Local Similarity 5.4%; Score 85.5; DB 6; Length 1794;  
RESULT 1466  
ID ABU54707 standard; protein; 1821 AA.  
DE Human CA125 amino terminal domain.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.

Query Match 5.4%; Score 85.5; DB 6; Length 1821;  
Best Local Similarity 27.2%; Pred. No. 3.7e+02;  
RESULT 1467  
ID ADE40509 standard; protein; 2055 AA.  
DE Human nuclear receptor coactivator ARAP3.  
PN DE10135787-A1.  
PD 13-FEB-2003.  
PA (JENP ) JENAPHARM GMBH & CO KG.  
Query Match 5.4%; Score 85.5; DB 8; Length 2055;  
Best Local Similarity 20.5%; Pred. No. 4.3e+02;  
RESULT 1468  
ID ABG95034 standard; protein; 2311 AA.  
DE Human translocation (4; 11)(q21; q23) protein #1.  
PN WO200269900-A2.  
PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Query Match 5.4%; Score 85.5; DB 5; Length 2311;  
Best Local Similarity 24.3%; Pred. No. 5.1e+02;  
RESULT 1469  
ID AEB29721 standard; protein; 2448 AA.  
DE Human Mucin 5 (subtypes A and C).  
PN WO2005067667-A2.  
PD 28-JUL-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 5.4%; Score 85.5; DB 9; Length 2448;  
Best Local Similarity 24.8%; Pred. No. 5.5e+02;  
RESULT 1470  
ID ABG31317 standard; protein; 2586 AA.  
DE Human 5+3 corrected OCP protein.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.4%; Score 85.5; DB 5; Length 2586;  
Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1471  
ID ABG32891 standard; protein; 2586 AA.  
DE Human osteoclast protein (OCP) #1.  
PN US2002086825-A1.  
PD 04-JUL-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 5.4%; Score 85.5; DB 5; Length 2586;  
Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1472  
ID ADL02231 standard; protein; 2586 AA.  
DE Human OCP protein #1.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.4%; Score 85.5; DB 8; Length 2586;  
Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1473  
ID ADL02234 standard; protein; 2586 AA.  
DE Human OCP protein #2.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.4%; Score 85.5; DB 8; Length 2586;  
Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1474  
ID AAB47935 standard; protein; 2587 AA.  
DE Human OCP.  
PN US2002022026-A1.  
PD 21-FEB-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 5.4%; Score 85.5; DB 5; Length 2587;

Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1475  
ID ABG32896 standard; protein; 2587 AA.  
DE Human osteoclast protein (OCP) #2.  
PN US2002086825-A1.  
PD 04-JUL-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 5.4%; Score 85.5; DB 5; Length 2587;  
Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1476  
ID ADL02236 standard; protein; 2587 AA.  
DE Human OCP protein #3.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.4%; Score 85.5; DB 8; Length 2587;  
Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1477  
ID ABG31323 standard; protein; 2589 AA.  
DE Human OCP protein.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.4%; Score 85.5; DB 5; Length 2589;  
Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1478  
ID ADL02244 standard; protein; 2589 AA.  
DE Human OCP protein #5.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 5.4%; Score 85.5; DB 8; Length 2589;  
Best Local Similarity 25.8%; Pred. No. 5.9e+02;  
RESULT 1479  
ID AAE34702 standard; protein; 5877 AA.  
DE Human mucin (MUC-16B).  
PN WO200292836-A2.  
PD 21-NOV-2002.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match 5.4%; Score 85.5; DB 6; Length 5877;  
Best Local Similarity 27.2%; Pred. No. 1.8e+03;  
RESULT 1480  
ID ABU54721 standard; protein; 11721 AA.  
DE Human CAL25 full length protein sequence.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 5.4%; Score 85.5; DB 6; Length 11721;  
Best Local Similarity 27.2%; Pred. No. 4.7e+03;  
RESULT 1481  
ID ADP84155 standard; protein; 22157 AA.  
DE Human CAL25 protein sequence SeqID 5.  
PN WO2004045553-A2.  
PD 03-JUN-2004.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 5.4%; Score 85.5; DB 8; Length 22157;  
Best Local Similarity 27.2%; Pred. No. 1.1e+04;  
RESULT 1482  
ID AAB39253 standard; protein; 280 AA.  
DE Gene 15 human secreted protein homologous amino acid sequence #133.  
PN WO200056754-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.4%; Score 85; DB 3; Length 280;  
Best Local Similarity 23.2%; Pred. No. 31;  
RESULT 1483  
ID ABM91067 standard; protein; 318 AA.  
DE M. xanthus protein sequence, seq id 10266.  
PN US6833447-B1.

PD 21-DEC-2004.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Query Match 5.4%; Score 85; DB 9; Length 318;  
Best Local Similarity 23.7%; Pred. No. 37;  
RESULT 1484  
ID ABB71546 standard; protein; 326 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 41430.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.4%; Score 85; DB 4; Length 326;  
Best Local Similarity 22.8%; Pred. No. 39;  
RESULT 1485  
ID ADQ25899 standard; protein; 472 AA.  
DE B amyloliquefaciens dipeptide synthesising protein SEQ ID NO: 7.  
PN EPI433791-A2.  
PD 30-JUN-2004.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 5.4%; Score 85; DB 8; Length 472;  
Best Local Similarity 20.3%; Pred. No. 64;  
RESULT 1486  
ID ADZ77694 standard; protein; 472 AA.  
DE Bacillus amyloliquefaciens IF03022 bacilysin synthetase enzyme Seq 25.  
PN EPI529837-A2.  
PD 11-MAY-2005.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 5.4%; Score 85; DB 9; Length 472;  
Best Local Similarity 20.3%; Pred. No. 64;  
RESULT 1487  
ID AEM61455 standard; protein; 472 AA.  
DE Dipeptide production microorganism protein, SEQ ID 7.  
PN WO2005052153-A1.  
PD 09-JUN-2005.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 5.4%; Score 85; DB 9; Length 472;  
Best Local Similarity 20.3%; Pred. No. 64;  
RESULT 1488  
ID ADV95930 standard; protein; 503 AA.  
DE Mouse stimulator of endothelial proliferation, mSEP.  
PN WO2004111085-A1.  
PD 23-DEC-2004.  
PA (XANT-) XANTOS BIOMEDICINE AG.  
Query Match 5.4%; Score 85; DB 9; Length 503;  
Best Local Similarity 23.0%; Pred. No. 70;  
RESULT 1489  
ID ADW43164 standard; protein; 503 AA.  
DE House mouse membrane-bound angiogenic factor SEP protein.  
PN WO2004111088-A2.  
PD 23-DEC-2004.  
PA (XANT-) XANTOS BIOMEDICINE AG.  
Query Match 5.4%; Score 85; DB 9; Length 503;  
Best Local Similarity 23.0%; Pred. No. 70;  
RESULT 1490  
ID ABR53289 standard; protein; 576 AA.  
DE Protein sequence #SEQ ID 1443.  
PN EPI258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 5.4%; Score 85; DB 6; Length 576;  
Best Local Similarity 21.0%; Pred. No. 84;  
RESULT 1491  
ID ADK63572 standard; protein; 576 AA.  
DE Disease treating protein complex-derived protein #867.  
PN EPI338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 5.4%; Score 85; DB 7; Length 576;  
Best Local Similarity 21.0%; Pred. No. 84;  
RESULT 1492  
ID ABB55236 standard; protein; 627 AA.  
DE Lactococcus lactis protein yffc.  
PN FR2807446-A1.  
PD 12-OCT-2001.

PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 5.4%; Score 85; DB 5; Length 627;  
Best Local Similarity 21.5%; Pred. No. 95;  
RESULT 1493  
ID ADS29466 standard; protein; 627 AA.  
DE Bacterial polypeptide #18499.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.4%; Score 85; DB 8; Length 627;  
Best Local Similarity 21.5%; Pred. No. 95;  
RESULT 1494  
ID ADX95894 standard; protein; 635 AA.  
DE Plant full length insert polypeptide seqid 58558.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 5.4%; Score 85; DB 8; Length 635;  
Best Local Similarity 23.3%; Pred. No. 96;  
RESULT 1495  
ID ADA55053 standard; protein; 637 AA.  
DE Human protein, SEQ ID 2621.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.4%; Score 85; DB 6; Length 637;  
Best Local Similarity 21.7%; Pred. No. 97;  
RESULT 1496  
ID AAB29654 standard; protein; 667 AA.  
DE Human membrane-associated protein HUMAP-11.  
PN WO200065054-A2.  
PD 02-NOV-2000.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.4%; Score 85; DB 3; Length 667;  
Best Local Similarity 21.7%; Pred. No. 1e+02;  
RESULT 1497  
ID ADU06855 standard; protein; 674 AA.  
DE Cell adhesion and extracellular matrix protein clone 7520409CD1.  
PN WO2004094623-A2.  
PD 04-NOV-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 5.4%; Score 85; DB 8; Length 674;  
Best Local Similarity 22.4%; Pred. No. 1e+02;  
RESULT 1498  
ID ADT56202 standard; protein; 782 AA.  
DE Plant polypeptide, SEQ ID 6279.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match 5.4%; Score 85; DB 8; Length 782;  
Best Local Similarity 19.7%; Pred. No. 1.3e+02;  
RESULT 1499  
ID ABB60387 standard; protein; 1049 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7953.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.4%; Score 85; DB 4; Length 1049;  
Best Local Similarity 22.1%; Pred. No. 1.9e+02;  
RESULT 1500  
ID AAU14240 standard; protein; 1061 AA.  
DE Human novel protein #111.  
PN WO200155437-A2.

PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC. 5.4%; Score 85; DB 4; Length 1061;  
Query Match 20.2%; Pred. No. 1.9e+02;  
Best Local Similarity

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OM protein - protein search, using sw model

Run on: March 20, 2006, 14:13:31 ; Search time 51.9623 Seconds  
(without alignments) 2460.550 Million cell updates/sec

Perfect score: 1575  
Sequence: 1 TRLLVQCSLRABELSIQVSC.....NPESKSPKSTTVRCLEAV 306

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100\$  
Listing first 1500 summaries

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Database : Published Applications_AA_Main.*
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6: /csn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
3	1575	100.0	322	3	US-09-905-291A-201	Sequence 201, App	
93	1575	100.0	322	4	US-10-223-085-32	Sequence 32, Appl	
94	1575	100.0	322	4	US-10-223-084-32	Sequence 32, Appl	
95	1575	100.0	322	4	US-10-223-080-32	Sequence 32, Appl	
96	1575	100.0	322	4	US-10-223-090-32	Sequence 32, Appl	
98	1575	100.0	322	4	US-10-223-087-32	Sequence 32, Appl	
101	1575	100.0	322	4	US-10-223-083-32	Sequence 32, Appl	
102	1575	100.0	322	4	US-10-079-111-1	Sequence 1, Appl	
103	1575	100.0	322	4	US-10-223-089-32	Sequence 32, Appl	
108	1575	100.0	322	4	US-10-298-976-201	Sequence 201, App	
136	1575	100.0	322	4	US-10-063-742-6	Sequence 6, Appl	
211	1575	100.0	322	4	US-10-299-937-201	Sequence 201, App	
214	1575	100.0	322	4	US-10-223-081-32	Sequence 32, Appl	
224	1575	100.0	322	4	US-10-223-082-32	Sequence 32, Appl	
230	1575	100.0	322	4	US-10-298-993-201	Sequence 201, App	
231	1575	100.0	322	4	US-10-305-654-32	Sequence 32, Appl	
232	1575	100.0	322	4	US-10-448-923-201	Sequence 201, App	
233	1575	100.0	322	4	US-10-443-656-201	Sequence 201, App	
234	1575	100.0	322	4	US-10-448-713-201	Sequence 201, App	
235	1575	100.0	322	4	US-10-425-447-201	Sequence 201, App	
236	1575	100.0	322	4	US-10-081-056-32	Sequence 32, Appl	
238	1575	100.0	322	4	US-10-215-371-201	Sequence 201, App	
239	1575	100.0	322	4	US-10-797-366-201	Sequence 201, App	
240	1575	100.0	322	4	US-10-771-187-201	Sequence 201, App	
241	1575	100.0	322	5	US-10-972-317-6	Sequence 6, Appl	
242	1575	100.0	322	5	US-10-963-467-201	Sequence 201, App	
243	1575	100.0	322	5	US-10-978-255-201	Sequence 201, App	
244	1575	100.0	322	5	US-10-820-474A-64	Sequence 64, Appl	

318	199.5	12.7	493	5	US-10-473-127-1301	Sequence 1301, Ap	391	131	8.3	649	4	US-10-189-123-63	Sequence 63, Appl
319	199.5	12.7	493	5	US-10-473-127-1303	Sequence 1303, Ap	392	131	8.3	649	4	US-10-188-495-63	Sequence 63, Appl
320	199.5	12.7	493	5	US-10-473-127-1305	Sequence 1305, Ap	393	131	8.3	649	4	US-10-741-790-333	Sequence 333, App
321	199.5	12.7	493	6	US-11-037-713-34	Sequence 34, Appl	394	131	8.3	671	3	US-09-759-130B-331	Sequence 331, App
322	199.5	12.7	700	4	US-10-012-969C-2	Sequence 2, Appli	395	131	8.3	671	4	US-10-189-123-61	Sequence 61, Appl
323	199	12.6	338	5	US-10-473-127-1271	Sequence 1271, Ap	396	131	8.3	671	4	US-10-188-495-61	Sequence 61, Appl
324	199	12.6	338	5	US-10-473-127-1315	Sequence 1315, Ap	397	131	8.3	671	4	US-10-741-790-331	Sequence 331, App
325	198	12.6	395	5	US-10-473-127-1281	Sequence 1281, Ap	406	131	8.3	911	4	US-10-237-535-52	Sequence 52, Appl
326	197	12.5	719	5	US-10-473-127-1270	Sequence 1270, Ap	415	131	8.3	911	4	US-10-239-196-52	Sequence 52, Appl
327	197	12.5	719	5	US-10-473-127-1316	Sequence 1316, Ap	506	131	8.3	911	4	US-10-312-352-24	Sequence 24, Appl
328	196.5	12.5	535	4	US-10-741-601-336	Sequence 336, App	507	131	8.3	911	5	US-10-936-626-89	Sequence 89, Appl
329	196.5	12.5	535	5	US-10-741-600-1044	Sequence 1044, Ap	508	131	8.3	911	5	US-10-938-061-89	Sequence 89, Appl
330	196.5	12.5	699	5	US-10-473-127-1274	Sequence 1274, Ap	509	131	8.3	911	5	US-10-983-340-21	Sequence 21, Appl
331	196.5	12.5	699	5	US-10-473-127-1280	Sequence 1280, Ap	510	130.5	8.3	883	3	US-09-759-130B-342	Sequence 342, App
332	196.5	12.5	699	5	US-10-473-127-1313	Sequence 1313, Ap	511	130.5	8.3	883	3	US-10-195-970-6	Sequence 6, Appli
333	196.5	12.5	699	5	US-10-696-639-71	Sequence 71, Appl	512	130.5	8.3	883	4	US-10-189-123-72	Sequence 72, Appl
334	196	12.4	293	5	US-10-473-127-1277	Sequence 1277, Ap	513	130.5	8.3	883	4	US-10-188-495-72	Sequence 72, Appl
335	196	12.4	294	5	US-10-473-127-1290	Sequence 1290, Ap	514	130.5	8.3	883	4	US-10-453-420-6	Sequence 6, Appli
336	196	12.4	294	5	US-10-473-127-1312	Sequence 1312, Ap	515	130.5	8.3	883	4	US-10-741-790-342	Sequence 342, App
337	196	12.4	395	4	US-10-741-601-345	Sequence 345, App	516	130.5	8.3	1082	4	US-10-264-237-2725	Sequence 2725, Ap
338	196	12.4	395	5	US-10-741-600-1052	Sequence 1052, Ap	517	130.5	8.3	2316	5	US-10-287-436A-566	Sequence 566, App
339	196	12.4	425	4	US-10-741-601-337	Sequence 337, App	518	129.5	8.2	457	5	US-10-960-275-5	Sequence 5, Appli
340	196	12.4	425	5	US-10-741-600-1045	Sequence 1045, Ap	519	129.5	8.2	2157	5	US-10-960-275-2	Sequence 2, Appli
341	196	12.4	493	4	US-10-741-601-343	Sequence 343, App	520	129.5	8.2	2570	4	US-10-028-248A-42	Sequence 42, Appl
342	196	12.4	493	5	US-10-741-600-1051	Sequence 1051, Ap	521	129.5	8.2	2570	4	US-10-107-782-42	Sequence 42, Appl
343	194.5	12.3	742	5	US-10-450-763-47430	Sequence 47430, A	522	128.5	8.2	95	5	US-10-473-127-1291	Sequence 1291, Ap
344	191.5	12.2	676	5	US-10-473-127-1268	Sequence 1268, Ap	523	128	8.1	2212	4	US-10-028-248A-43	Sequence 43, Appl
345	191.5	12.2	676	5	US-10-473-127-1318	Sequence 1318, Ap	524	128	8.1	2212	4	US-10-107-782-43	Sequence 43, Appl
346	191	12.1	271	5	US-10-473-127-1272	Sequence 1272, Ap	525	127.5	8.1	671	3	US-09-983-000A-14	Sequence 14, Appl
347	191	12.1	271	5	US-10-473-127-1314	Sequence 1314, Ap	526	127.5	8.1	671	5	US-10-652-981-14	Sequence 14, Appl
348	191	12.1	470	5	US-10-473-127-1269	Sequence 1269, Ap	527	127.5	8.1	671	5	US-10-936-626-90	Sequence 90, Appl
349	191	12.1	470	5	US-10-473-127-1317	Sequence 1317, Ap	528	127.5	8.1	671	5	US-10-938-061-90	Sequence 90, Appl
350	187	11.9	112	5	US-10-487-620-2	Sequence 2, Appli	529	127.5	8.1	671	5	US-10-852-335A-97	Sequence 97, Appl
351	186.5	11.8	113	5	US-10-487-620-6	Sequence 6, Appli	530	127.5	8.1	911	4	US-10-453-420-8	Sequence 8, Appli
352	185	11.7	112	5	US-10-487-620-8	Sequence 8, Appli	531	127.5	8.1	911	4	US-10-295-027-260	Sequence 260, App
353	183	11.6	112	5	US-10-487-620-10	Sequence 10, Appl	532	127	8.1	277	4	US-10-295-027-294	Sequence 294, App
354	182	11.6	112	5	US-10-487-620-4	Sequence 4, Appli	533	127	8.1	277	4	US-10-755-889-118	Sequence 118, App
355	181	11.5	112	5	US-10-487-620-12	Sequence 12, Appl	534	126.5	8.0	457	3	US-09-774-639-108	Sequence 108, App
356	175.5	11.1	920	5	US-10-450-763-47426	Sequence 47426, A	535	126.5	8.0	457	3	US-09-969-730-110	Sequence 110, App
357	170	10.8	34	3	US-09-864-761-47905	Sequence 47905, A	536	126.5	8.0	457	4	US-10-621-363-110	Sequence 110, App
358	161	10.2	90	3	US-09-799-118-3	Sequence 3, Appli	537	124.5	7.9	482	4	US-10-104-047-3794	Sequence 3794, Ap
359	153.5	9.7	90	3	US-09-927-463-8	Sequence 8, Appli	540	121.5	7.7	360	3	US-09-905-291A-213	Sequence 213, App
360	153.5	9.7	90	4	US-10-837-671-8	Sequence 8, Appli	1071	121.5	7.7	360	4	US-10-174-587-28	Sequence 28, Appl
361	150	9.5	510	4	US-10-104-047-2580	Sequence 2580, Ap	1106	121.5	7.7	360	4	US-10-299-976-213	Sequence 213, App
362	148.5	9.4	80	5	US-10-487-620-23	Sequence 23, Appl	1108	121.5	7.7	360	4	US-10-299-937-213	Sequence 213, App
363	145	9.2	277	3	US-09-799-118-2	Sequence 2, Appli	1118	121.5	7.7	360	4	US-10-298-993-213	Sequence 213, App
364	145	9.2	277	4	US-10-247-671-185	Sequence 185, App	1123	121.5	7.7	360	4	US-10-448-923-213	Sequence 213, App
365	145	9.2	277	4	US-10-295-027-292	Sequence 292, App	1124	121.5	7.7	360	4	US-10-449-656-213	Sequence 213, App
366	145	9.2	277	4	US-10-295-027-1237	Sequence 1237, Ap	1125	121.5	7.7	360	4	US-10-448-713-213	Sequence 213, App
367	145	9.2	277	5	US-10-723-860-4326	Sequence 4326, Ap	1127	121.5	7.7	360	4	US-10-425-447-213	Sequence 213, App
368	145	9.2	1069	4	US-10-028-248A-39	Sequence 39, Appl	1135	121.5	7.7	360	4	US-10-215-371-213	Sequence 213, App
369	145	9.2	1069	4	US-10-107-782-39	Sequence 39, Appl	1136	121.5	7.7	360	4	US-10-797-366-213	Sequence 213, App
370	145	9.2	2626	4	US-10-634-574-4	Sequence 4, Appli	1137	121.5	7.7	360	4	US-10-771-187-213	Sequence 213, App
371	144	9.1	275	5	US-10-960-275-12	Sequence 12, Appl	1138	121.5	7.7	360	5	US-10-963-467-213	Sequence 213, App
372	143.5	9.1	95	4	US-10-424-599-248857	Sequence 248857, Sequence 41, Appl	1139	121.5	7.7	360	5	US-10-978-255-213	Sequence 213, App
373	134	8.5	897	4	US-10-028-248A-41	Sequence 41, Appl	1143	121.5	7.7	360	5	US-10-970-823-213	Sequence 213, App
374	134	8.5	897	4	US-10-028-248A-211	Sequence 211, App	1144	121	7.7	528	3	US-09-759-130B-341	Sequence 341, App
375	134	8.5	897	4	US-10-107-782-41	Sequence 41, Appl	1145	121	7.7	528	4	US-10-189-123-71	Sequence 71, Appl
376	134	8.5	897	4	US-10-107-782-211	Sequence 211, App	1146	121	7.7	528	4	US-10-188-495-71	Sequence 71, Appl
377	134	8.5	2675	4	US-10-028-248A-2	Sequence 2, Appli	1147	121	7.7	528	4	US-10-741-790-341	Sequence 20, App
378	134	8.5	2675	4	US-10-107-782-2	Sequence 2, Appli	1148	121	7.7	528	5	US-10-314-942-20	Sequence 20, App
379	133	8.4	1192	4	US-10-028-248A-40	Sequence 40, Appl	1149	118.5	7.5	1642	5	US-10-741-600-1176	Sequence 1176, Ap
380	133	8.4	1192	4	US-10-107-782-40	Sequence 40, Appl	1150	118.5	7.5	1642	5	US-10-741-600-1178	Sequence 1178, Ap
381	133	8.4	1394	3	US-09-842-930A-25	Sequence 25, Appl	1151	118.5	7.5	3396	4	US-10-788-792-170	Sequence 170, App
382	133	8.4	1394	5	US-10-990-844-25	Sequence 25, Appl	1152	118.5	7.5	3396	5	US-10-741-600-1172	Sequence 1172, Ap
383	133	8.4	1416	4	US-10-133-172-4	Sequence 4, Appli	1153	118.5	7.5	3396	5	US-10-741-600-1173	Sequence 1173, Ap
384	133	8.4	1431	3	US-09-842-930A-2	Sequence 2, Appli	1154	118.5	7.5	3396	5	US-10-631-467-773	Sequence 773, App
385	133	8.4	1431	3	US-10-133-172-2	Sequence 2, Appli	1155	116	7.4	2397	5	US-10-631-467-1518	Sequence 1518, Ap
386	133	8.4	1431	5	US-10-990-844-2	Sequence 2, Appli	1156	114.5	7.3	1257	4	US-10-698-190-22	Sequence 22, Appl
387	133	8.4	1653	4	US-10-133-172-20	Sequence 20, Appl	1157	113.5	7.2	97	3	US-09-799-118-5	Sequence 5, Appli
388	131.5	8.3	883	4	US-10-195-970-3	Sequence 3, Appli	1158	112.5	7.1	287	3	US-09-764-853-576	Sequence 576, App
389	131.5	8.3	883	4	US-10-453-420-3	Sequence 3, Appli	1159	112.5	7.1	340	4	US-10-112-944-397	Sequence 397, App
390	131	8.3	649	3	US-09-759-130B-333	Sequence 333, App	1160	111.5	7.1	402	4	US-10-282-122A-64209	Sequence 64209, A

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1162	111	7.0	104	4	US-10-107-782-46	Sequence 46, Appl	1235	99	6.3	201	4	US-10-120-907A-40	Sequence 40, Appl
1163	111	7.0	655	4	US-10-270-253-2	Sequence 2, Appl	1236	99	6.3	201	4	US-10-120-907A-41	Sequence 41, Appl
1164	111	7.0	655	5	US-10-741-600-1174	Sequence 1174, Ap	1237	99	6.3	260	4	US-10-460-512-3	Sequence 3, Appl
1165	111	7.0	2409	4	US-10-177-293-90	Sequence 90, Appl	1238	99	6.3	260	5	US-10-897-911-3	Sequence 3, Appl
1166	111	7.0	2409	5	US-10-741-600-1175	Sequence 1175, Ap	1239	99	6.3	260	5	US-10-898-615-3	Sequence 3, Appl
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1168	111	7.0	2409	5	US-10-482-029-194	Sequence 194, Ap	1241	99	6.3	5376	4	US-10-028-248A-74	Sequence 74, Appl
1169	111	7.0	2409	5	US-10-853-335A-184	Sequence 184, Appl	1242	99	6.3	5376	4	US-10-107-782-74	Sequence 74, Appl
1170	109	6.9	353	5	US-10-960-275-11	Sequence 11, Appl	1243	98.5	6.3	1126	6	US-11-097-143-35952	Sequence 35952, A
1171	109	6.9	1321	4	US-10-241-220-82	Sequence 82, Appl	1244	98	6.2	2112	6	US-11-097-143-8001	Sequence 8001, Ap
1172	109	6.9	1321	4	US-10-238-027-282	Sequence 282, Appl	1245	98.5	6.1	585	5	US-10-868-381-58	Sequence 58, Appl
1173	109	6.9	1321	4	US-10-408-765A-1421	Sequence 1421, Ap	1246	95.5	6.1	1217	4	US-10-437-963-183891	Sequence 183891, A
1174	109	6.9	1321	4	US-10-698-190-18	Sequence 18, Appl	1247	95.5	6.1	5374	4	US-10-028-248A-75	Sequence 75, Appl
1175	109	6.9	1321	5	US-10-872-972-82	Sequence 82, Appl	1248	95.5	6.1	5374	4	US-10-107-782-75	Sequence 75, Appl
1176	109	6.9	1321	5	US-10-872-991-82	Sequence 82, Appl	1249	93.5	5.9	258	3	US-09-764-853-840	Sequence 840, App
1177	108	6.9	322	4	US-10-120-907A-32	Sequence 32, Appl	1250	93.5	5.9	258	4	US-10-091-438-205	Sequence 205, App
1178	108	6.9	322	4	US-10-120-907A-33	Sequence 33, Appl	1251	93.5	5.9	261	3	US-09-764-853-669	Sequence 669, App
1179	108	6.9	354	4	US-10-120-907A-3	Sequence 3, Appl	1252	93.5	5.9	261	4	US-10-091-438-144	Sequence 144, App
1180	108	6.9	354	4	US-10-120-907A-7	Sequence 7, Appl	1253	93.5	5.9	320	5	US-10-450-763-31869	Sequence 31869, A
1181	108	6.9	354	4	US-10-120-907A-9	Sequence 9, Appl	1254	93.5	5.9	339	5	US-10-391-939A-2	Sequence 2, Appl
1182	108	6.9	354	4	US-10-120-907A-11	Sequence 11, Appl	1255	93.5	5.9	339	5	US-10-391-939A-28	Sequence 28, Appl
1183	108	6.9	354	4	US-10-120-907A-13	Sequence 13, Appl	1256	93.5	5.9	359	4	US-10-188-012-17	Sequence 17, Appl
1184	108	6.9	354	4	US-10-120-907A-15	Sequence 15, Appl	1257	93.5	5.9	359	4	US-10-188-012-19	Sequence 19, Appl
1185	108	6.9	354	4	US-10-120-907A-17	Sequence 17, Appl	1258	93.5	5.9	359	4	US-10-188-012-23	Sequence 23, Appl
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1187	108	6.9	354	4	US-10-120-907A-21	Sequence 21, Appl	1260	93.5	5.9	359	4	US-10-188-832-64	Sequence 64, Appl
1188	108	6.9	354	4	US-10-120-907A-23	Sequence 23, Appl	1261	93.5	5.9	359	5	US-10-391-939A-4	Sequence 4, Appl
1189	108	6.9	354	4	US-10-120-907A-24	Sequence 24, Appl	1262	93.5	5.9	359	5	US-10-663-497-17	Sequence 17, Appl
1190	108	6.9	354	4	US-10-120-907A-28	Sequence 28, Appl	1263	93.5	5.9	359	5	US-10-663-497-19	Sequence 19, Appl
1191	108	6.9	354	4	US-10-120-907A-29	Sequence 29, Appl	1264	93.5	5.9	359	5	US-10-663-497-23	Sequence 23, Appl
1192	108	6.9	354	4	US-10-120-907A-30	Sequence 30, Appl	1265	93.5	5.9	359	5	US-10-718-321-8	Sequence 8, Appl
1193	108	6.9	354	4	US-10-120-907A-36	Sequence 36, Appl	1266	93.5	5.9	359	5	US-10-847-318-25	Sequence 25, Appl
1194	108	6.9	354	4	US-10-120-907A-38	Sequence 38, Appl	1267	93.5	5.9	366	5	US-10-450-763-38282	Sequence 38282, A
1195	108	6.9	354	4	US-10-120-907A-42	Sequence 42, Appl	1268	93.5	5.9	1595	5	US-10-484-218-20	Sequence 20, Appl
1196	108	6.9	354	4	US-10-120-907A-64	Sequence 64, Appl	1269	92.5	5.9	40	5	US-10-487-620-26	Sequence 26, Appl
1197	108	6.9	354	4	US-10-120-907A-66	Sequence 66, Appl	1270	92.5	5.9	300	3	US-09-953-499-10	Sequence 10, Appl
1198	108	6.9	354	5	US-10-754-473-19	Sequence 19, Appl	1271	92.5	5.9	300	4	US-10-265-542-10	Sequence 10, Appl
1199	108	6.9	354	5	US-10-754-473-22	Sequence 22, Appl	1272	92.5	5.9	300	4	US-10-633-008-10	Sequence 10, Appl
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1201	108	6.9	721	4	US-10-120-907A-25	Sequence 25, Appl	1274	92.5	5.9	300	4	US-10-785-221-10	Sequence 10, Appl
1202	108	6.9	721	4	US-10-120-907A-39	Sequence 39, Appl	1275	92.5	5.9	300	4	US-10-785-433-10	Sequence 10, Appl
1203	108	6.9	721	4	US-10-120-907A-31	Sequence 31, Appl	1276	92.5	5.9	300	4	US-10-767-904-10	Sequence 10, Appl
1204	108	6.9	721	4	US-10-120-907A-65	Sequence 65, Appl	1277	92.5	5.9	300	5	US-10-767-374-10	Sequence 10, Appl
1205	107	6.8	93	4	US-10-120-907A-67	Sequence 67, Appl	1278	92.5	5.9	300	5	US-10-785-607-10	Sequence 10, Appl
1206	107	6.8	315	4	US-10-133-172-5	Sequence 5, Appl	1279	92.5	5.9	300	5	US-10-785-351-12	Sequence 12, Appl
1207	107	6.8	315	4	US-10-667-723-4	Sequence 4, Appl	1280	92.5	5.9	365	4	US-10-188-012-21	Sequence 21, Appl
1208	107	6.8	339	5	US-10-754-473-21	Sequence 21, Appl	1281	92.5	5.9	569	4	US-10-369-493-1516	Sequence 1516, Ap
1209	107	6.8	354	4	US-10-120-907A-39	Sequence 39, Appl	1282	92.5	5.9	934	4	US-10-369-493-3228	Sequence 3228, Ap
1210	107	6.8	355	5	US-10-120-907A-31	Sequence 31, Appl	1283	92.5	5.9	934	4	US-10-032-2018-188	Sequence 188, App
1211	107	6.8	355	5	US-10-754-473-20	Sequence 20, Appl	1284	92	5.8	364	5	US-10-437-963-189767	Sequence 189767, A
1212	107	6.8	1268	4	US-10-960-275-9	Sequence 9, Appl	1285	92	5.8	364	5	US-10-704-781-3	Sequence 3, Appl
1213	107	6.8	1795	6	US-10-698-190-24	Sequence 24, Appl	1286	92	5.8	364	5	US-10-704-781-3	Sequence 3, Appl
1214	107	6.8	2420	4	US-11-097-143-36210	Sequence 36210, A	1287	92	5.8	966	3	US-10-425-114-66913	Sequence 66913, A
1215	107	6.8	2420	4	US-10-028-248A-4	Sequence 4, Appl	1288	92	5.8	966	3	US-10-425-115-32413	Sequence 32413, A
1216	105.5	6.7	341	3	US-10-107-782-40	Sequence 40, Appl	1289	91.5	5.8	166	4	US-10-425-115-32413	Sequence 17, Appl
1217	105.5	6.7	341	5	US-09-948-820-48	Sequence 48, Appl	1290	91.5	5.8	166	4	US-10-425-115-32413	Sequence 7350, Ap
1218	105	6.7	341	5	US-10-613-076-48	Sequence 48, Appl	1291	91.5	5.8	350	4	US-11-097-143-7350	Sequence 35049, A
1219	105	6.7	354	4	US-10-120-907A-37	Sequence 37, Appl	1292	91.5	5.8	350	4	US-10-188-012-27	Sequence 27, Appl
1220	104	6.6	98	3	US-10-754-473-18	Sequence 18, Appl	1293	91.5	5.8	350	4	US-10-663-497-27	Sequence 27, Appl
1221	104	6.6	139	4	US-09-799-118-4	Sequence 118, A	1294	91.5	5.8	350	4	US-10-663-497-27	Sequence 27, Appl
1222	104	6.6	139	5	US-10-741-601-342	Sequence 342, App	1295	91.5	5.8	350	4	US-10-663-497-27	Sequence 27, Appl
1223	104	6.6	139	5	US-10-473-127-2037	Sequence 2037, Ap	1296	91.5	5.8	350	4	US-10-663-497-27	Sequence 27, Appl
1224	104	6.6	139	5	US-10-473-127-2040	Sequence 2040, Ap	1297	91.5	5.8	350	4	US-10-663-497-27	Sequence 27, Appl
1225	104	6.6	139	5	US-10-741-600-1050	Sequence 1050, Ap	1298	91.5	5.8	350	4	US-10-663-497-27	Sequence 27, Appl
1226	102.5	6.5	183	6	US-11-097-143-8400	Sequence 8400, Ap	1299	91.5	5.8	350	4	US-10-663-497-27	Sequence 27, Appl
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127	79.5	5.0	2617	6	US-10-453-372-738	Sequence 738, App	201	75	4.8	1311	7	US-11-169-232-42	Sequence 42, Appl
128	79.5	5.0	2617	6	US-10-453-372-740	Sequence 740, App	202	75	4.8	1313	7	US-11-169-232-142	Sequence 142, App
129	79.5	5.0	2617	6	US-10-453-372-742	Sequence 742, App	203	75	4.8	1314	7	US-11-169-232-50	Sequence 50, Appl
130	79.5	5.0	2617	6	US-10-453-372-744	Sequence 744, App	204	75	4.8	1320	7	US-11-169-232-46	Sequence 46, Appl
131	79.5	5.0	2617	6	US-10-453-372-746	Sequence 746, App	205	75	4.8	1320	7	US-11-169-232-60	Sequence 60, Appl
132	79.5	5.0	2617	6	US-10-453-372-748	Sequence 748, App	206	75	4.8	1354	7	US-11-169-232-48	Sequence 48, Appl
133	79.5	5.0	2617	6	US-10-453-372-750	Sequence 750, App	207	75	4.8	1363	7	US-11-169-232-40	Sequence 40, Appl
134	79	5.0	92	7	US-11-128-059-70	Sequence 70, Appl	208	75	4.8	1363	7	US-11-169-232-52	Sequence 52, Appl
135	79	5.0	374	7	US-11-072-175-148	Sequence 148, App	209	75	4.8	1404	7	US-11-169-232-2	Sequence 2, Appli
136	79	5.0	781	6	US-10-330-773-671	Sequence 671, App	210	75	4.8	1404	7	US-11-169-232-62	Sequence 62, Appl
137	78.5	5.0	184	7	US-11-087-099-9675	Sequence 9675, Ap	211	75	4.8	1874	6	US-10-821-234-1182	Sequence 1182, Ap
138	78.5	5.0	181	7	US-11-096-568A-12137	Sequence 12137, A	212	74.5	4.7	249	7	US-11-128-059-56	Sequence 56, Appl
139	78.5	5.0	409	7	US-11-096-568A-7532	Sequence 7532, Ap	213	74.5	4.7	441	7	US-11-096-568A-30300	Sequence 30300, A
140	78.5	5.0	574	7	US-11-053-100-40	Sequence 40, Appl	214	74.5	4.7	671	7	US-11-087-099-8628	Sequence 8628, Ap
141	78.5	5.0	724	7	US-11-053-100-41	Sequence 41, Appl	215	74.5	4.7	681	7	US-11-096-568A-2501	Sequence 2501, Ap
142	78.5	5.0	874	7	US-11-053-100-42	Sequence 42, Appl	216	74.5	4.7	733	7	US-11-096-568A-24028	Sequence 24028, A
143	78.5	5.0	1174	7	US-11-053-100-43	Sequence 43, Appl	217	74.5	4.7	733	7	US-11-096-568A-24027	Sequence 24027, A
144	78.5	5.0	1722	6	US-10-714-995-48	Sequence 48, Appl	218	74.5	4.7	759	7	US-11-096-568A-24026	Sequence 24026, A
145	78	5.0	280	6	US-10-967-457-75	Sequence 75, Appl	219	74.5	4.7	764	7	US-11-096-568A-24026	Sequence 24026, A
146	78	5.0	453	7	US-11-087-099-7775	Sequence 7775, Ap	220	74.5	4.7	998	6	US-10-510-524-1	Sequence 1, Appli
147	77.5	4.9	348	7	US-11-096-568A-6734	Sequence 6734, Ap	221	74.5	4.7	998	6	US-11-203-251A-88	Sequence 88, Appl
148	77.5	4.9	472	7	US-11-165-211-6	Sequence 6, Appli	222	74	4.7	2801	6	US-10-330-773-630	Sequence 630, App
149	77.5	4.9	472	7	US-11-165-226-6	Sequence 6, Appli	223	74	4.7	124	7	US-11-128-059-64	Sequence 64, Appl
150	77.5	4.9	477	6	US-10-540-091-2	Sequence 2, Appli	224	74	4.7	339	6	US-10-498-026-35	Sequence 35, Appl
151	77.5	4.9	630	6	US-10-517-939-42	Sequence 42, Appl	225	74	4.7	339	6	US-10-498-026-36	Sequence 36, Appl
152	77.5	4.9	1249	7	US-11-126-022-30	Sequence 30, Appl	226	74	4.7	717	7	US-11-096-568A-28883	Sequence 28883, A
153	77	4.9	771	6	US-10-821-234-1271	Sequence 1271, Ap	227	74	4.7	860	7	US-11-022-562-217	Sequence 217, App
154	77	4.9	1007	6	US-10-517-939-84	Sequence 84, Appl	228	74	4.7	1594	7	US-11-052-554A-83	Sequence 83, Appl
155	76.5	4.9	1150	7	US-11-139-435-1	Sequence 1, Appli	229	73.5	4.7	232	6	US-10-527-500-37	Sequence 37, Appl
156	76.5	4.9	279	7	US-11-096-568A-8112	Sequence 8112, Ap	230	73.5	4.7	713	7	US-11-256-548-2	Sequence 194, App
157	76.5	4.9	283	7	US-11-096-568A-8111	Sequence 8111, Ap	231	73.5	4.7	826	6	US-10-873-528-194	Sequence 194, App
158	76.5	4.9	298	7	US-11-096-568A-8110	Sequence 8110, Ap	232	73	4.6	304	7	US-11-087-177-4	Sequence 4, Appli
159	76.5	4.9	311	7	US-11-096-568A-22963	Sequence 22963, A	233	73	4.6	311	7	US-11-096-568A-11193	Sequence 11193, A
160	76.5	4.9	536	6	US-10-453-372-6	Sequence 6, Appli	234	73	4.6	329	6	US-10-995-561-694	Sequence 694, App
161	76.5	4.9	536	6	US-10-453-372-24	Sequence 22, Appl	235	73	4.6	353	7	US-11-096-568A-11192	Sequence 11192, A
162	76.5	4.9	536	6	US-10-453-372-24	Sequence 24, Appl	236	73	4.6	488	7	US-11-202-330-5	Sequence 5, Appli
163	76.5	4.9	536	6	US-10-453-372-26	Sequence 26, Appl	237	73	4.6	512	7	US-11-108-172-1093	Sequence 1093, Ap
164	76.5	4.9	536	6	US-10-453-372-28	Sequence 28, Appl	238	73	4.6	558	7	US-11-052-554A-20	Sequence 20, Appl
166	76.5	4.9	653	6	US-10-917-905-2	Sequence 2, Appli	239	73	4.6	558	7	US-11-134-563-12	Sequence 12, Appl
167	76.5	4.9	653	6	US-10-973-115B-438	Sequence 438, App	240	73	4.6	646	6	US-10-995-561-695	Sequence 695, App
168	76.5	4.9	653	7	US-11-013-855-25	Sequence 25, Appl	241	73	4.6	708	6	US-10-636-320-2	Sequence 2, Appli
169	76.5	4.9	773	7	US-11-010-239-63	Sequence 63, Appl	242	73	4.6	750	7	US-11-124-368A-244	Sequence 244, App
170	76.5	4.9	1249	7	US-11-126-022-25	Sequence 25, Appl	243	73	4.6	750	6	US-11-124-368A-249	Sequence 249, App
171	76.5	4.9	1307	7	US-11-072-512-2438	Sequence 2438, Ap	244	73	4.6	918	6	US-10-995-561-696	Sequence 696, App
172	76	4.8	336	7	US-11-096-568A-34180	Sequence 34180, A	245	73	4.6	948	6	US-10-523-503-68	Sequence 68, Appl
173	76	4.8	367	7	US-11-096-568A-34179	Sequence 34179, A	246	73	4.6	1158	6	US-10-467-657-3112	Sequence 3112, Ap
174	76	4.8	393	7	US-11-096-568A-34178	Sequence 34178, A	247	73	4.6	1166	6	US-10-501-035-205	Sequence 205, App
175	76	4.8	400	7	US-11-087-099-8803	Sequence 8803, Ap	248	73	4.6	1207	6	US-10-821-234-1109	Sequence 1109, Ap
176	76	4.8	499	7	US-11-096-568A-32028	Sequence 32028, A	249	72.5	4.6	281	7	US-11-087-177-3	Sequence 3, Appli

250	72.5	4.6	302	7	US-11-096-568A-15531	Sequence 15531, A	324	70.5	4.5	750	7	US-11-096-568A-30499	Sequence 30499, A
251	72.5	4.6	389	7	US-11-096-568A-6654	Sequence 6654, Ap	325	70.5	4.5	885	7	US-11-096-568A-30498	Sequence 30498, A
252	72.5	4.6	445	6	US-10-793-626-1294	Sequence 1294, Ap	326	70.5	4.5	911	7	US-11-096-568A-30497	Sequence 30497, A
253	72.5	4.6	498	6	US-10-510-947-9	Sequence 9, Appli	327	70.5	4.5	989	6	US-10-821-234-975	Sequence 975, Ap
254	72.5	4.6	582	7	US-11-096-568A-24623	Sequence 24623, A	328	70.5	4.5	1980	7	US-11-179-624-3	Sequence 3, Appli
255	72.5	4.6	605	7	US-11-096-568A-24622	Sequence 24622, A	329	70	4.4	221	7	US-11-096-568A-28866	Sequence 28866, A
256	72.5	4.6	673	7	US-11-096-568A-24621	Sequence 24621, A	330	70	4.4	224	7	US-11-096-568A-7141	Sequence 7141, Ap
257	72.5	4.6	758	7	US-11-043-693-1	Sequence 1, Appli	331	70	4.4	256	7	US-11-096-568A-7140	Sequence 7140, Ap
258	72.5	4.6	1132	6	US-10-501-035-222	Sequence 222, Ap	332	70	4.4	289	7	US-11-096-568A-28865	Sequence 28865, A
259	72.5	4.6	1338	6	US-10-821-234-1622	Sequence 1622, Ap	333	70	4.4	323	7	US-11-096-568A-21688	Sequence 21688, A
260	72.5	4.6	1338	7	US-11-109-156-23	Sequence 23, Appli	334	70	4.4	393	5	US-09-930-864-1	Sequence 1, Appli
261	72.5	4.6	1338	7	US-11-075-047A-2	Sequence 2, Appli	335	70	4.4	427	7	US-11-096-568A-28864	Sequence 28864, A
262	72.5	4.6	2314	7	US-11-097-728-2	Sequence 2, Appli	336	70	4.4	467	7	US-11-087-099-2054	Sequence 2054, Ap
263	72.5	4.6	2353	7	US-11-097-728-6	Sequence 6, Appli	337	70	4.4	485	6	US-10-501-035-349	Sequence 349, App
264	72.5	4.6	2801	7	US-11-124-368A-305	Sequence 305, Ap	338	70	4.4	531	7	US-11-096-568A-19343	Sequence 19343, A
265	72.5	4.6	2801	7	US-11-124-367A-433	Sequence 433, Ap	339	70	4.4	578	6	US-10-821-234-1039	Sequence 1039, Ap
266	72.5	4.6	2896	7	US-11-124-368A-306	Sequence 306, Ap	340	70	4.4	609	7	US-11-110-082-40	Sequence 40, Appli
267	72.5	4.6	2896	7	US-11-124-367A-434	Sequence 434, Ap	341	70	4.4	733	7	US-11-096-568A-29645	Sequence 29645, A
268	72.5	4.6	2910	6	US-10-330-773-39	Sequence 39, Appli	342	70	4.4	735	7	US-11-096-568A-29645	Sequence 29645, A
269	72.5	4.6	3256	7	US-11-124-368A-304	Sequence 304, Ap	343	70	4.4	735	7	US-11-096-568A-31569	Sequence 31569, A
270	72.5	4.6	3256	7	US-11-124-367A-432	Sequence 432, Ap	344	70	4.4	768	7	US-11-096-568A-29644	Sequence 29644, A
271	72	4.6	245	7	US-11-087-099-299	Sequence 299, Ap	345	70	4.4	768	7	US-11-096-568A-31568	Sequence 31568, A
272	72	4.6	245	7	US-11-096-568A-33799	Sequence 33799, A	346	70	4.4	770	7	US-11-096-568A-31567	Sequence 31567, A
273	72	4.6	255	7	US-11-096-568A-7533	Sequence 7533, Ap	347	70	4.4	1256	6	US-10-517-696-111	Sequence 111, App
274	72	4.6	308	7	US-11-072-512-3898	Sequence 3898, Ap	348	70	4.4	1416	7	US-11-128-059-60	Sequence 60, Appli
275	72	4.6	458	6	US-10-540-091-24	Sequence 24, Appli	349	70	4.4	2011	7	US-11-080-991-56	Sequence 56, Appli
276	72	4.6	747	7	US-11-182-592-2	Sequence 2, Appli	350	69.5	4.4	106	7	US-11-096-568A-19298	Sequence 19298, A
277	72	4.6	784	6	US-10-467-657-5968	Sequence 5968, Ap	351	69.5	4.4	163	7	US-11-096-568A-641	Sequence 641, App
278	72	4.6	1009	6	US-10-514-531-11	Sequence 11, Appli	352	69.5	4.4	173	7	US-11-096-568A-452	Sequence 452, App
279	71.5	4.5	232	6	US-10-884-730-366	Sequence 366, App	353	69.5	4.4	173	7	US-11-096-568A-453	Sequence 453, App
280	71.5	4.5	353	7	US-11-096-568A-12810	Sequence 12810, A	354	69.5	4.4	175	7	US-11-087-099-6466	Sequence 6466, Ap
281	71.5	4.5	447	6	US-10-641-678-58	Sequence 58, Appli	355	69.5	4.4	215	6	US-10-467-657-476	Sequence 476, App
282	71.5	4.5	541	7	US-11-201-916-4	Sequence 4, Appli	356	69.5	4.4	312	6	US-10-973-115B-336	Sequence 336, App
283	71	4.5	250	7	US-11-128-059-62	Sequence 62, Appli	357	69.5	4.4	349	7	US-11-096-568A-10641	Sequence 10641, A
284	71	4.5	343	7	US-11-080-091-4	Sequence 4, Appli	358	69.5	4.4	453	7	US-11-052-554A-224	Sequence 224, App
285	71	4.5	345	7	US-11-087-177-19	Sequence 19, Appli	359	69.5	4.4	461	7	US-11-096-568A-10640	Sequence 10640, A
286	71	4.5	354	7	US-11-189-817-2	Sequence 2, Appli	360	69.5	4.4	519	7	US-11-087-099-9352	Sequence 9352, Ap
287	71	4.5	554	5	US-09-978-360A-410	Sequence 410, App	361	69.5	4.4	533	6	US-10-330-773-666	Sequence 666, App
288	71	4.5	578	7	US-11-087-099-542	Sequence 542, Ap	362	69.5	4.4	618	7	US-11-087-099-9161	Sequence 9161, Ap
289	71	4.5	579	7	US-11-087-099-6979	Sequence 6979, Ap	363	69.5	4.4	626	7	US-11-072-512-2827	Sequence 2827, Ap
290	71	4.5	579	7	US-11-087-099-7852	Sequence 7852, Ap	364	69.5	4.4	646	7	US-11-087-099-6754	Sequence 6754, Ap
291	71	4.5	581	7	US-11-087-099-2154	Sequence 2154, Ap	365	69.5	4.4	713	6	US-10-330-773-668	Sequence 668, App
292	71	4.5	581	7	US-11-087-099-2375	Sequence 2375, Ap	366	69.5	4.4	862	7	US-11-051-720-1443	Sequence 1443, Ap
293	71	4.5	581	7	US-11-087-099-3070	Sequence 3070, Ap	367	69.5	4.4	1007	7	US-11-051-720-1445	Sequence 1445, Ap
294	71	4.5	581	7	US-11-087-099-3327	Sequence 3327, Ap	368	69.5	4.4	1120	7	US-11-051-720-1733	Sequence 1733, Ap
295	71	4.5	581	7	US-11-087-099-3736	Sequence 3736, Ap	369	69.5	4.4	1305	7	US-11-051-720-1370	Sequence 1370, Ap
296	71	4.5	581	7	US-11-087-099-5261	Sequence 5261, Ap	370	69.5	4.4	16990	7	US-11-175-689-7	Sequence 7, Appli
297	71	4.5	581	7	US-11-087-099-7813	Sequence 7813, Ap	371	69.5	4.4	143	7	US-11-096-568A-8463	Sequence 8463, Ap
298	71	4.5	581	7	US-11-087-099-8783	Sequence 8783, Ap	372	69	4.4	180	7	US-11-096-568A-12758	Sequence 12758, A
299	71	4.5	581	7	US-11-087-099-9181	Sequence 9181, Ap	373	69	4.4	443	7	US-11-087-099-7683	Sequence 7683, Ap
300	71	4.5	581	7	US-11-087-099-10957	Sequence 10957, A	374	69	4.4	476	7	US-11-055-822-540	Sequence 540, App
301	71	4.5	581	7	US-11-087-099-11208	Sequence 11208, A	375	69	4.4	476	7	US-11-055-822-542	Sequence 542, App
302	71	4.5	581	7	US-11-087-099-11354	Sequence 11354, A	376	69	4.4	476	7	US-11-055-822-1122	Sequence 1122, Ap
303	71	4.5	581	7	US-11-087-099-12146	Sequence 12146, A	377	69	4.4	476	7	US-11-055-822-1124	Sequence 1124, Ap
304	71	4.5	582	7	US-11-087-099-4567	Sequence 4567, Ap	378	69	4.4	545	7	US-11-201-916-8	Sequence 8, Appli
305	71	4.5	626	7	US-11-010-748A-1	Sequence 1, Appli	379	69	4.4	654	6	US-10-528-031-1	Sequence 1, Appli
306	71	4.5	1118	7	US-11-113-751-42	Sequence 42, Appli	380	69	4.4	696	7	US-11-096-568A-29818	Sequence 29818, A
307	71	4.5	1153	7	US-11-113-751-44	Sequence 44, Appli	381	69	4.4	696	7	US-11-256-548-23	Sequence 23, Appli
308	71	4.5	1164	7	US-11-087-099-2278	Sequence 2278, Ap	382	69	4.4	705	7	US-11-087-099-10564	Sequence 10564, A
309	71	4.5	1164	7	US-11-087-099-9070	Sequence 9070, Ap	383	69	4.4	720	7	US-11-256-548-6	Sequence 6, Appli
310	70.5	4.5	163	7	US-11-096-568A-4288	Sequence 4288, Ap	384	69	4.4	761	6	US-10-485-517-232	Sequence 252, App
311	70.5	4.5	231	7	US-11-096-568A-1421	Sequence 1421, Ap	385	69	4.4	802	7	US-11-087-099-4982	Sequence 4882, Ap
312	70.5	4.5	232	6	US-10-884-730-363	Sequence 363, Ap	386	69	4.4	820	7	US-11-087-099-13246	Sequence 12246, A
313	70.5	4.5	232	6	US-10-884-730-364	Sequence 364, Ap	387	69	4.4	910	7	US-11-206-587-17	Sequence 17, Appli
314	70.5	4.5	232	6	US-10-884-730-365	Sequence 365, Ap	388	69	4.4	1158	7	US-11-075-646-6	Sequence 6, Appli
315	70.5	4.5	292	7	US-11-073-226-6	Sequence 6, Appli	389	69	4.4	245	7	US-11-096-568A-21710	Sequence 21710, A
316	70.5	4.5	308	7	US-11-096-568A-20980	Sequence 20980, A	390	68.5	4.3	330	7	US-11-098-686-10903	Sequence 10903, A
317	70.5	4.5	348	7	US-11-096-568A-20979	Sequence 20979, A	391	68.5	4.3	339	7	US-11-098-686-21709	Sequence 21709, A
318	70.5	4.5	368	7	US-11-096-568A-20978	Sequence 20978, A	392	68.5	4.3	341	7	US-11-096-568A-21708	Sequence 21708, A
319	70.5	4.5	497	7	US-11-072-512-3603	Sequence 3603, Ap	393	68.5	4.3	411	7	US-11-096-568A-7197	Sequence 7197, Ap
320	70.5	4.5	512	6	US-10-821-234-1032	Sequence 1032, Ap	394	68.5	4.3	436	7	US-11-124-368A-236	Sequence 236, App
321	70.5	4.5	678	7	US-11-102-240-34	Sequence 34, Appli	395	68.5	4.3	451	7	US-11-096-568A-7196	Sequence 7196, Ap
322	70.5	4.5	678	7	US-11-103-195-34	Sequence 34, Appli	396	68.5	4.3	455	7	US-11-087-099-10931	Sequence 10931, A
323	70.5	4.5	678	7			397	68.5	4.3				

398	68.5	4.3	464	7	US-11-096-568A-7530	Sequence 7530, Ap	471	67.5	4.3	1978	7	US-11-212-443-60	Sequence 60, Appl
399	68.5	4.3	467	7	US-11-096-568A-7195	Sequence 7195, Ap	472	67.5	4.3	4374	7	US-11-128-572-2	Sequence 2, Appl1
400	68.5	4.3	467	7	US-11-096-568A-7529	Sequence 7529, Ap	473	67	4.3	137	7	US-11-072-512-2849	Sequence 2849, Ap
401	68.5	4.3	509	7	US-11-096-568A-7528	Sequence 7528, Ap	474	67	4.3	149	7	US-11-096-568A-12138	Sequence 12138, A
402	68.5	4.3	529	7	US-11-210-316-28	Sequence 28, Appl	475	67	4.3	208	7	US-11-072-512-2188	Sequence 2188, Ap
403	68.5	4.3	589	7	US-11-096-568A-9189	Sequence 9189, Ap	476	67	4.3	209	7	US-11-096-568A-3341	Sequence 3341, Ap
404	68.5	4.3	589	7	US-11-096-568A-9191	Sequence 9191, Ap	477	67	4.3	246	7	US-11-073-226-1	Sequence 1, Appl1
405	68.5	4.3	605	7	US-11-096-568A-9188	Sequence 9188, Ap	478	67	4.3	304	7	US-11-080-091-10	Sequence 10, Appl
406	68.5	4.3	696	7	US-11-052-554A-100	Sequence 100, App	479	67	4.3	309	6	US-10-873-528-156	Sequence 9345, Ap
407	68.5	4.3	696	7	US-11-052-554A-101	Sequence 101, App	480	67	4.3	317	7	US-11-087-099-9345	Sequence 156, App
408	68.5	4.3	709	7	US-11-072-512-2349	Sequence 2349, Ap	481	67	4.3	332	7	US-11-096-568A-14684	Sequence 9345, Ap
409	68.5	4.3	748	6	US-10-330-773-394	Sequence 394, App	482	67	4.3	336	7	US-11-087-099-4886	Sequence 14684, A
410	68.5	4.3	825	7	US-11-087-099-1341	Sequence 1341, App	483	67	4.3	336	7	US-11-096-568A-5652	Sequence 4886, Ap
411	68.5	4.3	886	7	US-11-087-099-11456	Sequence 11456, A	484	67	4.3	344	7	US-11-174-816-47	Sequence 47, Appl
412	68.5	4.3	897	7	US-11-137-465-35	Sequence 35, Appl	485	67	4.3	344	7	US-11-174-819-32	Sequence 32, Appl
413	68.5	4.3	1070	7	US-11-087-099-5657	Sequence 5657, Ap	486	67	4.3	345	7	US-11-087-177-21	Sequence 21, Appl
414	68.5	4.3	1344	7	US-11-072-512-2452	Sequence 2452, Ap	487	67	4.3	362	7	US-11-080-091-12	Sequence 12, Appl
415	68.5	4.3	1669	6	US-10-330-773-392	Sequence 392, App	488	67	4.3	389	7	US-11-188-743-23	Sequence 23, Appl
416	68.5	4.3	2244	7	US-11-131-263-41	Sequence 41, Appl	489	67	4.3	402	7	US-11-096-568A-14683	Sequence 14683, A
417	68	4.3	246	7	US-11-052-554A-50	Sequence 50, Appl	490	67	4.3	413	7	US-11-096-568A-14682	Sequence 14682, A
418	68	4.3	263	7	US-11-096-568A-9712	Sequence 9712, Ap	491	67	4.3	472	7	US-11-165-211-1	Sequence 1, Appl1
419	68	4.3	269	6	US-10-839-799-109	Sequence 109, App	492	67	4.3	472	7	US-11-165-211-2	Sequence 2, Appl1
420	68	4.3	312	6	US-10-986-501-124	Sequence 124, App	493	67	4.3	472	7	US-11-165-211-3	Sequence 3, Appl1
421	68	4.3	347	7	US-11-096-568A-16579	Sequence 16579, A	494	67	4.3	472	7	US-11-165-211-5	Sequence 5, Appl1
422	68	4.3	406	7	US-11-096-568A-15346	Sequence 15346, A	495	67	4.3	472	7	US-11-165-226-1	Sequence 1, Appl1
423	68	4.3	415	7	US-11-096-568A-15345	Sequence 15345, A	496	67	4.3	472	7	US-11-165-226-2	Sequence 2, Appl1
424	68	4.3	422	7	US-11-169-041-224	Sequence 224, App	497	67	4.3	472	7	US-11-165-226-5	Sequence 5, Appl1
425	68	4.3	472	7	US-11-165-211-4	Sequence 4, Appl1	498	67	4.3	472	7	US-11-165-226-5	Sequence 1, Appl1
426	68	4.3	472	7	US-11-165-226-4	Sequence 4, Appl1	499	67	4.3	514	7	US-11-195-733-1	Sequence 1, Appl1
427	68	4.3	550	7	US-11-087-099-5463	Sequence 4, Appl1	500	67	4.3	521	7	US-11-096-568A-31277	Sequence 31277, A
428	68	4.3	648	7	US-11-096-568A-27576	Sequence 27576, A	501	67	4.3	536	7	US-11-018-868-42	Sequence 42, Appl
429	68	4.3	693	6	US-10-714-995-24	Sequence 24, Appl	502	67	4.3	543	7	US-11-096-568A-31276	Sequence 31276, A
430	68	4.3	1233	6	US-10-517-933-312	Sequence 312, App	503	67	4.3	552	7	US-11-087-099-10983	Sequence 10983, A
431	68	4.3	1340	7	US-11-013-759-9	Sequence 9, Appl1	504	67	4.3	581	7	US-11-096-568A-31275	Sequence 31275, A
432	68	4.3	2053	7	US-11-203-806A-11	Sequence 11, Appl	505	67	4.3	619	6	US-10-517-933-322	Sequence 352, App
433	68	4.3	2426	7	US-11-019-711-48	Sequence 48, Appl	506	67	4.3	644	7	US-11-087-099-11826	Sequence 11826, A
434	68	4.3	3712	7	US-11-019-711-51	Sequence 51, Appl	507	67	4.3	681	7	US-11-067-121-9	Sequence 3227, Ap
435	68	4.3	3712	7	US-11-019-711-51	Sequence 51, Appl	508	67	4.3	765	7	US-11-087-099-905	Sequence 9, Appl1
436	67.5	4.3	96	7	US-11-096-568A-6177	Sequence 6177, Ap	509	67	4.3	823	7	US-11-087-099-1971	Sequence 905, App
437	67.5	4.3	163	7	US-11-096-568A-9622	Sequence 9622, Ap	510	67	4.3	976	6	US-10-966-483-2	Sequence 1971, Ap
438	67.5	4.3	173	7	US-11-096-568A-9621	Sequence 9621, Ap	511	67	4.3	976	6	US-10-966-483-2	Sequence 2, Appl1
439	67.5	4.3	176	7	US-11-096-568A-9620	Sequence 9620, Ap	512	67	4.3	976	6	US-10-511-273-1	Sequence 1, Appl1
440	67.5	4.3	238	7	US-11-096-568A-26721	Sequence 26721, A	513	67	4.3	976	7	US-11-233-796-2	Sequence 2, Appl1
441	67.5	4.3	400	7	US-11-096-568A-3236	Sequence 3236, Ap	514	67	4.3	976	7	US-11-072-175-138	Sequence 138, App
442	67.5	4.3	411	7	US-11-024-953-330	Sequence 330, App	515	67	4.3	1218	7	US-11-203-251A-77	Sequence 77, Appl
443	67.5	4.3	413	7	US-11-096-568A-20771	Sequence 20771, A	516	67	4.3	1218	7	US-11-052-554A-123	Sequence 123, App
444	67.5	4.3	418	7	US-11-096-568A-3235	Sequence 3235, Ap	517	67	4.3	1279	6	US-10-793-628-3188	Sequence 3188, Ap
445	67.5	4.3	423	7	US-11-098-686-10135	Sequence 10135, A	518	67	4.3	1384	6	US-10-821-234-1120	Sequence 1120, Ap
446	67.5	4.3	436	7	US-11-096-568A-3234	Sequence 3234, Ap	519	66.5	4.2	160	7	US-11-087-099-4973	Sequence 4973, Ap
447	67.5	4.3	497	7	US-11-072-512-3773	Sequence 3773, Ap	520	66.5	4.2	180	7	US-11-096-568A-3993	Sequence 3992, Ap
448	67.5	4.3	532	7	US-11-087-099-8860	Sequence 8860, Ap	521	66.5	4.2	221	6	US-10-714-887-144	Sequence 144, App
449	67.5	4.3	577	7	US-11-201-916-31	Sequence 31, Appl	522	66.5	4.2	221	6	US-10-714-887-144	Sequence 144, App
450	67.5	4.3	600	7	US-11-072-512-3397	Sequence 3397, Ap	523	66.5	4.2	235	5	US-09-978-360A-782	Sequence 782, App
451	67.5	4.3	618	7	US-11-087-099-6625	Sequence 6625, Ap	524	66.5	4.2	298	7	US-11-080-091-9	Sequence 9, Appl1
452	67.5	4.3	623	7	US-11-096-568A-26597	Sequence 26597, A	526	66.5	4.2	310	6	US-10-973-115B-152	Sequence 152, App
453	67.5	4.3	630	7	US-11-236-198-5	Sequence 5, Appl1	527	66.5	4.2	310	7	US-11-043-806-394	Sequence 394, App
454	67.5	4.3	637	7	US-11-096-568A-27876	Sequence 27876, A	528	66.5	4.2	310	7	US-11-043-806-395	Sequence 395, App
455	67.5	4.3	649	7	US-11-236-198-3	Sequence 3, Appl1	529	66.5	4.2	314	7	US-11-096-568A-3237	Sequence 3237, Ap
456	67.5	4.3	704	7	US-11-096-568A-27875	Sequence 27875, A	530	66.5	4.2	314	7	US-11-096-568A-24347	Sequence 24347, A
457	67.5	4.3	725	7	US-11-096-568A-26596	Sequence 26596, A	531	66.5	4.2	319	7	US-11-256-548-3	Sequence 3, Appl1
458	67.5	4.3	732	7	US-11-096-568A-27874	Sequence 27874, A	532	66.5	4.2	362	7	US-11-087-099-1300	Sequence 1300, Ap
459	67.5	4.3	758	7	US-11-096-568A-26595	Sequence 26595, A	533	66.5	4.2	380	7	US-11-098-686-10593	Sequence 10593, A
460	67.5	4.3	961	7	US-11-113-424-35	Sequence 35, Appl	534	66.5	4.2	448	6	US-10-917-905-6	Sequence 6, Appl1
461	67.5	4.3	1026	7	US-11-169-041-205	Sequence 205, App	535	66.5	4.2	448	6	US-10-330-773-674	Sequence 674, App
462	67.5	4.3	1122	7	US-11-191-374-3	Sequence 3, Appl1	536	66.5	4.2	786	6	US-10-467-962B-103	Sequence 103, App
463	67.5	4.3	1122	7	US-11-191-375-3	Sequence 3, Appl1	537	66.5	4.2	786	6	US-10-467-962B-103	Sequence 126, App
464	67.5	4.3	1122	7	US-11-191-588-3	Sequence 3, Appl1	538	66.5	4.2	812	7	US-11-120-308-126	Sequence 11042, A
465	67.5	4.3	1267	7	US-11-096-568A-28960	Sequence 28960, A	539	66.5	4.2	897	7	US-11-087-099-11042	Sequence 35, Appl
466	67.5	4.3	1274	7	US-11-096-568A-28959	Sequence 28959, A	540	66.5	4.2	1267	7	US-11-109-156-35	Sequence 7791, Ap
467	67.5	4.3	1480	7	US-11-096-568A-28958	Sequence 28958, A	541	66	4.2	149	7	US-11-087-099-7791	Sequence 16, Appl
468	67.5	4.3	1574	7	US-11-212-443-179	Sequence 179, App	542	66	4.2	212	7	US-11-025-834A-16	Sequence 96, Appl
469	67.5	4.3	1678	7	US-11-124-367A-340	Sequence 340, App	543	66	4.2	292	7	US-11-129-143-96	Sequence 27037, A
470	67.5	4.3	1678	7	US-11-124-367A-341	Sequence 341, App	544	66	4.2	300	7	US-11-096-568A-27037	

545	66	4.2	333	7	US-11-096-568A-21892	Sequence 21892, A	620	65.5	4.2	14130	7	US-11-175-689-9	Sequence 9, Appli
546	66	4.2	334	7	US-11-096-568A-21891	Sequence 21891, A	621	65	4.1	162	6	US-10-467-657-9046	Sequence 9046, Ap
547	66	4.2	337	7	US-11-087-099-3435	Sequence 3435, A	622	65	4.1	181	6	US-10-746-959C-10	Sequence 10, Appl
548	66	4.2	340	6	US-10-501-035-354	Sequence 354, App	623	65	4.1	196	7	US-11-096-568A-24825	Sequence 24825, A
549	66	4.2	343	7	US-11-016-564-17	Sequence 17, Appl	624	65	4.1	204	7	US-11-054-554A-377	Sequence 377, App
550	66	4.2	344	7	US-11-174-816-46	Sequence 46, Appl	625	65	4.1	211	7	US-11-096-568A-24824	Sequence 24824, A
551	66	4.2	344	7	US-11-174-819-30	Sequence 30, Appl	626	65	4.1	234	7	US-11-096-568A-21717	Sequence 21717, A
552	66	4.2	367	7	US-11-072-512-2763	Sequence 2763, Ap	627	65	4.1	244	7	US-11-052-554A-60	Sequence 60, Appl
553	66	4.2	380	7	US-11-087-099-6673	Sequence 6673, Ap	628	65	4.1	244	7	US-11-096-568A-3713	Sequence 3713, Ap
554	66	4.2	434	7	US-11-096-568A-21798	Sequence 21798, A	629	65	4.1	248	7	US-11-096-568A-13135	Sequence 13135, A
555	66	4.2	462	7	US-11-177-648-27	Sequence 27, Appl	630	65	4.1	253	7	US-11-096-568A-21716	Sequence 21716, A
556	66	4.2	462	7	US-11-177-648-92	Sequence 92, Appl	631	65	4.1	305	6	US-10-055-877-136	Sequence 126, App
557	66	4.2	462	7	US-11-177-648-93	Sequence 93, Appl	632	65	4.1	305	6	US-10-055-877-264	Sequence 264, App
558	66	4.2	462	7	US-11-177-648-94	Sequence 94, Appl	633	65	4.1	305	7	US-11-080-091-2	Sequence 2, Appli
559	66	4.2	462	7	US-11-177-648-95	Sequence 95, Appl	634	65	4.1	305	7	US-11-087-177-7	Sequence 7, Appli
560	66	4.2	464	7	US-11-096-568A-21797	Sequence 21797, A	635	65	4.1	309	7	US-11-037-243-118	Sequence 118, App
562	66	4.2	490	6	US-10-973-115B-356	Sequence 356, App	636	65	4.1	379	7	US-11-087-099-10889	Sequence 10889, A
563	66	4.2	508	7	US-11-087-099-10016	Sequence 10016, A	637	65	4.1	380	7	US-11-087-099-4525	Sequence 4525, Ap
564	66	4.2	525	7	US-11-074-176-146	Sequence 146, App	638	65	4.1	380	7	US-11-087-099-4810	Sequence 4810, Ap
565	66	4.2	567	7	US-11-016-503-2	Sequence 2, Appli	639	65	4.1	432	7	US-11-055-822-1096	Sequence 1096, Ap
567	66	4.2	607	6	US-10-973-115B-344	Sequence 344, App	640	65	4.1	445	7	US-11-072-512-2209	Sequence 2209, Ap
568	66	4.2	607	7	US-11-176-863-2	Sequence 2, Appli	642	65	4.1	449	6	US-10-973-115B-224	Sequence 224, App
569	66	4.2	648	7	US-11-098-686-10873	Sequence 10873, A	643	65	4.1	462	7	US-11-177-648-96	Sequence 96, Appl
570	66	4.2	690	6	US-10-613-744-19	Sequence 19, Appl	644	65	4.1	509	7	US-11-008-727-16	Sequence 16, Appl
571	66	4.2	690	6	US-10-511-657-2	Sequence 2, Appli	645	65	4.1	555	7	US-11-072-512-2330	Sequence 2330, Ap
572	66	4.2	738	6	US-10-880-881-23	Sequence 23, Appl	646	65	4.1	557	7	US-11-016-503-4	Sequence 4, Appli
573	66	4.2	780	7	US-11-087-099-251	Sequence 251, App	647	65	4.1	567	7	US-11-016-503-10	Sequence 10, Appl
574	66	4.2	793	7	US-11-060-914-2	Sequence 2, Appli	648	65	4.1	619	7	US-11-136-244-3	Sequence 3, Appli
575	66	4.2	799	6	US-10-493-909-8	Sequence 8, Appli	649	65	4.1	625	7	US-11-072-512-3210	Sequence 3210, Ap
576	66	4.2	822	6	US-10-493-909-48	Sequence 48, Appl	650	65	4.1	628	7	US-11-037-243-86	Sequence 86, Appl
577	66	4.2	823	7	US-11-087-099-11109	Sequence 11109, A	651	65	4.1	640	7	US-11-136-244-4	Sequence 4, Appli
578	66	4.2	874	6	US-10-510-386-28	Sequence 28, Appl	652	65	4.1	653	6	US-10-501-035-358	Sequence 358, App
579	66	4.2	928	7	US-11-130-594-8	Sequence 8, Appli	653	65	4.1	764	7	US-11-072-512-2379	Sequence 2379, Ap
580	66	4.2	928	7	US-11-201-801-8	Sequence 8, Appli	654	65	4.1	764	7	US-11-124-368A-186	Sequence 186, App
581	66	4.2	931	7	US-11-230-145-2	Sequence 2, Appli	655	65	4.1	922	7	US-11-072-512-2694	Sequence 2694, Ap
582	66	4.2	1035	6	US-10-966-483-20	Sequence 20, Appl	656	65	4.1	1036	7	US-11-096-568A-28315	Sequence 28315, A
583	66	4.2	1035	6	US-11-021-441-4	Sequence 4, Appli	657	65	4.1	1070	7	US-11-096-568A-28314	Sequence 28314, A
584	66	4.2	1047	6	US-10-510-386-200	Sequence 200, App	658	65	4.1	1131	6	US-11-072-512-2866	Sequence 2866, Ap
585	66	4.2	1161	7	US-11-075-646-8	Sequence 8, Appli	659	65	4.1	1198	6	US-10-451-375-4	Sequence 4, Appli
586	66	4.2	1551	7	US-11-087-099-10366	Sequence 10366, A	660	65	4.1	1276	7	US-11-096-568A-28313	Sequence 28313, A
587	66	4.2	1647	7	US-11-052-554A-260	Sequence 260, App	661	65	4.1	1981	6	US-10-374-954-23	Sequence 23, Appl
588	65.5	4.2	145	6	US-10-793-626-1504	Sequence 1504, Ap	662	65	4.1	1992	7	US-11-013-759-3	Sequence 3, Appli
589	65.5	4.2	192	7	US-11-096-568A-3893	Sequence 3893, Ap	663	65	4.1	1992	7	US-11-013-759-13	Sequence 13, Appl
590	65.5	4.2	205	7	US-11-096-568A-3892	Sequence 3892, Ap	664	65	4.1	1998	6	US-10-374-954-21	Sequence 21, Appl
591	65.5	4.2	257	7	US-11-096-568A-25250	Sequence 25250, A	665	65	4.1	2009	6	US-10-374-954-2	Sequence 2, Appli
592	65.5	4.2	436	7	US-11-024-959-394	Sequence 394, App	666	65	4.1	2047	7	US-11-013-759-4	Sequence 4, Appli
593	65.5	4.2	445	6	US-10-467-657-5092	Sequence 5092, Ap	667	65	4.1	2047	7	US-11-013-759-7	Sequence 7, Appli
594	65.5	4.2	470	6	US-10-878-556A-101	Sequence 101, App	668	64.5	4.1	160	6	US-10-533-811-13	Sequence 13, Appl
595	65.5	4.2	485	7	US-11-096-568A-26552	Sequence 26552, A	669	64.5	4.1	223	7	US-11-087-099-7197	Sequence 7197, Ap
596	65.5	4.2	539	7	US-11-096-568A-13358	Sequence 13358, A	670	64.5	4.1	250	7	US-11-096-568A-3195	Sequence 3195, Ap
597	65.5	4.2	541	7	US-11-201-916-17	Sequence 17, Appl	671	64.5	4.1	264	7	US-11-096-568A-5205	Sequence 5205, Ap
598	65.5	4.2	560	7	US-11-018-868-40	Sequence 40, Appl	672	64.5	4.1	282	6	US-10-055-877-137	Sequence 127, App
599	65.5	4.2	567	6	US-10-485-517-216	Sequence 216, App	673	64.5	4.1	282	7	US-11-087-177-9	Sequence 9, Appli
600	65.5	4.2	612	6	US-10-467-657-3988	Sequence 3988, Ap	674	64.5	4.1	315	7	US-11-072-512-2198	Sequence 2198, Ap
601	65.5	4.2	652	6	US-10-821-234-1016	Sequence 1016, Ap	675	64.5	4.1	370	7	US-11-096-568A-3216	Sequence 3216, Ap
602	65.5	4.2	683	7	US-11-124-368A-243	Sequence 243, App	676	64.5	4.1	370	7	US-11-096-568A-3217	Sequence 3217, Ap
603	65.5	4.2	707	7	US-11-072-512-3162	Sequence 3162, App	677	64.5	4.1	371	6	US-10-467-657-1926	Sequence 1926, Ap
604	65.5	4.2	777	7	US-11-124-368A-238	Sequence 238, App	678	64.5	4.1	378	7	US-11-087-099-8872	Sequence 8872, Ap
605	65.5	4.2	778	7	US-11-124-368A-240	Sequence 240, App	679	64.5	4.1	378	7	US-11-087-099-11183	Sequence 11183, A
606	65.5	4.2	791	7	US-11-124-368A-245	Sequence 245, App	680	64.5	4.1	380	7	US-11-087-099-5374	Sequence 5374, Ap
607	65.5	4.2	836	7	US-11-124-368A-246	Sequence 246, App	681	64.5	4.1	381	7	US-11-087-099-12159	Sequence 12159, A
608	65.5	4.2	877	6	US-10-485-517-200	Sequence 200, App	682	64.5	4.1	388	7	US-11-087-099-4330	Sequence 4330, Ap
609	65.5	4.2	925	6	US-10-453-372-1124	Sequence 1124, Ap	683	64.5	4.1	393	7	US-11-096-568A-3215	Sequence 3215, Ap
610	65.5	4.2	966	6	US-10-877-346-32	Sequence 32, Appl	684	64.5	4.1	407	7	US-11-096-568A-5204	Sequence 5204, Ap
611	65.5	4.2	972	6	US-10-453-372-1128	Sequence 1128, Ap	685	64.5	4.1	433	7	US-11-096-568A-5203	Sequence 5203, Ap
612	65.5	4.2	997	7	US-11-080-991-50	Sequence 50, Appl	686	64.5	4.1	482	6	US-10-821-234-972	Sequence 972, App
613	65.5	4.2	999	7	US-11-113-424-36	Sequence 36, App	687	64.5	4.1	519	7	US-11-087-099-5406	Sequence 5406, Ap
614	65.5	4.2	2432	6	US-10-821-234-899	Sequence 899, App	688	64.5	4.1	579	7	US-11-072-512-2360	Sequence 2360, Ap
615	65.5	4.2	2551	7	US-11-052-554A-368	Sequence 368, App	689	64.5	4.1	645	7	US-11-072-512-3418	Sequence 3418, Ap
616	65.5	4.2	3069	7	US-11-235-732-2	Sequence 2, Appli	691	64.5	4.1	649	7	US-11-102-240-132	Sequence 132, App
617	65.5	4.2	3095	7	US-11-235-732-4	Sequence 4, Appli	692	64.5	4.1	649	7	US-11-103-195-132	Sequence 132, App
618	65.5	4.2	3100	7	US-11-235-732-7	Sequence 7, Appli	693	64.5	4.1	651	7	US-11-198-819-22	Sequence 22, Appl
619	65.5	4.2	3567	6	US-10-453-372-1112	Sequence 1112, Ap	694	64.5	4.1	729	7	US-11-096-568A-19858	Sequence 19858, A

695	64.5	4.1	754	6	US-10-467-962B-63	Sequence 63, Appl	769	63.5	4.0	290	7	US-11-096-568A-18388	Sequence 18388, A
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697	64.5	4.1	848	7	US-11-096-568A-19856	Sequence 19856, A	771	63.5	4.0	316	6	US-10-517-696-126	Sequence 126, App
698	64.5	4.1	1075	7	US-11-098-686-10295	Sequence 10295, A	772	63.5	4.0	319	7	US-11-087-099-9069	Sequence 9069, Ap
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701	64.5	4.1	2910	7	US-11-087-084-2	Sequence 2, Appl	775	63.5	4.0	336	6	US-10-517-696-153	Sequence 153, App
702	64.5	4.1	2910	7	US-11-087-085-2	Sequence 2, Appl	776	63.5	4.0	336	6	US-11-096-568A-5367	Sequence 5367, Ap
703	64	4.1	122	7	US-11-087-099-6151	Sequence 6151, Ap	777	63.5	4.0	350	6	US-10-517-696-125	Sequence 125, App
704	64	4.1	131	7	US-11-096-568A-12238	Sequence 12238, A	778	63.5	4.0	358	7	US-11-096-568A-21943	Sequence 21943, A
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707	64	4.1	198	7	US-11-087-099-11173	Sequence 11173, A	781	63.5	4.0	375	7	US-11-096-568A-21942	Sequence 21942, A
708	64	4.1	203	7	US-11-050-857-488	Sequence 488, App	782	63.5	4.0	379	6	US-10-517-696-150	Sequence 150, App
709	64	4.1	203	7	US-11-043-806-370	Sequence 370, App	783	63.5	4.0	384	7	US-11-096-568A-33509	Sequence 33509, A
710	64	4.1	262	7	US-11-096-568A-11276	Sequence 11276, A	784	63.5	4.0	388	7	US-11-096-568A-33508	Sequence 33508, A
711	64	4.1	266	7	US-11-096-568A-11275	Sequence 11275, A	785	63.5	4.0	393	6	US-11-052-554A-254	Sequence 254, App
712	64	4.1	276	7	US-11-096-568A-30981	Sequence 30981, A	786	63.5	4.0	396	6	US-10-517-696-147	Sequence 147, App
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714	64	4.1	319	6	US-10-793-626-2008	Sequence 792, App	788	63.5	4.0	397	7	US-11-230-180-6	Sequence 6, Appl
715	64	4.1	319	6	US-10-793-626-2008	Sequence 792, App	788	63.5	4.0	398	6	US-10-517-696-136	Sequence 136, App
716	64	4.1	335	6	US-10-873-528-4	Sequence 4, Appl	790	63.5	4.0	409	6	US-10-517-696-149	Sequence 149, App
717	64	4.1	338	7	US-11-096-568A-30980	Sequence 30980, A	791	63.5	4.0	420	6	US-10-517-696-141	Sequence 141, App
718	64	4.1	342	6	US-10-980-388-118	Sequence 118, App	792	63.5	4.0	446	7	US-11-102-621-138	Sequence 138, App
719	64	4.1	342	7	US-11-174-816-18	Sequence 18, Appl	793	63.5	4.0	458	7	US-11-096-568A-21941	Sequence 21941, A
720	64	4.1	342	7	US-11-174-819-71	Sequence 71, Appl	794	63.5	4.0	463	6	US-10-517-696-121	Sequence 121, App
721	64	4.1	346	7	US-11-096-568A-30979	Sequence 30979, A	795	63.5	4.0	475	6	US-10-501-035-309	Sequence 309, App
722	64	4.1	349	6	US-10-973-115B-424	Sequence 424, App	796	63.5	4.0	475	6	US-10-517-696-117	Sequence 117, App
723	64	4.1	373	6	US-10-498-026-113	Sequence 113, App	797	63.5	4.0	484	6	US-10-517-696-132	Sequence 132, App
724	64	4.1	379	7	US-11-087-099-8341	Sequence 8341, Ap	798	63.5	4.0	484	6	US-10-517-696-120	Sequence 120, App
725	64	4.1	381	7	US-11-096-568A-17861	Sequence 17861, A	799	63.5	4.0	485	6	US-10-517-696-142	Sequence 142, App
726	64	4.1	382	7	US-11-096-568A-17860	Sequence 17860, A	800	63.5	4.0	492	6	US-10-517-696-131	Sequence 131, App
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728	64	4.1	387	6	US-10-895-064-611	Sequence 13774, A	802	63.5	4.0	517	6	US-10-517-696-144	Sequence 144, App
729	64	4.1	387	7	US-11-129-741-611	Sequence 611, App	803	63.5	4.0	524	6	US-10-517-696-122	Sequence 122, App
730	64	4.1	387	7	US-11-096-568A-13773	Sequence 13773, A	804	63.5	4.0	524	6	US-11-087-099-12268	Sequence 12268, A
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732	64	4.1	388	7	US-11-096-568A-27930	Sequence 27930, A	806	63.5	4.0	541	7	US-11-201-916-14	Sequence 14, Appl
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737	64	4.1	446	7	US-11-087-099-8235	Sequence 8235, Ap	811	63.5	4.0	614	6	US-10-517-696-128	Sequence 128, App
738	64	4.1	447	6	US-10-967-527A-14	Sequence 14, Appl	812	63.5	4.0	654	6	US-10-510-947-6	Sequence 6, Appl
739	64	4.1	462	7	US-11-177-648-97	Sequence 97, Appl	813	63.5	4.0	654	6	US-10-995-561-632	Sequence 632, App
740	64	4.1	462	7	US-11-087-099-6811	Sequence 6811, Ap	814	63.5	4.0	693	7	US-11-085-185-4	Sequence 4, Appl
741	64	4.1	513	7	US-11-096-568A-12983	Sequence 12983, A	815	63.5	4.0	778	6	US-10-821-234-1276	Sequence 1276, Ap
742	64	4.1	537	7	US-11-087-099-4695	Sequence 4695, Ap	816	63.5	4.0	1009	6	US-10-912-971-16	Sequence 16, Appl
743	64	4.1	548	7	US-11-096-568A-12982	Sequence 12982, A	817	63.5	4.0	1053	6	US-10-517-939-52	Sequence 52, Appl
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745	64	4.1	619	6	US-10-999-886-3	Sequence 3, Appl	819	63.5	4.0	1230	7	US-11-087-099-8922	Sequence 8922, Ap
746	64	4.1	640	6	US-10-999-886-4	Sequence 4, Appl	820	63.5	4.0	1255	7	US-11-050-857-487	Sequence 487, App
747	64	4.1	756	6	US-10-055-877-188	Sequence 188, App	821	63.5	4.0	1255	7	US-11-043-806-398	Sequence 398, App
748	64	4.1	860	7	US-11-087-099-6246	Sequence 6246, Ap	822	63.5	4.0	1315	6	US-10-995-561-630	Sequence 630, App
749	64	4.1	972	7	US-11-177-894-17	Sequence 17, Appl	823	63.5	4.0	1607	7	US-11-098-686-10178	Sequence 10178, A
750	64	4.1	976	7	US-11-148-770-31	Sequence 31, Appl	824	63.5	4.0	1607	7	US-11-098-686-10178	Sequence 58, Appl
751	64	4.1	976	7	US-11-177-894-15	Sequence 15, Appl	825	63.5	4.0	1992	7	US-11-069-834-58	Sequence 58, Appl
752	64	4.1	976	7	US-11-177-894-16	Sequence 16, Appl	826	63.5	4.0	2000	7	US-11-069-834-56	Sequence 56, Appl
753	64	4.1	976	7	US-11-177-894-18	Sequence 18, Appl	827	63.5	4.0	2015	7	US-11-052-554A-374	Sequence 374, App
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755	64	4.1	976	7	US-11-177-894-20	Sequence 20, Appl	829	63.5	4.0	2176	7	US-11-193-561-25	Sequence 25, Appl
756	64	4.1	976	7	US-11-177-894-21	Sequence 21, Appl	830	63.5	4.0	2176	7	US-11-193-789-25	Sequence 25, Appl
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759	64	4.1	1123	7	US-11-037-243-77	Sequence 77, Appl	833	63.5	4.0	2296	6	US-11-193-561-23	Sequence 23, Appl
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762	64	4.1	1637	6	US-10-055-877-144	Sequence 144, App	836	63.5	4.0	2296	7	US-11-193-806-23	Sequence 23, Appl
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765	63.5	4.0	249	6	US-10-821-234-1125	Sequence 1125, Ap	839	63.5	4.0	3487	7	US-11-087-099-10423	Sequence 10423, A
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768	63.5	4.0	273	7	US-11-096-568A-22109	Sequence 22109, A							



842	63	4.0	192	7	US-11-072-512-3585	Sequence 3585, Ap	915	63	4.0	2224	7	US-11-043-806-393	Sequence 393, App
843	63	4.0	193	7	US-11-096-568A-24769	Sequence 24769, A	916	62.5	4.0	146	6	US-10-467-657-5594	Sequence 5594, Ap
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848	63	4.0	327	6	US-10-055-877-183	Sequence 183, App	921	62.5	4.0	271	6	US-10-353-783-52	Sequence 52, Appl
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852	63	4.0	344	7	US-11-174-819-28	Sequence 28, Appl	926	62.5	4.0	299	7	US-11-000-463-747	Sequence 747, App
853	63	4.0	359	7	US-11-087-099-7177	Sequence 7177, Ap	927	62.5	4.0	299	7	US-11-000-463-748	Sequence 748, App
854	63	4.0	362	7	US-11-087-099-7379	Sequence 7379, Ap	928	62.5	4.0	299	7	US-11-173-037-7	Sequence 7, Appl
855	63	4.0	363	7	US-11-087-099-9842	Sequence 9842, Ap	929	62.5	4.0	343	7	US-11-098-686-11280	Sequence 11280, A
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857	63	4.0	386	7	US-11-055-822-586	Sequence 586, App	931	62.5	4.0	410	7	US-11-089-551A-28	Sequence 28, Appl
858	63	4.0	408	7	US-11-096-568A-31339	Sequence 31339, A	932	62.5	4.0	440	7	US-11-087-099-8456	Sequence 8456, Ap
859	63	4.0	471	7	US-11-087-099-8817	Sequence 8817, Ap	933	62.5	4.0	442	7	US-11-102-621-136	Sequence 126, App
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863	63	4.0	472	7	US-11-165-226-13	Sequence 13, Appl	937	62.5	4.0	489	7	US-11-096-568A-32213	Sequence 32213, A
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866	63	4.0	497	6	US-10-501-035-337	Sequence 337, App	940	62.5	4.0	515	6	US-10-517-696-114	Sequence 114, App
867	63	4.0	501	6	US-10-485-517-381	Sequence 381, App	941	62.5	4.0	524	6	US-10-517-696-113	Sequence 113, App
868	63	4.0	513	6	US-10-641-678-66	Sequence 66, Appl	942	62.5	4.0	539	7	US-11-096-568A-32212	Sequence 32212, A
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870	63	4.0	546	7	US-11-072-512-2051	Sequence 2051, Ap	944	62.5	4.0	545	7	US-11-096-568A-32211	Sequence 32211, A
871	63	4.0	548	7	US-11-096-568A-402	Sequence 402, App	945	62.5	4.0	558	7	US-11-096-568A-25748	Sequence 25748, A
872	63	4.0	581	7	US-11-236-198-7	Sequence 7, Appl	946	62.5	4.0	573	7	US-11-090-617-2	Sequence 2, Appl
873	63	4.0	615	7	US-11-096-568A-401	Sequence 401, App	947	62.5	4.0	575	7	US-11-096-568A-27577	Sequence 27577, A
874	63	4.0	615	7	US-11-096-568A-403	Sequence 403, App	948	62.5	4.0	577	7	US-11-124-368A-232	Sequence 232, App
875	63	4.0	629	7	US-11-096-568A-29173	Sequence 29173, A	949	62.5	4.0	585	7	US-11-108-172-1067	Sequence 1067, Ap
876	63	4.0	643	7	US-11-096-568A-400	Sequence 400, App	950	62.5	4.0	588	7	US-11-196-475-122	Sequence 122, App
877	63	4.0	645	6	US-10-485-517-244	Sequence 244, App	951	62.5	4.0	603	7	US-11-096-568A-25747	Sequence 25747, A
878	63	4.0	678	7	US-11-096-568A-29172	Sequence 29172, A	952	62.5	4.0	880	7	US-11-087-099-950	Sequence 950, App
879	63	4.0	706	7	US-11-087-099-4237	Sequence 4237, Ap	953	62.5	4.0	915	7	US-11-156-084-119	Sequence 119, App
880	63	4.0	719	7	US-11-096-568A-29171	Sequence 29171, A	954	62.5	4.0	965	7	US-11-113-424-2	Sequence 2, Appl
881	63	4.0	726	6	US-11-096-568A-28626	Sequence 28626, A	955	62.5	4.0	1001	6	US-10-330-773-510	Sequence 510, App
882	63	4.0	728	6	US-10-530-340-14	Sequence 14, Appl	956	62.5	4.0	1162	6	US-10-451-375-3	Sequence 3, Appl
883	63	4.0	743	7	US-11-072-512-2340	Sequence 2340, Ap	957	62.5	4.0	2059	7	US-11-087-100-4	Sequence 4, Appl
884	63	4.0	756	7	US-11-096-568A-28625	Sequence 28625, A	958	62.5	4.0	2059	7	US-11-087-084-4	Sequence 4, Appl
885	63	4.0	786	7	US-11-096-568A-32685	Sequence 32685, A	959	62.5	4.0	2059	7	US-11-087-085-4	Sequence 4, Appl
886	63	4.0	793	7	US-11-096-568A-28222	Sequence 28222, A	960	62.5	4.0	2304	6	US-10-330-773-310	Sequence 310, App
887	63	4.0	798	7	US-11-096-568A-28221	Sequence 28221, A	961	62.5	4.0	2367	7	US-11-051-453-42	Sequence 42, Appl
888	63	4.0	801	7	US-11-096-568A-28220	Sequence 28220, A	962	62.5	4.0	2472	7	US-11-203-806A-2	Sequence 2, Appl
889	63	4.0	808	7	US-11-087-099-7073	Sequence 7073, Ap	963	62.5	4.0	2871	7	US-11-169-041-131	Sequence 131, App
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891	63	4.0	902	7	US-11-182-016-36	Sequence 36, Appl	965	62.5	4.0	3487	7	US-11-087-099-9068	Sequence 9068, Ap
892	63	4.0	1083	7	US-11-113-751-40	Sequence 40, Appl	966	62	3.9	146	7	US-11-096-568A-14379	Sequence 14379, A
893	63	4.0	1393	7	US-11-096-568A-32145	Sequence 32145, A	967	62	3.9	162	7	US-11-096-568A-21263	Sequence 21263, A
894	63	4.0	1637	6	US-10-821-234-1204	Sequence 1204, Ap	968	62	3.9	165	6	US-10-821-234-1539	Sequence 1539, Ap
895	63	4.0	1645	7	US-11-043-806-364	Sequence 364, App	969	62	3.9	175	6	US-10-967-527A-7	Sequence 7, Appl
896	63	4.0	1928	6	US-10-480-330-30	Sequence 30, Appl	970	62	3.9	195	7	US-11-096-568A-14743	Sequence 14743, A
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898	63	4.0	1966	6	US-10-480-330-2	Sequence 2, Appl	972	62	3.9	226	7	US-11-132-285-5	Sequence 5, Appl
899	63	4.0	1966	6	US-10-480-330-6	Sequence 6, Appl	973	62	3.9	231	7	US-11-132-285-61	Sequence 61, Appl
900	63	4.0	1966	6	US-10-480-330-8	Sequence 8, Appl	974	62	3.9	233	7	US-11-096-568A-18993	Sequence 18993, A
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902	63	4.0	1966	6	US-10-480-330-12	Sequence 12, Appl	976	62	3.9	235	7	US-11-219-359-5	Sequence 5, Appl
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907	63	4.0	1966	6	US-10-480-330-22	Sequence 22, Appl	981	62	3.9	321	7	US-11-096-568A-21893	Sequence 21893, A
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910	63	4.0	2074	6	US-10-480-330-28	Sequence 28, Appl	984	62	3.9	341	7	US-11-240-769-72	Sequence 72, Appl
911	63	4.0	2074	6	US-11-043-806-365	Sequence 365, App	985	62	3.9	341	7	US-11-096-568A-23537	Sequence 23537, A
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914	63	4.0	2224	7	US-11-043-806-392	Sequence 392, App	989	62	3.9	346	6	US-10-967-457-77	Sequence 77, Appl

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1005	62	3.9	489	7	US-11-264-728-4	Sequence 4, Appl	1078	61.5	3.9	541	7	US-11-169-041-136	Sequence 136, App
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1177	61	3.9	214	7	US-11-080-991-94	Sequence 94, Appl	1251	60.5	3.8	761	6	US-11-213-443-22	Sequence 22, Appl
1178	61	3.9	223	6	US-10-895-064-388	Sequence 388, Appl	1252	60.5	3.8	773	6	US-10-995-561-852	Sequence 852, App
1179	61	3.9	2723	7	US-11-129-741-388	Sequence 388, Appl	1253	60.5	3.8	803	6	US-10-821-234-1643	Sequence 1643, Ap
1180	61	3.9	2828	7	US-11-080-991-54	Sequence 54, Appl	1254	60.5	3.8	840	7	US-11-108-172-1102	Sequence 1102, Ap
1181	61	3.9	2828	7	US-11-186-284-49	Sequence 49, Appl	1255	60.5	3.8	858	6	US-10-995-561-854	Sequence 854, App
1182	60.5	3.8	53	7	US-11-096-568A-6179	Sequence 6179, Ap	1256	60.5	3.8	871	7	US-11-077-550-8	Sequence 2, Appl1
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1184	60.5	3.8	132	7	US-11-087-099-3992	Sequence 3992, Ap	1258	60.5	3.8	871	7	US-11-077-550-26	Sequence 26, Appl
1185	60.5	3.8	154	6	US-10-475-075-802	Sequence 802, Appl	1259	60.5	3.8	871	7	US-11-077-550-153	Sequence 153, App
1186	60.5	3.8	161	7	US-11-096-568A-6182	Sequence 6182, Ap	1260	60.5	3.8	873	7	US-11-077-550-6	Sequence 6, Appl1
1187	60.5	3.8	171	7	US-11-096-568A-13784	Sequence 13784, A	1261	60.5	3.8	873	7	US-11-077-550-149	Sequence 149, App
1188	60.5	3.8	221	7	US-11-112-481C-2	Sequence 2, Appl1	1262	60.5	3.8	873	7	US-11-077-550-151	Sequence 151, App
1189	60.5	3.8	237	6	US-10-884-730-336	Sequence 336, Appl	1263	60.5	3.8	879	7	US-11-077-550-159	Sequence 159, App
1190	60.5	3.8	245	7	US-11-186-284-167	Sequence 167, Appl	1264	60.5	3.8	894	7	US-11-077-550-4	Sequence 4, Appl1
1191	60.5	3.8	248	6	US-11-176-830-528	Sequence 528, Appl	1265	60.5	3.8	907	7	US-11-087-099-3272	Sequence 3272, Ap
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1193	60.5	3.8	266	7	US-11-087-099-5491	Sequence 5491, Ap	1267	60.5	3.8	965	7	US-11-147-047-51	Sequence 51, Appl
1194	60.5	3.8	266	7	US-11-087-099-7758	Sequence 7758, Ap	1268	60.5	3.8	1127	7	US-11-077-550-40	Sequence 40, Appl
1195	60.5	3.8	272	7	US-11-087-099-8109	Sequence 8109, Ap	1269	60.5	3.8	1129	7	US-11-077-550-42	Sequence 42, Appl
1196	60.5	3.8	272	7	US-11-087-099-9485	Sequence 9485, Ap	1270	60.5	3.8	1137	7	US-11-072-762-70	Sequence 70, Appl
1197	60.5	3.8	273	6	US-10-353-783-42	Sequence 42, Appl	1271	60.5	3.8	1137	6	US-11-012-761-81	Sequence 81, App
1198	60.5	3.8	276	6	US-11-020-602-224	Sequence 224, Appl	1272	60.5	3.8	1178	7	US-10-995-561-851	Sequence 293, Appl
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1201	60.5	3.8	278	6	US-10-861-934-26	Sequence 26, Appl	1275	60.5	3.8	1337	7	US-11-112-304A-33	Sequence 33, Appl
1202	60.5	3.8	278	7	US-11-072-512-3938	Sequence 3938, Ap	1276	60.5	3.8	1532	7	US-11-212-443-62	Sequence 62, Appl
1203	60.5	3.8	279	6	US-10-861-934-24	Sequence 24, Appl	1277	60.5	3.8	1995	7	US-11-069-834-60	Sequence 60, Appl
1204	60.5	3.8	279	6	US-10-861-934-32	Sequence 32, Appl	1278	60.5	3.8	2244	7	US-11-131-263-9	Sequence 9, Appl1
1205	60.5	3.8	279	7	US-11-032-797-5	Sequence 5, Appl1	1279	60.5	3.8	2244	7	US-11-131-263-18	Sequence 18, Appl
1206	60.5	3.8	283	7	US-11-096-568A-30112	Sequence 30112, A	1280	60.5	3.8	2244	7	US-11-131-263-30	Sequence 30, Appl
1207	60.5	3.8	293	6	US-10-821-234-1374	Sequence 1374, Ap	1281	60.5	3.8	2314	7	US-11-013-759-11	Sequence 11, Appl
1208	60.5	3.8	306	7	US-11-096-568A-16235	Sequence 16235, A	1282	60.5	3.8	2766	6	US-10-877-346-62	Sequence 62, Appl
1209	60.5	3.8	307	6	US-10-401-386B-31	Sequence 31, Appl	1283	60.5	3.8	8746	7	US-11-098-686-10232	Sequence 10232, A

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1285	60	3.8	112	7	US-11-096-568A-7599	Sequence 7599, Ap	1360	60	3.8	756	6	US-10-055-877-34	Sequence 34, Appl
1286	60	3.8	135	7	US-11-077-619-106	Sequence 106, App	1361	60	3.8	756	6	US-10-055-877-187	Sequence 187, App
1287	60	3.8	142	7	US-11-186-284-105	Sequence 105, App	1362	60	3.8	756	6	US-10-055-877-189	Sequence 189, App
1288	60	3.8	150	6	US-10-467-657-2040	Sequence 2040, Ap	1363	60	3.8	771	7	US-11-147-047-34	Sequence 34, Appl
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1302	60	3.8	324	7	US-11-087-099-8018	Sequence 8018, Ap	1377	60	3.8	1171	7	US-11-087-099-9917	Sequence 9917, Ap
1303	60	3.8	324	7	US-11-087-099-9180	Sequence 9180, Ap	1378	60	3.8	1570	6	US-10-330-773-936	Sequence 936, App
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1322	60	3.8	390	7	US-11-098-686-10913	Sequence 10913, A	1397	59.5	3.8	251	7	US-11-096-568A-1074	Sequence 1074, App
1323	60	3.8	412	7	US-11-096-568A-21231	Sequence 21231, A	1398	59.5	3.8	251	7	US-11-096-568A-16236	Sequence 16236, A
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1326	60	3.8	438	7	US-11-074-176-152	Sequence 152, App	1401	59.5	3.8	266	7	US-11-087-099-4585	Sequence 4585, Ap
1327	60	3.8	440	7	US-11-096-568A-32490	Sequence 32490, A	1402	59.5	3.8	266	7	US-11-087-099-6865	Sequence 6865, Ap
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1342	60	3.8	554	7	US-11-096-568A-10891	Sequence 10891, A	1417	59.5	3.8	331	7	US-11-096-568A-3911	Sequence 3911, Ap
1343	60	3.8	556	7	US-11-124-368A-303	Sequence 303, App	1418	59.5	3.8	332	7	US-11-096-568A-22442	Sequence 22442, A
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1346	60	3.8	663	7	US-11-216-245-1	Sequence 1, Appl	1421	59.5	3.8	347	6	US-10-821-234-1379	Sequence 1379, Ap
1347	60	3.8	682	7	US-11-072-175-154	Sequence 154, App	1422	59.5	3.8	375	7	US-11-087-099-7023	Sequence 7023, Ap
1348	60	3.8	682	7	US-11-072-175-154	Sequence 154, App	1423	59.5	3.8	406	7	US-11-107-028-7	Sequence 7, Appl
1349	60	3.8	690	6	US-10-973-115B-306	Sequence 306, App	1424	59.5	3.8	408	7	US-11-072-512-2274	Sequence 2274, Ap
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1356	60	3.8					1431	59.5	3.8	463	6	US-10-973-115B-360	Sequence 360, App
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1435	59.5	3.8	480	6	US-10-510-386-12	Sequence 12, Appli
1436	59.5	3.8	481	7	US-11-031-206-76	Sequence 76, Appli
1437	59.5	3.8	487	7	US-11-096-568A-22133	Sequence 22133, A
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1443	59.5	3.8	519	7	US-11-096-568A-22132	Sequence 22132, A
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1446	59.5	3.8	545	7	US-11-065-943-73	Sequence 73, Appli
1447	59.5	3.8	553	7	US-11-055-822-266	Sequence 266, App
1448	59.5	3.8	593	7	US-11-154-673-3	Sequence 3, Appli
1449	59.5	3.8	629	7	US-11-098-686-11359	Sequence 11359, A
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1452	59.5	3.8	726	7	US-11-096-568A-2446	Sequence 2446, Ap
1453	59.5	3.8	727	7	US-11-096-568A-2445	Sequence 2445, Ap
1454	59.5	3.8	736	6	US-10-330-773-813	Sequence 813, App
1455	59.5	3.8	749	6	US-10-330-773-536	Sequence 536, App
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1457	59.5	3.8	836	7	US-11-096-568A-2444	Sequence 2444, Ap
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1459	59.5	3.8	871	7	US-11-077-550-155	Sequence 155, App
1460	59.5	3.8	873	7	US-11-077-550-163	Sequence 163, App
1461	59.5	3.8	873	7	US-11-077-550-165	Sequence 165, App
1462	59.5	3.8	874	7	US-11-087-099-10263	Sequence 10263, A
1463	59.5	3.8	887	7	US-11-077-550-161	Sequence 161, App
1464	59.5	3.8	919	7	US-11-074-176-284	Sequence 284, App
1465	59.5	3.8	933	7	US-11-072-512-2928	Sequence 2928, Ap
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1468	59.5	3.8	1121	7	US-11-113-751-24	Sequence 24, Appli
1469	59.5	3.8	1121	7	US-11-024-959-459	Sequence 459, App
1470	59.5	3.8	1159	7	US-11-113-751-27	Sequence 27, Appli
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1472	59.5	3.8	1203	7	US-11-096-568A-33183	Sequence 33183, A
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1477	59.5	3.8	1770	7	US-11-103-957-21	Sequence 21, Appli
1478	59.5	3.8	1770	7	US-11-018-868-17	Sequence 17, Appli
1479	59.5	3.8	1970	6	US-10-821-234-1641	Sequence 1641, Ap
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1481	59	3.7	121	7	US-11-087-099-10410	Sequence 10410, A
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1488	59	3.7	208	7	US-11-128-440-6	Sequence 6, Appli
1489	59	3.7	214	7	US-11-096-568A-1416	Sequence 1416, Ap
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1492	59	3.7	226	7	US-11-096-568A-2890	Sequence 2890, Ap
1493	59	3.7	226	7	US-11-096-568A-7534	Sequence 7534, Ap
1494	59	3.7	248	7	US-11-176-830-524	Sequence 524, App
1495	59	3.7	264	7	US-11-096-568A-8571	Sequence 8571, Ap
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154	86.5	5.5	807	2	US-09-294-663-4	Sequence 4, Appl	227	81.5	5.2	687	2	US-08-521-872-4	Sequence 4, Appl
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168	84	5.3	216	2	US-09-588-995A-8	Sequence 8, Appl	241	81	5.1	1322	2	US-09-197-970B-7	Sequence 7, Appl
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285	79.5	5.0	461	6	5395760-2	Patent No. 5395760	358	78	5.0	280	2	US-09-903-603A-325	Sequence 325, App
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296	79.5	5.0	1114	2	US-09-262-537-34	Sequence 34, Appl	369	78	5.0	308	2	US-09-248-796A-14578	Sequence 14578, A
297	79.5	5.0	1123	2	US-09-262-537-4	Sequence 4, Appli	370	78	5.0	434	2	US-09-248-796A-16546	Sequence 16546, A
298	79.5	5.0	1177	2	US-09-262-537-2	Sequence 2, Appli	371	78	5.0	564	2	US-10-069-540A-2	Sequence 2, Appli
299	79.5	5.0	1403	2	US-09-262-537-6	Sequence 6, Appli	372	78	5.0	609	2	US-09-198-452A-579	Sequence 579, App
300	79	5.0	175	2	US-08-700-651-12	Sequence 12, Appl	373	78	5.0	849	1	US-08-405-392-18	Sequence 18, Appl
301	79	5.0	175	2	US-08-928-361B-17	Sequence 17, Appl	374	78	5.0	849	2	US-08-487-691-18	Sequence 18, Appl
302	79	5.0	175	2	US-08-988-995A-17	Sequence 17, Appl	375	78	5.0	849	2	US-08-189-738A-19	Sequence 19, Appl
303	79	5.0	334	2	US-09-107-532A-6336	Sequence 6336, Ap	376	78	5.0	905	1	US-08-405-392-2	Sequence 2, Appli
304	79	5.0	374	2	US-09-489-847-166	Sequence 166, App	377	78	5.0	905	2	US-08-487-691-2	Sequence 2, Appli
305	79	5.0	382	2	US-09-907-794A-137	Sequence 137, App	378	78	5.0	905	2	US-08-666-221B-4	Sequence 4, Appli
306	79	5.0	382	2	US-09-905-125A-137	Sequence 137, App	379	78	5.0	905	2	US-08-189-738A-2	Sequence 2, Appli
307	79	5.0	382	2	US-09-902-775A-137	Sequence 137, App	380	78	5.0	1006	2	US-09-949-016-7897	Sequence 7897, Ap
308	79	5.0	382	2	US-09-906-700-137	Sequence 137, App	381	78	5.0	1442	1	US-08-015-986A-3	Sequence 3, Appli
309	79	5.0	382	2	US-09-903-603A-137	Sequence 137, App	382	78	5.0	1442	1	US-08-446-363-3	Sequence 3, Appli
310	79	5.0	382	2	US-09-904-920A-137	Sequence 137, App	383	78	5.0	1744	2	US-09-438-185A-542	Sequence 542, App
311	79	5.0	382	2	US-09-905-064-137	Sequence 137, App	384	78	5.0	2176	2	US-09-949-016-9923	Sequence 9923, Ap
312	79	5.0	382	2	US-09-905-381A-137	Sequence 137, App	385	77.5	4.9	497	2	US-09-377-557-10	Sequence 10, Appl
313	79	5.0	382	2	US-09-906-618-137	Sequence 137, App	386	77.5	4.9	514	2	US-08-738-168B-15	Sequence 15, Appl
314	79	5.0	382	2	US-09-906-646-137	Sequence 137, App	387	77.5	4.9	1252	2	US-09-107-433-5067	Sequence 5067, Ap
315	79	5.0	382	2	US-09-904-462-137	Sequence 137, App	388	77.5	4.9	1475	2	US-09-538-092-1160	Sequence 1160, Ap
316	79	5.0	382	2	US-09-902-736A-137	Sequence 137, App	389	77.5	4.9	3969	2	US-08-061-376-5	Sequence 5, Appli
317	79	5.0	382	2	US-09-906-722A-137	Sequence 137, App	390	77.5	4.9	3969	2	US-09-538-092-1262	Sequence 1262, Ap
318	79	5.0	398	2	US-09-248-796A-21599	Sequence 21599, A	391	77	4.9	162	2	US-09-068-140A-2	Sequence 2, Appli
319	79	5.0	455	2	US-09-949-016-10519	Sequence 10519, A	392	77	4.9	173	2	US-09-068-140A-13	Sequence 13, Appli

393	77	4.9	249	2	US-08-700-651-15	Sequence 15, Appl	466	76	4.8	1401	2	US-08-781-891-206	Sequence 206, Appl
394	77	4.9	249	2	US-08-928-361B-20	Sequence 20, Appl	467	76	4.8	1401	2	US-09-618-166-206	Sequence 206, Appl
395	77	4.9	249	2	US-09-588-995A-20	Sequence 20, Appl	468	76	4.8	1426	2	US-09-136-574A-43	Sequence 43, Appl
396	77	4.9	624	2	US-09-877-730-24	Sequence 24, Appl	469	76	4.8	1645	2	US-09-976-594-769	Sequence 769, Appl
397	77	4.9	712	2	US-09-877-730-22	Sequence 22, Appl	470	75.5	4.8	258	2	US-08-961-083-90	Sequence 90, Appl
398	77	4.9	714	2	US-09-949-016-7038	Sequence 7038, Ap	471	75.5	4.8	258	2	US-09-536-784-90	Sequence 90, Appl
399	77	4.9	793	2	US-09-877-730-28	Sequence 28, Appl	472	75.5	4.8	258	2	US-09-765-271-90	Sequence 90, Appl
400	77	4.9	905	2	US-08-666-221B-10	Sequence 10, Appl	473	75.5	4.8	258	2	US-09-765-272A-90	Sequence 90, Appl
401	77	4.9	908	2	US-09-949-016-7580	Sequence 7580, Ap	474	75.5	4.8	348	1	US-08-035-392-2	Sequence 2, Appl
402	77	4.9	991	2	US-09-877-730-12	Sequence 12, Appl	475	75.5	4.8	348	1	US-08-504-511A-2	Sequence 2, Appl
403	77	4.9	1069	2	US-09-877-730-2	Sequence 2, Appl	476	75.5	4.8	430	1	US-08-035-392-4	Sequence 4, Appl
404	77	4.9	1072	2	US-09-877-730-18	Sequence 18, Appl	477	75.5	4.8	430	1	US-08-504-511A-4	Sequence 4, Appl
405	77	4.9	1140	2	US-09-538-092-647	Sequence 647, App	478	75.5	4.8	451	2	US-09-134-001C-4461	Sequence 4461, Ap
406	77	4.9	1150	2	US-09-877-730-8	Sequence 8, Appl	479	75.5	4.8	453	2	US-09-230-225B-4	Sequence 4, Appl
407	77	4.9	1401	2	US-09-127-670-6	Sequence 6, Appl	480	75.5	4.8	484	1	US-08-127-499A-26	Sequence 26, Appl
408	77	4.9	2123	2	US-08-968-685A-10	Sequence 10, Appl	481	75.5	4.8	484	1	US-08-482-847-26	Sequence 26, Appl
409	76.5	4.9	134	2	US-09-248-796A-27317	Sequence 27317, A	482	75.5	4.8	510	2	US-09-270-767-43633	Sequence 43633, A
410	76.5	4.9	240	1	US-08-114-555A-8	Sequence 8, Appl	483	75.5	4.8	511	1	US-08-220-151-17	Sequence 17, Appl
411	76.5	4.9	240	2	US-08-559-397A-14	Sequence 14, Appl	484	75.5	4.8	511	1	US-08-413-118-17	Sequence 17, Appl
412	76.5	4.9	303	2	US-09-248-796A-14269	Sequence 14269, A	485	75.5	4.8	511	2	US-08-473-446-17	Sequence 17, Appl
413	76.5	4.9	334	2	US-10-012-231A-41	Sequence 41, Appl	486	75.5	4.8	565	2	US-08-961-083-218	Sequence 218, App
414	76.5	4.9	334	2	US-10-015-389A-41	Sequence 41, Appl	487	75.5	4.8	565	2	US-09-536-784-218	Sequence 218, App
415	76.5	4.9	334	2	US-10-006-768A-41	Sequence 41, Appl	488	75.5	4.8	565	2	US-09-765-271-218	Sequence 218, App
416	76.5	4.9	334	2	US-10-015-671A-41	Sequence 41, Appl	489	75.5	4.8	565	2	US-09-765-272A-218	Sequence 218, App
417	76.5	4.9	334	2	US-10-015-393A-41	Sequence 41, Appl	490	75.5	4.8	639	2	US-09-949-016-6812	Sequence 6812, Ap
418	76.5	4.9	334	2	US-10-011-833A-41	Sequence 41, Appl	491	75.5	4.8	641	2	US-10-164-595-46	Sequence 46, Appl
419	76.5	4.9	334	2	US-10-006-041A-41	Sequence 41, Appl	492	75.5	4.8	652	2	US-09-949-016-7323	Sequence 7323, Ap
420	76.5	4.9	334	2	US-10-012-064A-41	Sequence 41, Appl	493	75	4.8	210	2	US-09-270-767-32951	Sequence 32951, A
421	76.5	4.9	348	2	US-09-216-295-16	Sequence 16, Appl	494	75	4.8	210	2	US-09-270-767-48168	Sequence 48168, A
422	76.5	4.9	348	2	US-09-632-570-16	Sequence 16, Appl	495	75	4.8	424	1	US-08-419-414-2	Sequence 2, Appl
423	76.5	4.9	348	2	US-09-632-575-46	Sequence 46, Appl	496	75	4.8	425	1	US-09-748-537-14	Sequence 14, Appl
424	76.5	4.9	382	1	US-08-415-818-7	Sequence 7, Appl	497	75	4.8	554	1	US-08-524-051-2	Sequence 2, Appl
425	76.5	4.9	382	1	US-08-894-236-7	Sequence 7, Appl	498	75	4.8	554	2	US-09-052-778-16	Sequence 16, Appl
426	76.5	4.9	382	1	US-08-555-268A-14	Sequence 14, Appl	499	75	4.8	557	2	US-09-248-796A-26892	Sequence 26892, A
427	76.5	4.9	382	2	US-09-430-775-36	Sequence 36, Appl	500	75	4.8	904	2	US-09-198-484-2	Sequence 2, Appl
428	76.5	4.9	382	4	PCT-US96-01444-7	Sequence 7, Appl	501	75	4.8	920	1	US-07-718-575-10	Sequence 10, Appl
429	76.5	4.9	397	2	US-09-198-452A-201	Sequence 201, App	502	75	4.8	920	1	US-08-481-206-10	Sequence 10, Appl
430	76.5	4.9	397	2	US-09-438-185A-188	Sequence 188, App	503	75	4.8	920	1	US-08-486-269A-10	Sequence 10, Appl
431	76.5	4.9	452	2	US-09-248-796A-16219	Sequence 16219, A	504	75	4.8	941	2	US-07-757-022B-14	Sequence 14, Appl
432	76.5	4.9	653	2	US-09-991-181-229	Sequence 229, App	505	75	4.8	1022	2	US-07-757-022B-84	Sequence 84, Appl
433	76.5	4.9	653	2	US-09-990-444-229	Sequence 229, App	506	75	4.8	1038	2	US-07-757-022B-74	Sequence 74, Appl
434	76.5	4.9	653	2	US-09-997-333-229	Sequence 229, App	507	75	4.8	1049	2	US-07-757-022B-58	Sequence 58, Appl
435	76.5	4.9	653	2	US-09-992-598-229	Sequence 229, App	508	75	4.8	1140	2	US-07-757-022B-104	Sequence 104, App
436	76.5	4.9	901	2	US-09-248-796A-14747	Sequence 14747, A	509	75	4.8	1151	1	US-08-286-889-37	Sequence 37, Appl
437	76.5	4.9	1013	2	US-08-860-886-2	Sequence 2, Appl	510	75	4.8	1151	1	US-08-485-618-37	Sequence 37, Appl
438	76.5	4.9	1307	2	US-10-104-047-2438	Sequence 2438, Ap	511	75	4.8	1151	1	US-08-362-652-37	Sequence 37, Appl
439	76.5	4.9	5037	2	US-09-424-783-4	Sequence 4, Appl	512	75	4.8	1151	1	US-08-605-672-37	Sequence 37, Appl
440	76	4.8	154	2	US-09-270-767-61124	Sequence 61124, A	513	75	4.8	1151	1	US-08-482-293A-37	Sequence 37, Appl
441	76	4.8	299	2	US-09-270-767-44350	Sequence 44350, A	514	75	4.8	1151	1	US-08-943-363-37	Sequence 37, Appl
442	76	4.8	321	2	US-09-248-796A-20146	Sequence 20146, A	515	75	4.8	1151	2	US-09-193-043-37	Sequence 37, Appl
443	76	4.8	345	2	US-09-543-681A-6150	Sequence 6150, Ap	516	75	4.8	1151	2	US-09-688-307A-37	Sequence 37, Appl
444	76	4.8	380	2	US-09-134-001C-4558	Sequence 4558, Ap	517	75	4.8	1151	2	US-09-350-259-37	Sequence 37, Appl
445	76	4.8	386	2	US-09-328-352-4722	Sequence 4722, Ap	518	75	4.8	1161	2	US-09-193-043-55	Sequence 55, Appl
446	76	4.8	402	2	US-09-270-767-45612	Sequence 45612, A	519	75	4.8	1161	2	US-09-688-307A-55	Sequence 55, Appl
447	76	4.8	509	2	US-09-907-794A-315	Sequence 315, App	520	75	4.8	1161	2	US-09-350-259-55	Sequence 55, Appl
448	76	4.8	509	2	US-09-905-125A-315	Sequence 315, App	521	75	4.8	1162	1	US-08-728-323A-2	Sequence 2, Appl
449	76	4.8	509	2	US-09-902-775A-315	Sequence 315, App	522	75	4.8	1162	2	US-09-298-568-2	Sequence 2, Appl
450	76	4.8	509	2	US-09-906-700-315	Sequence 315, App	523	75	4.8	1162	2	US-09-410-399-2	Sequence 2, Appl
451	76	4.8	509	2	US-09-903-603A-315	Sequence 315, App	524	75	4.8	1162	2	US-09-894-273-2	Sequence 2, Appl
452	76	4.8	509	2	US-09-904-920A-315	Sequence 315, App	525	75	4.8	1310	2	US-07-757-022B-44	Sequence 44, Appl
453	76	4.8	509	2	US-09-909-064-315	Sequence 315, App	526	75	4.8	1311	2	US-07-757-022B-42	Sequence 42, Appl
454	76	4.8	509	2	US-09-905-381A-315	Sequence 315, App	527	75	4.8	1313	2	US-07-757-022B-142	Sequence 142, App
455	76	4.8	509	2	US-09-906-618-315	Sequence 315, App	528	75	4.8	1314	2	US-07-757-022B-50	Sequence 50, Appl
456	76	4.8	509	2	US-09-906-646-315	Sequence 315, App	529	75	4.8	1320	2	US-07-757-022B-46	Sequence 46, Appl
457	76	4.8	509	2	US-09-904-462-315	Sequence 315, App	530	75	4.8	1320	2	US-10-164-595-58	Sequence 58, Appl
458	76	4.8	509	2	US-09-902-736A-315	Sequence 315, App	531	75	4.8	1320	2	US-10-164-595-58	Sequence 58, Appl
459	76	4.8	509	2	US-09-906-722A-315	Sequence 315, App	532	75	4.8	1354	2	US-07-757-022B-48	Sequence 48, Appl
460	76	4.8	563	2	US-09-949-016-10405	Sequence 10405, A	533	75	4.8	1361	2	US-07-757-022B-40	Sequence 40, Appl
461	76	4.8	985	2	US-09-248-796A-16090	Sequence 16090, A	534	75	4.8	1363	2	US-07-757-022B-52	Sequence 52, Appl
462	76	4.8	1014	2	US-09-078-347A-3	Sequence 3, Appl	535	75	4.8	1404	2	US-07-757-022B-2	Sequence 2, Appl
463	76	4.8	1014	2	US-09-596-248D-25	Sequence 25, Appl	536	75	4.8	1404	2	US-07-757-022B-62	Sequence 62, Appl
464	76	4.8	1014	2	US-09-296-662-35	Sequence 35, Appl	537	75	4.8	1404	2	US-10-164-595-78	Sequence 78, Appl
465	76	4.8	1063	2	US-09-596-248D-47	Sequence 47, Appl	538	75	4.8	1404	2	US-09-298-970A-1	Sequence 1, Appl

539	4.8	1404	2	US-09-897-188-1	Sequence 1, Appli	612	73.5	4.7	128	2	US-08-700-651-7	Sequence 7, Appli
540	4.8	1411	2	US-09-949-016-10827	Sequence 10827, A	613	73.5	4.7	128	2	US-08-928-361B-12	Sequence 12, Appl
541	4.7	109	2	US-09-107-532A-4999	Sequence 4999, Ap	614	73.5	4.7	128	2	US-09-588-995A-12	Sequence 12, Appl
542	4.7	145	2	US-08-808-599A-41	Sequence 41, Appl	615	73.5	4.7	130	2	US-08-700-651-8	Sequence 8, Appli
543	4.7	186	2	US-09-252-991A-20433	Sequence 20433, A	616	73.5	4.7	130	2	US-08-928-361B-13	Sequence 13, Appl
544	4.7	216	2	US-09-248-796A-25076	Sequence 25076, A	617	73.5	4.7	130	2	US-09-588-995A-13	Sequence 13, Appl
545	4.7	270	2	US-09-134-000C-3553	Sequence 3553, Ap	618	73.5	4.7	138	2	US-08-700-651-10	Sequence 10, Appl
546	4.7	312	2	US-09-248-796A-20143	Sequence 20143, A	619	73.5	4.7	138	2	US-08-928-361B-15	Sequence 15, Appl
547	4.7	333	2	US-09-107-532A-6475	Sequence 6475, Ap	620	73.5	4.7	138	2	US-09-588-995A-15	Sequence 15, Appl
548	4.7	386	2	US-09-270-767-44120	Sequence 44120, A	621	73.5	4.7	217	2	US-09-949-016-11174	Sequence 11174, A
549	4.7	429	2	US-09-949-016-81883	Sequence 81883, Ap	622	73.5	4.7	262	2	US-09-248-796A-21451	Sequence 21451, A
550	4.7	429	2	US-09-949-016-81884	Sequence 81884, Ap	623	73.5	4.7	382	2	US-09-248-796A-17276	Sequence 17276, A
551	4.7	478	1	US-08-456-670B-40	Sequence 40, Appl	624	73.5	4.7	397	2	US-08-991-426-4	Sequence 4, Appli
552	4.7	478	2	US-09-372-036-40	Sequence 40, Appl	625	73.5	4.7	397	2	US-09-143-470-4	Sequence 4, Appli
553	4.7	530	2	US-09-912-035-38	Sequence 38, Appl	626	73.5	4.7	397	2	US-08-649-006A-4	Sequence 4, Appli
554	4.7	564	2	US-09-949-016-6898	Sequence 6898, Ap	627	73.5	4.7	397	2	US-09-771-023-4	Sequence 4, Appli
555	4.7	565	2	US-09-949-016-6902	Sequence 6902, Ap	628	73.5	4.7	427	1	US-08-282-197C-53	Sequence 53, Appl
556	4.7	587	2	US-09-815-923-4	Sequence 4, Appli	629	73.5	4.7	499	2	US-09-561-763-2	Sequence 2, Appli
557	4.7	639	2	US-09-248-796A-20583	Sequence 20583, A	630	73.5	4.7	499	2	US-09-431-367B-2	Sequence 2, Appli
558	4.7	758	2	US-09-949-016-8288	Sequence 8288, Ap	631	73.5	4.7	570	2	US-09-565-501A-104	Sequence 104, App
559	4.7	794	2	US-09-252-991A-28569	Sequence 28569, A	632	73.5	4.7	570	2	US-09-639-206A-104	Sequence 104, App
560	4.7	998	1	US-08-449-645A-20	Sequence 20, Appl	633	73.5	4.7	570	2	US-09-874-923-104	Sequence 104, App
561	4.7	998	1	US-08-702-367A-20	Sequence 20, Appl	634	73.5	4.7	638	1	US-08-463-262A-11	Sequence 11, Appl
562	4.7	998	2	PCT-US95-04681-20	Sequence 20, Appl	635	73.5	4.7	638	1	US-08-463-989-11	Sequence 11, Appl
563	4.7	1638	2	US-09-071-035-258	Sequence 258, App	636	73.5	4.7	638	1	US-09-003-574-11	Sequence 11, Appl
564	4.7	1638	2	US-09-071-035-262	Sequence 262, App	637	73.5	4.7	638	2	US-09-003-570-11	Sequence 11, Appl
565	4.7	1638	2	US-09-071-035-266	Sequence 266, App	638	73.5	4.7	638	2	US-09-864-541A-11	Sequence 11, Appl
566	4.7	1638	2	US-10-206-576-258	Sequence 258, App	639	73.5	4.7	646	2	US-09-902-540-12044	Sequence 12044, A
567	4.7	1638	2	US-10-206-576-262	Sequence 262, App	640	73.5	4.7	712	2	US-09-949-016-10600	Sequence 10600, A
568	4.7	1638	2	US-10-206-576-266	Sequence 266, App	641	73.5	4.7	712	2	US-08-899-437-2	Sequence 2, Appli
569	4.7	1747	2	US-09-134-000C-5999	Sequence 5999, Ap	642	73.5	4.7	713	2	US-09-126-121-2	Sequence 2, Appli
570	4.7	197	2	US-09-513-999C-7852	Sequence 7852, Ap	643	73.5	4.7	713	2	US-09-961-083-66	Sequence 66, Appl
571	4.7	257	2	US-09-567-458A-2	Sequence 2, Appli	644	73.5	4.7	763	2	US-09-536-784-66	Sequence 66, Appl
572	4.7	279	2	US-09-248-796A-16859	Sequence 16859, A	645	73.5	4.7	763	2	US-09-765-271-66	Sequence 66, Appl
573	4.7	299	2	US-09-107-433-3811	Sequence 3811, Ap	646	73.5	4.7	763	2	US-09-765-272A-66	Sequence 66, Appl
574	4.7	323	2	US-09-270-767-44688	Sequence 44688, A	647	73.5	4.7	780	2	US-09-248-796A-16702	Sequence 16702, A
575	4.7	339	1	US-08-433-854-4	Sequence 4, Appli	648	73.5	4.7	795	2	US-09-193-562D-11	Sequence 11, Appl
576	4.7	339	1	US-08-174-745A-4	Sequence 4, Appli	649	73.5	4.7	795	2	US-10-055-412B-11	Sequence 11, Appl
577	4.7	339	1	US-08-195-947-4	Sequence 4, Appli	650	73.5	4.7	819	2	US-09-468-656A-10	Sequence 10, Appl
578	4.7	339	1	US-08-433-885-4	Sequence 4, Appli	651	73.5	4.7	821	2	US-09-133-562D-12	Sequence 12, Appl
579	4.7	339	1	US-08-433-908B-4	Sequence 4, Appli	652	73.5	4.7	821	2	US-10-055-412B-12	Sequence 12, Appl
580	4.7	339	1	US-08-410-614-4	Sequence 4, Appli	653	73.5	4.7	826	2	US-09-769-787-194	Sequence 194, App
581	4.7	370	2	US-09-270-767-37418	Sequence 37418, A	654	73.5	4.7	866	2	US-08-405-392-17	Sequence 17, Appl
582	4.7	370	2	US-09-270-767-52635	Sequence 52635, A	655	73.5	4.7	866	2	US-08-487-691-17	Sequence 17, Appl
583	4.7	395	2	US-09-949-016-9564	Sequence 9564, Ap	656	73.5	4.7	905	2	US-09-193-562D-2	Sequence 2, Appli
584	4.7	422	2	US-09-949-016-8251	Sequence 8251, Ap	657	73.5	4.7	905	2	US-10-055-412B-2	Sequence 2, Appli
585	4.7	428	2	US-09-134-000C-6457	Sequence 6457, Ap	658	73.5	4.7	919	2	US-09-949-016-6954	Sequence 6954, Ap
586	4.7	472	2	US-09-625-188-6	Sequence 6, Appli	659	73.5	4.7	1101	2	US-09-561-709B-5	Sequence 5, Appli
587	4.7	493	2	US-09-248-796A-17819	Sequence 17819, A	660	73.5	4.7	1761	2	US-09-561-709B-1	Sequence 1, Appli
588	4.7	778	2	US-09-248-796A-16358	Sequence 16358, A	661	73.5	4.7	1876	2	US-09-418-710-71	Sequence 71, Appl
589	4.7	823	2	US-09-248-796A-16699	Sequence 16699, A	662	73.5	4.7	1876	2	US-09-839-479-70	Sequence 70, Appl
590	4.7	910	2	US-09-270-767-42083	Sequence 42083, A	663	73.5	4.7	1878	2	US-09-418-710-13	Sequence 13, Appl
591	4.7	1021	2	US-08-902-540-16773	Sequence 16773, A	664	73.5	4.7	1878	2	US-09-839-479-13	Sequence 13, Appl
592	4.7	1693	2	US-08-840-316-1	Sequence 1, Appli	665	73	4.6	155	2	US-09-252-991A-22634	Sequence 22634, A
593	4.7	1693	2	US-08-809-523-1	Sequence 1, Appli	666	73	4.6	162	2	US-08-700-651-13	Sequence 13, Appl
594	4.7	1693	2	US-08-471-971-1	Sequence 1, Appli	667	73	4.6	326	2	US-09-248-796A-19891	Sequence 19891, A
595	4.7	1693	2	US-09-402-776-1	Sequence 1, Appli	668	73	4.6	326	2	US-09-313-942-10	Sequence 10, Appl
596	4.7	1693	2	US-08-470-246-1	Sequence 1, Appli	669	73	4.6	332	2	US-10-282-162-10	Sequence 10, Appl
597	4.7	1693	2	US-08-316-765-1	Sequence 1, Appli	670	73	4.6	340	2	US-09-248-796A-24600	Sequence 24600, A
598	4.7	1693	2	US-09-724-475-1	Sequence 1, Appli	671	73	4.6	380	2	US-09-270-767-43987	Sequence 43987, A
599	4.7	1693	4	PCT-US93-08849A-1	Sequence 1, Appli	672	73	4.6	488	2	US-09-991-181-513	Sequence 513, App
600	4.7	1693	4	PCT-US93-08849-1	Sequence 1, Appli	673	73	4.6	482	2	US-09-990-444-513	Sequence 513, App
601	4.7	1729	2	US-09-134-000C-5675	Sequence 5675, Ap	674	73	4.6	482	2	US-09-897-333-513	Sequence 513, App
602	4.7	2414	1	US-08-227-536-2	Sequence 2, Appli	675	73	4.6	482	2	US-09-992-598-513	Sequence 513, App
603	4.7	2414	2	US-09-538-092-1289	Sequence 1289, Ap	676	73	4.6	488	1	US-08-599-455B-5	Sequence 5, Appli
604	4.7	2414	4	PCT-US95-04682-2	Sequence 2, Appli	677	73	4.6	488	1	US-09-069-781B-5	Sequence 5, Appli
605	4.7	3224	1	US-08-705-660-34	Sequence 34, Appl	678	73	4.6	488	2	US-09-137-132-5	Sequence 5, Appli
606	4.7	3224	2	US-08-989-045-34	Sequence 34, Appl	679	73	4.6	488	2	US-08-864-564A-5	Sequence 5, Appli
607	4.7	3224	2	US-09-538-092-1161	Sequence 1161, Ap	680	73	4.6	488	2	US-09-094-410-5	Sequence 5, Appli
608	4.7	3224	2	US-09-315-355A-34	Sequence 34, Appl	681	73	4.6	488	2	US-08-708-123D-5	Sequence 5, Appli
609	4.7	124	2	US-08-700-651-11	Sequence 11, Appl	682	73	4.6	488	2	US-08-583-153A-5	Sequence 5, Appli
610	4.7	124	2	US-08-928-361B-16	Sequence 16, Appl	683	73	4.6	488	2	US-08-638-524B-5	Sequence 5, Appli
611	4.7	124	2	US-09-588-995A-16	Sequence 16, Appl	684	73	4.6	497	2	US-08-956-171B-5234	Sequence 5234, Ap

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686	73	4.6	579	2	US-09-198-452A-918	Sequence 918, App	759	72.5	4.6	758	2	US-10-105-901A-1	Sequence 1, Appli
687	73	4.6	605	2	US-09-438-185A-853	Sequence 853, App	760	72.5	4.6	780	1	US-08-232-538-14	Sequence 14, Appl
688	73	4.6	646	2	US-09-270-767-42233	Sequence 42233, A	761	72.5	4.6	780	1	US-08-786-164-14	Sequence 14, Appl
689	73	4.6	650	2	US-08-362-525-2	Sequence 2, Appli	762	72.5	4.6	786	2	US-09-270-767-42988	Sequence 42988, A
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691	73	4.6	658	2	US-09-312-611-4	Sequence 4, Appli	764	72.5	4.6	827	2	US-09-270-767-46276	Sequence 46276, A
692	73	4.6	708	1	US-07-797-556-2	Sequence 2, Appli	765	72.5	4.6	841	2	US-09-949-016-9669	Sequence 9669, Ap
693	73	4.6	708	1	US-08-308-881-2	Sequence 2, Appli	766	72.5	4.6	878	2	US-09-556-706B-2	Sequence 2, Appli
694	73	4.6	708	1	US-09-058-263-2	Sequence 2, Appli	767	72.5	4.6	878	2	US-09-724-418A-2	Sequence 2, Appli
695	73	4.6	708	1	US-09-059-099-2	Sequence 2, Appli	768	72.5	4.6	907	2	US-08-783-774-2	Sequence 2, Appli
696	73	4.6	708	2	US-09-058-264-2	Sequence 2, Appli	769	72.5	4.6	907	2	US-09-328-599A-1	Sequence 1, Appli
697	73	4.6	708	2	US-09-455-962-2	Sequence 2, Appli	770	72.5	4.6	907	4	PCT-US95-04611A-19	Sequence 19, Appli
698	73	4.6	708	4	PCT-US95-06530-2	Sequence 2, Appli	771	72.5	4.6	922	2	US-03-248-796A-16269	Sequence 16269, A
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701	73	4.6	852	2	US-09-206-551-19	Sequence 19, Appl	774	72.5	4.6	1338	2	US-08-750-141A-3	Sequence 3, Appli
702	73	4.6	859	2	US-09-313-942-7	Sequence 7, Appli	775	72.5	4.6	1338	2	US-09-119-014D-6	Sequence 6, Appli
703	73	4.6	859	2	US-10-282-162-7	Sequence 7, Appli	776	72.5	4.6	2308	1	US-08-015-973-1	Sequence 1, Appli
704	73	4.6	918	1	US-08-825-558-6	Sequence 6, Appli	777	72.5	4.6	2308	1	US-08-448-164-1	Sequence 1, Appli
705	73	4.6	918	2	US-09-312-611-6	Sequence 6, Appli	778	72.5	4.6	2308	2	US-08-081-929-2	Sequence 2, Appli
706	73	4.6	918	2	US-09-853-180B-3	Sequence 3, Appli	779	72.5	4.6	2308	2	US-10-000-954-2	Sequence 2, Appli
707	73	4.6	918	2	US-09-949-002-333	Sequence 333, App	780	72.5	4.6	2314	2	US-09-816-703A-2	Sequence 2, Appli
708	73	4.6	933	1	US-08-682-847-2	Sequence 2, Appli	781	72.5	4.6	3069	2	US-09-712-363-246	Sequence 246, App
709	73	4.6	937	2	US-09-949-002-536	Sequence 536, App	782	72.5	4.6	3256	2	US-09-919-172-98	Sequence 98, Appl
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711	73	4.6	951	2	US-10-282-162-9	Sequence 9, Appli	784	72.5	4.6	3256	2	US-09-919-039-21	Sequence 21, Appl
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714	73	4.6	1168	2	US-09-313-942-24	Sequence 24, Appl	787	72	4.6	303	2	US-09-270-767-57613	Sequence 57613, A
715	73	4.6	1168	2	US-10-282-162-24	Sequence 24, Appl	788	72	4.6	308	2	US-10-104-047-3898	Sequence 3898, Ap
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717	73	4.6	1702	2	US-09-839-996-5	Sequence 5, Appli	790	72	4.6	327	2	US-09-270-767-42324	Sequence 42324, A
718	73	4.6	1702	2	US-10-080-505-5	Sequence 5, Appli	791	72	4.6	342	2	US-09-949-016-10365	Sequence 10365, A
719	73	4.6	1702	2	US-10-645-655-5	Sequence 5, Appli	792	72	4.6	401	2	US-09-270-767-44680	Sequence 44680, A
720	73	4.6	1702	4	PCT-US95-10661A-5	Sequence 5, Appli	793	72	4.6	456	2	US-09-058-389A-2	Sequence 2, Appli
721	73	4.6	2285	2	US-09-308-375-2	Sequence 2, Appli	794	72	4.6	456	2	US-09-611-781-2	Sequence 2, Appli
722	73	4.6	2736	2	US-09-932-183A-2	Sequence 2, Appli	795	72	4.6	457	2	US-09-949-016-7211	Sequence 7211, Ap
723	73	4.6	2736	2	US-09-252-991A-30227	Sequence 30227, A	796	72	4.6	462	1	US-08-865-597A-2	Sequence 2, Appli
724	72.5	4.6	150	2	US-08-928-361B-18	Sequence 18, Appl	797	72	4.6	489	2	US-09-545-814-29	Sequence 29, Appl
725	72.5	4.6	150	2	US-09-588-995A-18	Sequence 18, Appl	798	72	4.6	559	2	US-09-545-814-14	Sequence 14, Appl
726	72.5	4.6	167	2	US-08-956-171E-5216	Sequence 5216, Ap	799	72	4.6	583	2	US-09-545-814-2	Sequence 2, Appli
727	72.5	4.6	167	2	US-08-781-986A-5216	Sequence 5216, Ap	800	72	4.6	583	2	US-09-545-814-5	Sequence 5, Appli
728	72.5	4.6	185	2	US-09-248-796A-18311	Sequence 18311, A	801	72	4.6	599	1	US-08-910-551B-2	Sequence 2, Appli
729	72.5	4.6	206	2	US-09-902-540-14080	Sequence 14080, A	802	72	4.6	635	2	US-09-545-814-32	Sequence 32, Appli
730	72.5	4.6	206	2	US-09-198-452A-879	Sequence 879, App	803	72	4.6	785	2	US-08-374-077C-3	Sequence 3, Appli
731	72.5	4.6	206	2	US-09-438-185A-822	Sequence 822, App	804	72	4.6	785	2	US-08-895-530-3	Sequence 3, Appli
732	72.5	4.6	293	2	US-09-496-320-5	Sequence 5, Appli	805	72	4.6	785	2	US-09-539-879A-3	Sequence 3, Appli
733	72.5	4.6	315	2	US-09-328-352-5948	Sequence 5948, Ap	806	72	4.6	801	1	US-08-725-012-2	Sequence 2, Appli
734	72.5	4.6	328	2	US-09-489-039A-12803	Sequence 12803, A	807	72	4.6	813	2	US-09-964-899-25	Sequence 25, Appl
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736	72.5	4.6	378	2	US-09-248-796A-18526	Sequence 18526, A	809	72	4.6	903	2	US-09-623-624-18	Sequence 18, Appl
737	72.5	4.6	428	2	US-09-489-039A-10901	Sequence 10901, A	810	72	4.6	903	2	US-10-055-412B-46	Sequence 46, Appl
738	72.5	4.6	445	2	US-09-710-279-1294	Sequence 1294, Ap	811	72	4.6	903	2	US-10-270-595-18	Sequence 18, Appl
739	72.5	4.6	462	6	5171671-2	Patent No. 5171671	812	72	4.6	915	2	US-09-270-767-43656	Sequence 43656, A
740	72.5	4.6	463	1	US-08-162-402B-9	Sequence 9, Appli	813	72	4.6	1129	2	US-09-023-905A-2	Sequence 2, Appli
741	72.5	4.6	494	2	US-09-902-540-9960	Sequence 9960, Ap	814	72	4.6	1203	2	US-09-351-200-2	Sequence 2, Appli
742	72.5	4.6	510	2	US-09-211-417-1	Sequence 1, Appli	815	72	4.6	1389	1	US-08-193-198-5	Sequence 5, Appli
743	72.5	4.6	608	2	US-09-949-016-11148	Sequence 11148, A	816	72	4.6	2441	1	US-08-194-468-2	Sequence 2, Appli
744	72.5	4.6	608	2	US-09-949-016-11149	Sequence 11149, A	817	72	4.6	2441	2	US-08-961-739-2	Sequence 2, Appli
745	72.5	4.6	608	2	US-09-949-016-11150	Sequence 11150, A	818	72	4.6	2441	2	US-09-514-247A-8	Sequence 8, Appli
746	72.5	4.6	608	2	US-09-949-016-11151	Sequence 11151, A	819	72	4.6	2441	2	US-09-686-316-2	Sequence 2, Appli
747	72.5	4.6	652	2	US-09-310-463-4	Sequence 4, Appli	820	71.5	4.5	135	2	US-09-252-991A-17514	Sequence 17514, A
748	72.5	4.6	652	2	US-08-842-248A-4	Sequence 4, Appli	821	71.5	4.5	142	2	US-09-107-532A-6315	Sequence 6315, Ap
749	72.5	4.6	687	1	US-08-232-538-6	Sequence 6, Appli	822	71.5	4.5	218	2	US-09-605-703B-2490	Sequence 2490, Ap
750	72.5	4.6	687	1	US-08-786-164-6	Sequence 6, Appli	823	71.5	4.5	232	2	US-09-333-809-217	Sequence 217, App
751	72.5	4.6	687	2	US-09-427-353-2	Sequence 2, Appli	824	71.5	4.5	232	2	US-09-746-311B-366	Sequence 366, App
752	72.5	4.6	707	2	US-09-228-986-80	Sequence 80, Appl	825	71.5	4.5	240	2	US-09-107-532A-4430	Sequence 4430, Ap
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754	72.5	4.6	719	2	US-09-949-016-7766	Sequence 7766, Ap	827	71.5	4.5	326	2	US-09-134-000C-5607	Sequence 5607, Ap
755	72.5	4.6	758	1	US-08-874-678-1	Sequence 1, Appli	828	71.5	4.5	342	2	US-09-605-703B-250	Sequence 250, App
756	72.5	4.6	758	2	US-08-643-839-1	Sequence 1, Appli	829	71.5	4.5	386	2	US-09-248-796A-18312	Sequence 18312, A
757	72.5	4.6	758	2	US-09-051-363-24	Sequence 24, Appl	830	71.5	4.5	442	1	US-08-363-255-4	Sequence 4, Appli

831	71.5	4.5	442	1	US-08-363-255-11	Sequence 11, Appl	904	70.5	4.5	401	2	US-09-949-016-7956	Sequence 7956, Ap
832	71.5	4.5	442	1	US-08-687-559-6	Sequence 6, Appl	905	70.5	4.5	432	2	US-09-134-000C-3498	Sequence 3498, Ap
833	71.5	4.5	442	1	US-09-401-415-6	Sequence 6, Appl	906	70.5	4.5	441	2	US-08-248-796A-20171	Sequence 20171, A
834	71.5	4.5	540	2	US-09-583-110-3685	Sequence 3685, Ap	907	70.5	4.5	445	2	US-09-270-767-46629	Sequence 46629, A
835	71.5	4.5	540	2	US-09-538-092-793	Sequence 793, App	908	70.5	4.5	462	1	US-08-417-330A-16	Sequence 16, Appl
836	71.5	4.5	556	2	US-09-949-016-11052	Sequence 11052, A	909	70.5	4.5	491	2	US-09-248-796A-18483	Sequence 18483, A
837	71.5	4.5	641	2	US-09-613-303-51	Sequence 51, Appl	910	70.5	4.5	497	2	US-10-104-047-3603	Sequence 3603, Ap
838	71.5	4.5	641	2	US-10-267-311-51	Sequence 51, Appl	911	70.5	4.5	522	2	US-09-538-092-1096	Sequence 1096, Ap
839	71.5	4.5	650	2	US-09-134-000C-5177	Sequence 5177, Ap	912	70.5	4.5	526	2	US-09-487-558B-362	Sequence 362, App
840	71.5	4.5	681	2	US-08-760-615-4	Sequence 4, Appl	913	70.5	4.5	574	2	US-09-248-796A-16162	Sequence 16162, A
841	71.5	4.5	681	2	US-09-336-910A-2	Sequence 2, Appl	914	70.5	4.5	639	2	US-09-252-991A-24474	Sequence 24474, A
842	71.5	4.5	732	2	US-09-134-000C-6359	Sequence 6359, Ap	915	70.5	4.5	676	2	US-09-003-570-34	Sequence 34, Appl
843	71.5	4.5	920	2	US-09-538-092-1197	Sequence 1197, Ap	916	70.5	4.5	676	2	US-09-003-570-34	Sequence 34, Appl
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845	71.5	4.5	1724	2	US-09-607-510-2	Sequence 2, Appl	918	70.5	4.5	678	2	US-09-91-181-179	Sequence 179, App
846	71.5	4.5	1751	1	US-09-136-574A-44	Sequence 44, Appl	919	70.5	4.5	678	2	US-09-990-444-179	Sequence 179, App
847	71.5	4.5	3174	1	US-08-477-451-3	Sequence 3, Appl	920	70.5	4.5	678	2	US-09-992-598-179	Sequence 179, App
848	71	4.5	144	2	US-09-252-991A-23388	Sequence 23388, A	921	70.5	4.5	678	2	US-09-992-598-179	Sequence 179, App
849	71	4.5	169	2	US-09-248-796A-14699	Sequence 32019, A	922	70.5	4.5	979	2	US-09-538-092-990	Sequence 990, App
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851	71	4.5	189	2	US-09-270-767-54674	Sequence 54674, A	924	70.5	4.5	1168	2	US-09-762-311-5	Sequence 5, Appl
852	71	4.5	189	2	US-09-328-352-7443	Sequence 7443, Ap	925	70.5	4.5	1187	2	US-09-949-016-6513	Sequence 6513, Ap
853	71	4.5	230	2	US-09-248-796A-16743	Sequence 16743, A	926	70.5	4.5	1591	2	US-09-270-767-45698	Sequence 45698, A
854	71	4.5	230	2	US-09-248-796A-16743	Sequence 16743, A	927	70.5	4.5	1591	2	US-09-914-272A-3	Sequence 3, Appl
855	71	4.5	251	2	US-09-248-796A-16743	Sequence 16743, A	928	70.5	4.5	1980	2	US-10-638-333-3	Sequence 3, Appl
856	71	4.5	251	2	US-09-248-796A-16743	Sequence 16743, A	929	70.5	4.5	1980	2	US-10-638-333-3	Sequence 3, Appl
857	71	4.5	272	2	US-09-504-358-10	Sequence 10, Appl	930	70.5	4.5	2169	2	US-09-949-016-6930	Sequence 3, Appl
858	71	4.5	316	2	US-09-954-314-10	Sequence 10, Appl	931	70.5	4.5	2169	2	US-09-949-016-6930	Sequence 3, Appl
859	71	4.5	316	2	US-10-230-562-10	Sequence 10, Appl	932	70.5	4.5	2442	2	US-09-514-247A-10	Sequence 10, Appl
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861	71	4.5	401	6	5252556-1	Sequence 8, Appl	934	70	4.4	135	2	US-09-270-767-35728	Sequence 35728, A
862	71	4.5	554	2	US-09-599-360B-78	Sequence 78, Appl	935	70	4.4	135	2	US-09-270-767-35728	Sequence 35728, A
863	71	4.5	610	1	US-07-821-717B-6	Sequence 6, Appl	936	70	4.4	135	2	US-09-270-767-35728	Sequence 35728, A
864	71	4.5	610	1	US-08-113-262B-6	Sequence 6, Appl	937	70	4.4	222	2	US-09-252-991A-27628	Sequence 27628, A
865	71	4.5	610	1	US-08-135-929A-11	Sequence 11, Appl	938	70	4.4	236	2	US-09-492-709A-350	Sequence 350, App
866	71	4.5	610	1	US-08-234-265A-11	Sequence 11, Appl	939	70	4.4	317	6	5340934-11	Patent No. 5340934
867	71	4.5	630	2	US-09-485-529-8	Sequence 8, Appl	940	70	4.4	340	2	US-09-492-709A-262	Sequence 262, App
868	71	4.5	633	2	US-09-248-796A-20407	Sequence 20407, A	941	70	4.4	352	2	US-09-413-814-24	Sequence 24, Appl
869	71	4.5	893	2	US-08-189-738A-18	Sequence 18, Appl	942	70	4.4	353	1	US-09-902-540-9867	Sequence 9867, Ap
870	71	4.5	1011	2	US-09-602-362E-27	Sequence 27, Appl	943	70	4.4	353	1	US-08-458-555-2	Sequence 2, Appl
871	71	4.5	1239	2	US-10-076-622-57	Sequence 57, App	944	70	4.4	360	2	US-09-807-933B-5	Sequence 5, Appl
872	71	4.5	1374	2	US-09-771-161A-267	Sequence 267, App	945	70	4.4	372	2	US-09-489-039A-13193	Sequence 13193, A
873	71	4.5	1841	2	US-09-477-962-99	Sequence 99, Appl	946	70	4.4	410	2	US-09-248-796A-19334	Sequence 19334, A
874	71	4.5	1938	2	US-09-949-016-6609	Sequence 6609, Ap	947	70	4.4	416	2	US-09-543-681A-5962	Sequence 5962, Ap
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878	71	4.5	2045	2	US-09-949-016-10491	Sequence 10491, A	951	70	4.4	525	2	US-09-107-532A-5095	Sequence 5095, Ap
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888	70.5	4.5	232	2	US-09-333-809-214	Sequence 214, App	961	70	4.4	915	2	US-08-988-242-2	Sequence 2, Appl
889	70.5	4.5	232	2	US-09-333-809-215	Sequence 215, App	962	70	4.4	1004	2	US-09-138-735-2	Sequence 2, Appl
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896	70.5	4.5	237	2	US-09-248-796A-22928	Sequence 22928, A	969	69.5	4.4	219	1	US-08-463-388-91	Sequence 91, Appl
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998	69.5	4.4	406	2	US-09-248-796A-20860	Sequence 20860, A	1071	68.5	4.3	331	2	US-09-248-796A-20795	Sequence 20795, A
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1001	69.5	4.4	586	2	US-09-171-156A-30	Sequence 30, Appli	1074	68.5	4.3	391	2	US-09-200-090-4	Sequence 4, Appli
1002	69.5	4.4	586	2	US-09-004-730A-30	Sequence 30, Appli	1075	68.5	4.3	440	2	US-09-270-767-37864	Sequence 37864, A
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1007	69.5	4.4	551	2	US-09-248-796A-18743	Sequence 18743, A	1080	68.5	4.3	529	2	US-09-291-922-28	Sequence 28, Appli
1008	69.5	4.4	812	2	US-09-248-796A-20875	Sequence 20875, A	1081	68.5	4.3	600	2	US-09-693-746-2	Sequence 2, Appli
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1016	69.5	4.4	2468	2	US-09-538-092-1135	Sequence 1135, Ap	1089	68.5	4.3	756	2	US-09-085-199B-9	Sequence 9, Appli
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1021	69	4.4	171	2	US-09-248-796A-19229	Sequence 19229, A	1094	68.5	4.3	906	2	US-10-307-389-6	Sequence 6, Appli
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1049	69	4.4	817	2	US-09-248-796A-20276	Sequence 20276, A	1122	68	4.3	516	1	US-08-762-106-8	Sequence 8, Appli



1123	68	4.3	516	2	US-08-745-404-2	Sequence 2, Appli	1196	68	4.3	3712	2	US-10-037-417-48	Sequence 48, Appl
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1128	68	4.3	527	2	US-08-940-244-144	Sequence 144, App	1201	67.5	4.3	107	2	US-09-765-272A-150	Sequence 150, App
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1132	68	4.3	563	2	US-09-949-016-7419	Sequence 7419, Ap	1205	67.5	4.3	157	2	US-09-248-796A-21632	Sequence 21632, A
1133	68	4.3	599	1	US-08-222-619-2	Sequence 2, Appli	1206	67.5	4.3	159	2	US-09-252-991A-20138	Sequence 20138, A
1134	68	4.3	599	2	US-08-221-767-24	Sequence 24, Appli	1207	67.5	4.3	160	2	US-09-270-767-59046	Sequence 59046, A
1135	68	4.3	599	4	PCT-US95-04075-2	Sequence 2, Appli	1208	67.5	4.3	201	2	US-09-408-020-54	Sequence 54, Appl
1136	68	4.3	646	2	US-09-248-796A-16701	Sequence 16701, A	1209	67.5	4.3	223	2	US-09-248-796A-17645	Sequence 17645, A
1137	68	4.3	654	2	US-09-315-127-11	Sequence 11, Appli	1210	67.5	4.3	223	2	US-09-270-767-46344	Sequence 46344, A
1138	68	4.3	654	2	US-09-315-127-12	Sequence 12, Appli	1211	67.5	4.3	284	2	US-09-270-767-46346	Sequence 3246, A
1139	68	4.3	672	2	US-09-248-796A-26995	Sequence 26995, A	1212	67.5	4.3	290	2	US-09-270-767-50463	Sequence 50463, A
1140	68	4.3	709	2	US-09-248-796A-19045	Sequence 19045, A	1213	67.5	4.3	291	2	US-09-248-796A-14273	Sequence 72, Appl
1141	68	4.3	785	2	US-09-487-558B-348	Sequence 348, App	1214	67.5	4.3	301	1	PCT-US93-08528-72	Sequence 72, Appl
1142	68	4.3	833	2	US-09-949-016-9530	Sequence 9530, Ap	1215	67.5	4.3	301	4	US-09-270-767-43688	Sequence 43688, A
1143	68	4.3	859	2	US-09-538-092-717	Sequence 717, App	1216	67.5	4.3	313	2	US-08-832-399-2	Sequence 2, Appli
1144	68	4.3	863	1	US-08-380-182-20	Sequence 20, Appli	1217	67.5	4.3	319	2	US-09-372-498-2	Sequence 2, Appli
1145	68	4.3	873	1	US-08-571-758-6	Sequence 6, Appli	1218	67.5	4.3	362	1	US-08-437-027-21	Sequence 21, Appl
1146	68	4.3	873	1	US-08-909-984A-6	Sequence 6, Appli	1219	67.5	4.3	365	1	US-08-437-027-20	Sequence 20, Appl
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1149	68	4.3	878	2	US-09-141-212-8	Sequence 8, Appli	1222	67.5	4.3	383	2	US-09-248-796A-26759	Sequence 26759, A
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1152	68	4.3	879	2	US-09-561-138-6	Sequence 6, Appli	1225	67.5	4.3	410	2	US-09-472-880-2	Sequence 2, Appli
1153	68	4.3	908	2	US-09-949-016-6669	Sequence 6669, Ap	1226	67.5	4.3	410	2	US-09-826-509-537	Sequence 537, App
1154	68	4.3	974	1	US-08-868-786-6	Sequence 6, Appli	1227	67.5	4.3	427	2	US-09-248-796A-24117	Sequence 24117, A
1155	68	4.3	974	1	US-08-673-789-8	Sequence 8, Appli	1228	67.5	4.3	427	2	US-09-328-352-5205	Sequence 5205, Ap
1156	68	4.3	977	1	US-08-673-789-8	Sequence 8, Appli	1229	67.5	4.3	437	2	US-09-353-332-2	Sequence 2, Appli
1157	68	4.3	1026	2	US-09-949-016-6777	Sequence 6777, Ap	1230	67.5	4.3	437	2	US-09-353-332-2	Sequence 6012, Ap
1158	68	4.3	1034	2	US-09-949-016-10870	Sequence 10870, A	1231	67.5	4.3	451	2	US-09-328-352-6012	Sequence 14133, A
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1161	68	4.3	1155	1	US-08-362-652-46	Sequence 46, Appl	1234	67.5	4.3	498	2	US-09-583-110-2949	Sequence 2949, Ap
1162	68	4.3	1155	1	US-08-605-672-46	Sequence 46, Appl	1235	67.5	4.3	522	2	US-09-107-433-2618	Sequence 2618, Ap
1163	68	4.3	1155	1	US-08-482-293A-46	Sequence 46, Appl	1236	67.5	4.3	522	2	US-09-198-452A-480	Sequence 480, App
1164	68	4.3	1155	1	US-08-943-363-46	Sequence 46, Appl	1237	67.5	4.3	549	1	US-08-325-071-61	Sequence 61, Appl
1165	68	4.3	1155	2	US-09-193-043-46	Sequence 46, Appl	1238	67.5	4.3	549	2	US-08-461-004A-61	Sequence 61, Appl
1166	68	4.3	1155	2	US-09-688-307A-46	Sequence 46, Appl	1239	67.5	4.3	555	2	US-09-107-532A-6422	Sequence 6422, Ap
1167	68	4.3	1155	2	US-09-350-259-46	Sequence 46, Appl	1240	67.5	4.3	591	2	US-09-949-016-10914	Sequence 10914, A
1168	68	4.3	1161	1	US-08-485-618-53	Sequence 53, Appl	1241	67.5	4.3	591	2	US-09-949-016-10915	Sequence 10915, A
1169	68	4.3	1161	1	US-08-485-618-55	Sequence 55, Appl	1242	67.5	4.3	600	2	US-10-104-047-3397	Sequence 3397, Ap
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1172	68	4.3	1161	1	US-08-605-672-53	Sequence 53, Appl	1245	67.5	4.3	630	1	US-08-956-268-3	Sequence 3, Appli
1173	68	4.3	1161	1	US-08-605-672-55	Sequence 55, Appl	1246	67.5	4.3	630	1	US-09-499-522-16	Sequence 16, Appl
1174	68	4.3	1161	1	US-08-482-293A-53	Sequence 53, Appl	1247	67.5	4.3	630	2	US-09-269-939A-10	Sequence 10, Appl
1175	68	4.3	1161	1	US-08-482-293A-55	Sequence 55, Appl	1248	67.5	4.3	649	2	US-09-499-522-14	Sequence 14, Appl
1176	68	4.3	1161	1	US-08-943-363-53	Sequence 53, Appl	1249	67.5	4.3	650	1	US-08-325-071-63	Sequence 8, Appli
1177	68	4.3	1161	1	US-08-943-363-55	Sequence 55, Appl	1250	67.5	4.3	650	2	US-08-461-004A-63	Sequence 63, Appl
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1179	68	4.3	1161	2	US-09-588-307A-53	Sequence 53, Appl	1252	67.5	4.3	656	2	US-09-214-564A-4	Sequence 4, Appli
1180	68	4.3	1161	2	US-09-350-259-53	Sequence 53, Appl	1253	67.5	4.3	664	2	US-09-538-092-1250	Sequence 1250, Ap
1181	68	4.3	1181	2	US-09-540-236-3804	Sequence 3804, Ap	1254	67.5	4.3	802	2	US-09-107-532A-7252	Sequence 7252, Ap
1182	68	4.3	1309	2	US-09-862-027-82	Sequence 82, App	1255	67.5	4.3	802	2	US-09-081-345-18	Sequence 18, Appl
1183	68	4.3	1341	2	US-09-949-016-6890	Sequence 6890, Ap	1256	67.5	4.3	812	1	US-08-446-794A-4	Sequence 4, Appli
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1186	68	4.3	1541	2	US-09-839-396-3	Sequence 3, Appli	1259	67.5	4.3	877	1	US-08-972-629-2	Sequence 2, Appli
1187	68	4.3	1541	2	US-10-080-505-3	Sequence 3, Appli	1260	67.5	4.3	877	1	US-08-972-630-2	Sequence 2, Appli
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1189	68	4.3	1541	4	PCT-US95-10661A-3	Sequence 3, Appli	1262	67.5	4.3	877	1	US-09-225-170-2	Sequence 2, Appli
1190	68	4.3	1541	2	US-08-296-791-4	Sequence 4, Appli	1263	67.5	4.3	973	2	US-09-430-723-2	Sequence 455, App
1191	68	4.3	1545	2	US-09-839-396-4	Sequence 4, Appli	1264	67.5	4.3	999	2		
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1193	68	4.3	1545	2	US-10-645-655-4	Sequence 4, Appli	1266	67.5	4.3				
1194	68	4.3	1545	4	PCT-US95-10661A-4	Sequence 4, Appli	1267	67.5	4.3				
1195	68	4.3	1675	2	US-09-540-236-1994	Sequence 1994, Ap	1268	67.5	4.3				

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1270	67.5	4.3	1020	2	US-09-538-092-911	Sequence 911, App	1343	67	4.3	503	2	US-08-123-934A-10	Sequence 10, Appl
1271	67.5	4.3	1122	2	US-10-771-708-3	Sequence 3, Appl	1344	67	4.3	503	2	US-09-874-628-10	Sequence 10, Appl
1272	67.5	4.3	1150	1	US-08-589-756-3	Sequence 3, Appl	1345	67	4.3	503	4	PCT-US94-10080-10	Sequence 10, Appl
1273	67.5	4.3	1150	2	US-09-206-800-3	Sequence 3, Appl	1346	67	4.3	514	2	US-09-712-363-154	Sequence 154, App
1274	67.5	4.3	1150	2	US-09-206-898-3	Sequence 3, Appl	1347	67	4.3	541	2	US-09-248-796A-25057	Sequence 25057, A
1275	67.5	4.3	1150	2	US-09-870-122A-3	Sequence 3, Appl	1348	67	4.3	543	2	US-09-949-016-8822	Sequence 8822, Ap
1276	67.5	4.3	1301	2	US-09-071-035-234	Sequence 234, App	1349	67	4.3	570	2	US-08-826-246-2	Sequence 2, Appl
1277	67.5	4.3	1301	2	US-09-071-035-238	Sequence 238, App	1350	67	4.3	570	2	US-08-944-495-2	Sequence 2, Appl
1278	67.5	4.3	1301	2	US-09-071-035-242	Sequence 242, App	1351	67	4.3	570	2	US-09-126-640-7	Sequence 7, Appl
1279	67.5	4.3	1301	2	US-10-206-576-234	Sequence 234, App	1352	67	4.3	570	2	US-08-925-588-2	Sequence 2, Appl
1280	67.5	4.3	1301	2	US-10-206-576-238	Sequence 238, App	1353	67	4.3	570	2	US-09-288-292A-7	Sequence 7, Appl
1281	67.5	4.3	1301	2	US-10-206-576-242	Sequence 242, App	1354	67	4.3	570	2	US-09-372-044-2	Sequence 2, Appl
1282	67.5	4.3	1574	2	US-09-302-626B-179	Sequence 179, App	1355	67	4.3	570	2	US-08-825-446-2	Sequence 2, Appl
1283	67.5	4.3	1978	2	US-09-302-626B-60	Sequence 60, Appl	1356	67	4.3	570	2	US-08-826-248-2	Sequence 2, Appl
1284	67.5	4.3	2453	2	US-09-632-033B-4	Sequence 60, Appl	1357	67	4.3	598	2	US-09-538-092-1083	Sequence 1083, Ap
1285	67.5	4.3	3913	2	US-09-949-016-10933	Sequence 10933, A	1358	67	4.3	623	2	US-09-485-529-7	Sequence 7, Appl
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1287	67	4.3	135	2	US-09-908-322-51	Sequence 51, Appl	1360	67	4.3	661	1	US-08-232-538-12	Sequence 12, Appl
1288	67	4.3	137	2	US-10-104-047-2849	Sequence 2849, Ap	1361	67	4.3	661	1	US-08-786-164-12	Sequence 12, Appl
1289	67	4.3	149	2	US-09-513-999C-4813	Sequence 4813, Ap	1362	67	4.3	688	2	US-09-477-962-96	Sequence 96, Appl
1290	67	4.3	185	2	US-09-902-540-13687	Sequence 13687, A	1363	67	4.3	699	2	US-09-949-016-6158	Sequence 6158, Ap
1291	67	4.3	197	2	US-09-107-532A-7229	Sequence 7229, Ap	1364	67	4.3	702	2	US-09-949-016-11476	Sequence 11476, A
1292	67	4.3	206	2	US-09-328-352-6224	Sequence 6224, Ap	1365	67	4.3	702	2	US-09-949-016-11477	Sequence 11477, A
1293	67	4.3	208	2	US-10-104-047-2188	Sequence 2188, Ap	1366	67	4.3	784	2	US-09-538-092-1254	Sequence 1254, Ap
1294	67	4.3	210	1	US-07-667-276A-2	Sequence 2, Appl	1367	67	4.3	786	2	US-09-949-016-10170	Sequence 10170, A
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1297	67	4.3	246	1	US-08-294-386C-1	Sequence 1, Appl	1370	67	4.3	976	1	US-08-702-367A-18	Sequence 18, Appl
1298	67	4.3	246	1	US-08-294-386C-3	Sequence 3, Appl	1371	67	4.3	976	1	US-09-949-016-6499	Sequence 6499, Ap
1299	67	4.3	246	1	US-08-299-249A-1	Sequence 1, Appl	1372	67	4.3	976	4	PCT-US95-04681-18	Sequence 18, Appl
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1302	67	4.3	246	2	US-08-852-020-1	Sequence 1, Appl	1375	67	4.3	1132	2	US-09-528-784A-87	Sequence 87, Appl
1303	67	4.3	246	4	PCT-US94-06543-1	Sequence 1, Appl	1376	67	4.3	1132	2	US-09-569-098A-87	Sequence 87, Appl
1304	67	4.3	246	4	PCT-US95-10224-1	Sequence 1, Appl	1377	67	4.3	1231	2	US-09-071-035-420	Sequence 420, App
1305	67	4.3	246	4	PCT-US95-10224-3	Sequence 3, Appl	1378	67	4.3	1231	2	US-10-206-576-420	Sequence 420, App
1306	67	4.3	267	2	US-09-949-016-7941	Sequence 7941, Ap	1379	67	4.3	1265	2	US-09-071-035-418	Sequence 418, App
1307	67	4.3	272	2	US-08-248-796A-16689	Sequence 16689, A	1380	67	4.3	1265	2	US-10-206-576-418	Sequence 418, App
1308	67	4.3	277	2	US-08-469-633A-4	Sequence 4, Appl	1381	67	4.3	1278	2	US-09-134-000C-6043	Sequence 6043, Ap
1309	67	4.3	289	2	US-08-961-083-20	Sequence 20, Appl	1382	67	4.3	1279	2	US-09-710-279-3188	Sequence 3188, Ap
1310	67	4.3	289	2	US-09-536-784-20	Sequence 20, Appl	1383	67	4.3	1900	2	US-09-538-092-564	Sequence 564, App
1311	67	4.3	289	2	US-09-765-271-20	Sequence 20, Appl	1384	67	4.3	1900	2	US-09-487-558B-390	Sequence 390, App
1312	67	4.3	289	2	US-09-765-272A-20	Sequence 20, Appl	1385	67	4.3	2005	2	US-08-836-325-7	Sequence 7, Appl
1313	67	4.3	309	2	US-09-270-767-46802	Sequence 46802, A	1386	67	4.3	2005	2	US-09-457-571-7	Sequence 7, Appl
1314	67	4.3	309	2	US-09-769-787-156	Sequence 156, App	1387	67	4.3	2476	1	US-08-276-967-2	Sequence 2, Appl
1315	67	4.3	320	2	US-09-248-796A-20167	Sequence 20167, A	1388	67	4.3	3696	2	US-09-134-001C-5080	Sequence 5080, Ap
1316	67	4.3	342	2	US-09-107-433-3903	Sequence 3903, Ap	1389	67	4.3	4377	2	US-09-949-016-6978	Sequence 6978, Ap
1317	67	4.3	343	2	US-09-401-636-7	Sequence 7, Appl	1390	66.5	4.2	91	2	US-08-700-651-14	Sequence 14, Appl
1318	67	4.3	373	2	US-09-270-767-46313	Sequence 46313, A	1391	66.5	4.2	91	2	US-08-928-361B-19	Sequence 19, Appl
1319	67	4.3	387	2	US-09-314-847A-4	Sequence 4, Appl	1392	66.5	4.2	91	2	US-09-588-995A-19	Sequence 19, Appl
1320	67	4.3	387	2	US-09-570-778A-2	Sequence 2, Appl	1393	66.5	4.2	154	2	US-09-252-991A-32034	Sequence 32034, A
1321	67	4.3	387	2	US-09-570-778A-7	Sequence 7, Appl	1394	66.5	4.2	173	2	US-09-328-352-5235	Sequence 5235, Ap
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1323	67	4.3	387	2	US-09-570-778A-9	Sequence 9, Appl	1396	66.5	4.2	205	2	US-09-252-991A-21933	Sequence 21933, A
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1325	67	4.3	387	2	US-09-991-138-7	Sequence 7, Appl	1398	66.5	4.2	206	2	US-09-041-889-6	Sequence 6, Appl
1326	67	4.3	387	2	US-09-991-138-8	Sequence 8, Appl	1399	66.5	4.2	206	2	US-08-837-058-6	Sequence 6, Appl
1327	67	4.3	387	2	US-09-991-138-9	Sequence 9, Appl	1400	66.5	4.2	235	2	US-09-247-155-126	Sequence 126, App
1328	67	4.3	387	2	US-10-037-677A-4	Sequence 4, Appl	1401	66.5	4.2	235	2	US-09-903-190-126	Sequence 126, App
1329	67	4.3	387	2	US-10-037-677A-6	Sequence 6, Appl	1402	66.5	4.2	236	2	US-09-148-545-202	Sequence 202, App
1330	67	4.3	389	2	US-09-788-657-23	Sequence 23, Appl	1403	66.5	4.2	236	2	US-09-621-011-202	Sequence 202, App
1331	67	4.3	389	2	US-10-641-068-23	Sequence 23, Appl	1404	66.5	4.2	239	2	US-09-248-796A-21096	Sequence 21096, A
1332	67	4.3	412	2	US-09-538-092-835	Sequence 835, App	1405	66.5	4.2	249	2	US-09-189-760-6	Sequence 6, Appl
1333	67	4.3	416	2	US-09-601-478-1	Sequence 1, Appl	1406	66.5	4.2	249	2	US-09-188-811-6	Sequence 6, Appl
1334	67	4.3	416	2	US-09-601-478-4	Sequence 4, Appl	1407	66.5	4.2	249	2	US-09-514-422-6	Sequence 6, Appl
1335	67	4.3	435	2	US-09-949-016-9133	Sequence 9133, Ap	1408	66.5	4.2	252	2	US-09-270-767-43125	Sequence 43125, A
1336	67	4.3	454	2	US-09-949-016-9823	Sequence 9823, Ap	1409	66.5	4.2	265	2	US-09-918-288-39	Sequence 39, Appl
1337	67	4.3	465	2	US-08-845-258-30	Sequence 30, Appl	1410	66.5	4.2	265	2	US-09-282-357-39	Sequence 39, Appl
1338	67	4.3	465	2	US-08-990-571-30	Sequence 30, Appl	1411	66.5	4.2	284	2	US-09-248-796A-20639	Sequence 20639, A
1339	67	4.3	465	2	US-08-723-142A-30	Sequence 30, Appl	1412	66.5	4.2	305	2	US-09-134-001C-5038	Sequence 5038, Ap
1340	67	4.3	465	2	US-09-528-784A-30	Sequence 30, Appl	1413	66.5	4.2	319	2	US-09-107-532A-4723	Sequence 4723, Ap
1341	67	4.3	465	2	US-09-569-098A-30	Sequence 30, Appl	1414	66.5	4.2	326	2	US-09-058-389A-3	Sequence 3, Appl



1415	66.5	4.2	326	2	US-09-611-781-3	Sequence 3, Appli	1488	66	4.2	268	2	US-09-536-784-208	Sequence 208, App
1416	66.5	4.2	331	2	US-08-808-720-5	Sequence 5, Appli	1489	66	4.2	268	2	US-09-765-271-208	Sequence 208, App
1417	66.5	4.2	331	2	US-09-467-638-5	Sequence 5, Appli	1490	66	4.2	268	2	US-09-765-272A-208	Sequence 208, App
1418	66.5	4.2	362	2	US-08-899-437-3	Sequence 3, Appli	1491	66	4.2	309	1	US-08-715-131-2	Sequence 2, Appli
1419	66.5	4.2	362	2	US-09-126-121-3	Sequence 3, Appli	1492	66	4.2	309	2	US-09-221-753-2	Sequence 2, Appli
1420	66.5	4.2	376	2	US-09-270-767-42614	Sequence 42614, A	1493	66	4.2	309	2	US-09-613-092B-2	Sequence 2, Appli
1421	66.5	4.2	381	2	US-09-270-767-38365	Sequence 38365, A	1494	66	4.2	309	2	US-09-754-809-2	Sequence 2, Appli
1422	66.5	4.2	381	2	US-09-270-767-53582	Sequence 53582, A	1495	66	4.2	310	2	US-09-248-796A-15375	Sequence 15375, A
1423	66.5	4.2	387	2	US-09-489-847-372	Sequence 372, App	1496	66	4.2	334	2	US-09-902-540-13842	Sequence 13842, A
1424	66.5	4.2	407	1	US-08-776-585-3	Sequence 3, Appli	1497	66	4.2	340	1	US-08-446-875-16	Sequence 16, Appl
1425	66.5	4.2	436	2	US-09-248-796A-17505	Sequence 17505, A	1498	66	4.2	342	2	US-09-252-991A-19903	Sequence 19903, A
1426	66.5	4.2	459	2	US-09-691-220-4	Sequence 4, Appli	1499	66	4.2	344	2	US-09-904-615-131	Sequence 131, App
1427	66.5	4.2	485	2	US-10-172-502-18	Sequence 18, Appl	1500	66	4.2	344	2	US-10-054-988-131	Sequence 131, App
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1429	66.5	4.2	499	2	US-09-049-672A-1	Sequence 1, Appli							
1430	66.5	4.2	517	2	US-09-189-760-2	Sequence 2, Appli							
1431	66.5	4.2	517	2	US-09-514-422-2	Sequence 2, Appli							
1432	66.5	4.2	522	2	US-10-172-502-17	Sequence 17, Appl							
1433	66.5	4.2	562	2	US-09-487-558B-82	Sequence 82, Appl							
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1437	66.5	4.2	582	2	US-09-489-039A-12055	Sequence 12055, A							
1438	66.5	4.2	584	2	US-09-693-746-22	Sequence 22, Appl							
1439	66.5	4.2	612	2	US-09-248-796A-24557	Sequence 24557, A							
1440	66.5	4.2	619	1	US-08-372-652-5	Sequence 5, Appli							
1441	66.5	4.2	619	4	PCT-US95-16311-5	Sequence 5, Appli							
1442	66.5	4.2	620	1	US-08-325-071-65	Sequence 65, Appl							
1443	66.5	4.2	620	2	US-08-461-004A-65	Sequence 65, Appl							
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1445	66.5	4.2	650	2	US-08-461-004A-67	Sequence 67, Appl							
1446	66.5	4.2	655	2	US-09-632-538C-36	Sequence 36, Appl							
1447	66.5	4.2	681	2	US-08-760-615-6	Sequence 6, Appli							
1448	66.5	4.2	682	2	US-09-270-767-45389	Sequence 45389, A							
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1450	66.5	4.2	694	1	US-08-701-240-2	Sequence 2, Appli							
1451	66.5	4.2	694	2	US-09-138-236-2	Sequence 2, Appli							
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1453	66.5	4.2	815	2	US-09-914-259-18	Sequence 18, Appl							
1454	66.5	4.2	872	2	US-08-337-797A-2	Sequence 2, Appli							
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1459	66.5	4.2	980	2	US-08-473-446-5	Sequence 5, Appli							
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1463	66.5	4.2	993	2	US-09-558-340-1	Sequence 1, Appli							
1464	66.5	4.2	1059	2	US-09-800-729-217	Sequence 217, App							
1465	66.5	4.2	1068	2	US-09-248-796A-16119	Sequence 16119, A							
1466	66.5	4.2	1068	2	US-09-487-558B-242	Sequence 242, App							
1467	66.5	4.2	1095	2	US-09-107-532A-3855	Sequence 3855, Ap							
1468	66.5	4.2	1416	1	US-08-061-465-4	Sequence 4, Appli							
1469	66.5	4.2	1457	2	US-09-436-874-2	Sequence 2, Appli							
1470	66.5	4.2	1457	2	US-09-713-273A-18	Sequence 18, Appl							
1471	66.5	4.2	2137	2	US-09-134-001C-4463	Sequence 4463, Ap							
1472	66.5	4.2	2466	2	US-09-080-855-12	Sequence 12, Appl							
1473	66.5	4.2	2466	2	US-09-566-076-12	Sequence 12, Appl							
1474	66.5	4.2	2466	4	PCT-US94-09943-2	Sequence 2, Appli							
1475	66.5	4.2	2485	2	US-09-290-640-46	Sequence 46, Appl							
1476	66.5	4.2	2485	2	US-09-665-615B-46	Sequence 46, Appl							
1477	66.5	4.2	2457	1	US-08-416-603-4	Sequence 4, Appli							
1478	66.5	4.2	4572	2	US-10-042-665A-4	Sequence 4, Appli							
1479	66	4.2	137	2	US-09-248-796A-26561	Sequence 26561, A							
1480	66	4.2	173	2	US-09-830-230A-659	Sequence 659, App							
1481	66	4.2	187	2	US-09-248-796A-21855	Sequence 21855, A							
1482	66	4.2	194	2	US-09-489-039A-14065	Sequence 14065, A							
1483	66	4.2	198	2	US-09-252-991A-29162	Sequence 29162, A							
1484	66	4.2	208	2	US-09-248-796A-21781	Sequence 21781, A							
1485	66	4.2	231	2	US-09-717-364A-13	Sequence 13, Appl							
1486	66	4.2	234	2	US-09-248-796A-20570	Sequence 20570, A							
1487	66	4.2	268	2	US-08-961-083-208	Sequence 208, App							

## ALIGNMENTS

## RESULT 1

US-09-232-160-21  
; Sequence 21, Application US/09232160  
; Patent No. 6368794  
; GENERAL INFORMATION:  
; APPLICANT: Steve Daniel  
; APPLICANT: James Gilmore  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Laura Stuve  
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL  
; TITLE OF INVENTION: PROLIFERATION  
; FILE REFERENCE: PA-0003 US  
; CURRENT APPLICATION NUMBER: US/09/232,160  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PERL Program  
; SEQ ID NO 21  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 3044710  
US-09-232-160-21

Query Match 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2, 2e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TRLLVQSLRAEELSIOVSCRINGITLVSKKANQQLNFTTEAKRLLGLSLAGKQOVET	60
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Qy	61	ALKASPTCSYGVWGVDFVVISRISPNPKGKGVGLVWKVPSVQPAAYCNSSDTWT	120
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Qy	121	NSCIPRIITKDPINFTQTATOTTEFIVSDTSVSVASPYSTIPATTTTTPAPASTSIPRR	180
Db	137	NSCIPRIITKDPINFTQTATOTTEFIVSDTSVSVASPYSTIPATTTTTPAPASTSIPRR	196
Qy	181	KKLCICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFGVPTALLVLLFFGAAAGLGF	240
Db	197	KKLCICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFGVPTALLVLLFFGAAAGLGF	256
Qy	241	CYVKRYVKAFFPTNKQKQEMETKVKVBEKANSDNPNEESKKTIDKNPESKSPSKTTVVR	300
Db	257	CYVKRYVKAFFPTNKQKQEMETKVKVBEKANSDNPNEESKKTIDKNPESKSPSKTTVVR	316
Qy	301	CLEAEV 306	
Db	317	CLEAEV 322	

## RESULT 2

US-09-907-794A-201



;; PRIOR APPLICATION NUMBER: US 60/146,222  
;; PRIOR FILING DATE: 1999-07-28  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/20944  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
;; PRIOR FILING DATE: 1999-11-29  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 201  
;; LENGTH: 322  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic protein  
US-09-905-125A-201

Query Match 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.2e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB |||||  
QY 17 TRLVQSLRAELSLQVSCRMIGITLVSKKANQQLNFTKEAKCRLLGLSLAGKQVET 76  
DB |||||  
QY 61 ALKASFETCSYGVWGDGFVVISRISPNPKCKGNGVGLVWKVPVSRQFAAYCYNSSDTWT 120  
DB |||||  
QY 77 ALKASFETCSYGVWGDGFVVISRISPNPKCKGNGVGLVWKVPVSRQFAAYCYNSSDTWT 136  
DB |||||  
QY 121 NSCIPELIITTKDPIFNQTQTATOTTEFIVSDSTYVSPSTIPAPTTTPPAPASTSPRR 180  
DB |||||  
QY 137 NSCIPELIITTKDPIFNQTQTATOTTEFIVSDSTYVSPSTIPAPTTTPPAPASTSPRR 196  
DB |||||  
QY 181 KGLICVTEVFMETSTMSTETEPFVENKAAFPNEAAGFGVPTALLVLLFFGAAAGLGF 240  
DB |||||  
QY 197 KGLICVTEVFMETSTMSTETEPFVENKAAFPNEAAGFGVPTALLVLLFFGAAAGLGF 256  
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DB |||||  
QY 257 CYVKRYKAPFTTNKQCKMIETKVVEKANDSNNEESKKTDKNPEESKSPSKTTVR 316  
DB |||||  
QY 301 CLEAEV 306  
DB |||||  
QY 317 CLEAEV 322

## RESULT 4

US-09-902-775A-201  
; Sequence 201, Application US/09902775A  
; Patent No. 6686451  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi

;; APPLICANT: Botstein, David  
;; APPLICANT: Deanoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, A.  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, Christopher J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth, J.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Mather, Jennie P.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William, I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: 10466-14  
;; CURRENT APPLICATION NUMBER: US/09/902,775A  
;; CURRENT FILING DATE: 2001-07-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: 2000-02-22  
;; PRIOR APPLICATION NUMBER: US 60/143,048  
;; PRIOR FILING DATE: 1999-07-07  
;; PRIOR APPLICATION NUMBER: US 60/145,698  
;; PRIOR FILING DATE: 1999-07-26  
;; PRIOR APPLICATION NUMBER: US 60/146,222  
;; PRIOR FILING DATE: 1999-07-28  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/20944  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
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;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
;; PRIOR FILING DATE: 1999-11-29  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 201  
;; LENGTH: 322  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic protein  
US-09-902-775A-201

Query Match 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.2e-151;

Matches	306;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	17	TRLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKACRLILGLSLAGKDQVET	76						
Qy	61	ALKASFETCSYGWVGDFVWISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDPTWT	120						
Db	77	ALKASFETCSYGWVGDFVWISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDPTWT	136						
Qy	121	NSCIPETITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIIPAPTTTTPPAPASTSPRR	180						
Db	137	NSCIPETITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIIPAPTTTTPPAPASTSPRR	196						
Qy	181	KKLLCVTEVFMTETSMSTETEPFVENKAAFKNEAAGFGVPTALLVLALLPFGAAAGLGF	240						
Db	197	KKLLCVTEVFMTETSMSTETEPFVENKAAFKNEAAGFGVPTALLVLALLPFGAAAGLGF	256						
Qy	241	CYVKRYVKAFFPTNKNOQKEMIEYKVKKEEKANDSNPNEESKKTDKNPEESKSPSKTIVR	300						
Db	257	CYVKRYVKAFFPTNKNOQKEMIEYKVKKEEKANDSNPNEESKKTDKNPEESKSPSKTIVR	316						
Qy	301	CLEAEV 306							
Db	317	CLEAEV 322							

## RESULT 5

US-09-906-700-201  
; Sequence 201, Application US/09906700

; FILE# NO. 6723333  
: GENERAL INFORMATION:

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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Tra
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/90
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/0
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/2
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/2

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, PRIOR FILING DATE: 1999-09-13
, PRIOR APPLICATION NUMBER: PCT/US99/21090
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/21547
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/23089
, PRIOR FILING DATE: 1999-10-05
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, PRIOR APPLICATION NUMBER: PCT/US99/28313
, PRIOR FILING DATE: 1999-11-30
, PRIOR APPLICATION NUMBER: PCT/US99/28564
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/28565
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: 1999-12-16
, PRIOR APPLICATION NUMBER: PCT/US99/30911
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 201
, LENGTH: 322
, TYPE: PRT
, ORGANISM: Artificial sequence
, FEATURE:
, OTHER INFORMATION: Synthetic protein
US-09-306-700-201

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Query Match      100.0%; Score 1575; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.2e-151;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	TRLIVQSGLSRAEELSIQVSCRIMGITLVSQKANOQLNFTAEKACRLJGLSLAGKDQVET	60
Db	17	TRLIVQSGLSRAEELSIQVSCRIMGITLVSQKANOQLNFTAEKACRLJGLSLAGKDQVET	76
Qy	61	ALKASFTCSYGVWYGDGFVWLSRISPNPKCGKNGVGVLWKVPVSRQFAAYCYNSSDWT	120
Db	77	ALKASFTCSYGVWYGDGFVWLSRISPNPKCGKNGVGVLWKVPVSRQFAAYCYNSSDWT	136
Qy	121	NSCIPELIITTKDPIFNQTQTQTTEFIVSDSTYSVASPYSTIPATPTTTPPAPASTSI	180
Db	137	NSCIPELIITTKDPIFNQTQTQTTEFIVSDSTYSVASPYSTIPATPTTTPPAPASTSI	196
Qy	181	KKLTCVTEVPMETSTMSTETETEPFVENKAAFNEAAGFGVPTALLVLALLFPGAAGLGF	240
Db	197	KKLTCVTEVPMETSTMSTETETEPFVENKAAFNEAAGFGVPTALLVLALLFPGAAGLGF	256
Qy	241	CYVKRYVKAFFPTNKNQOKEMIETKVKKEKANDSNPNEESKTKTDKNPEESKPSKTTVR	300
Db	257	CYVKRYVKAFFPTNKNQOKEMIETKVKKEKANDSNPNEESKTKTDKNPEESKPSKTTVR	316
Qy	301	CLEAEV 306	
Db	317	CLEAEV 322	

RESIT.T 6

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US-09-09303-603A-201
; Sequence 201, Application US/0990303603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

```

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: GNE.1618P2C12  
CURRENT APPLICATION NUMBER: US/09/903.603A  
CURRENT FILING DATE: 2001-07-11  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 201  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic protein  
US-09-903-603A-201

Query Match 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.2e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRLLVQGLRAEELSIVQVSRINGITLVSKKANQQLNFTKAEACRLGLSLAGKQVET 60  
DB 17 TRLLVQGLRAEELSIVQVSRINGITLVSKKANQQLNFTKAEACRLGLSLAGKQVET 76

QY 61 ALKASPETCSYGVWGDGVVVISRISPNPKCKGKNGVGLWKVPVSRQFAAYCYNSSDTWT 120  
DB 77 ALKASPETCSYGVWGDGVVVISRISPNPKCKGKNGVGLWKVPVSRQFAAYCYNSSDTWT 136  
QY 121 NSCIPEIITTKODIFNTQTATQTTEFIVSDSTVSASPYSTIPAPTTTPAPASTSIPIRR 180  
DB 137 NSCIPEIITTKODIFNTQTATQTTEFIVSDSTVSASPYSTIPAPTTTPAPASTSIPIRR 196  
QY 181 KKLICVTEVFMTSTMTSTETEPVENKAAAFKNEAAGGGVPTALLVLALLPFGAAGLGF 240  
DB 197 KKLICVTEVFMTSTMTSTETEPVENKAAAFKNEAAGGGVPTALLVLALLPFGAAGLGF 256  
QY 241 CYVKRYVKAFFPTNKNQKQKEMIETKVVKBEKANDSNPNESKKTDKNPEESKSPSKTTTVR 300  
DB 257 CYVKRYVKAFFPTNKNQKQKEMIETKVVKBEKANDSNPNESKKTDKNPEESKSPSKTTTVR 316  
QY 301 CLEARV 306  
DB 317 CLEARV 322

## RESULT 7

US-09-904-920A-201  
Sequence 201, Application US/09904920A  
Patent No. 6806352  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,920A  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15



QY 121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPSTIPAPTTTPAPASTSIPRR 180  
DB 137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPSTIPAPTTTPAPASTSIPRR 196  
QY 181 KKLICVTEVFMTSTMTSTETEPFVFNKAAPFNEAAGFGGVTALLVLALLFFGAAAGLGF 240  
DB 197 KKLICVTEVFMTSTMTSTETEPFVFNKAAPFNEAAGFGGVTALLVLALLFFGAAAGLGF 256  
QY 241 CVKRYVKAPFTNKNQOKEMIEYKVKKEKANDSNPNEESKTKDKNPEESKSPSKTTVR 300  
DB 257 CVKRYVKAPFTNKNQOKEMIEYKVKKEKANDSNPNEESKTKDKNPEESKSPSKTTVR 316  
QY 301 CLEAEV 306  
DB 317 CLEAEV 322

## RESULT 9

US-09-905-381A-201  
; Sequence 201, Application US/09905381A  
; Patent No. 6818746

## GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,381A

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-09-905-381A-201

Query Match 100.0%; Score 1575; DB 2; Length 322;

Best Local Similarity 100.0%; Pred. No. 2.2e-151;

Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRLLVQSLRAEELSIQVSCRIMGITLVSKKANQOLNFTKEACRLGLSLAGKQOQVET 60  
DB 17 TRLLVQSLRAEELSIQVSCRIMGITLVSKKANQOLNFTKEACRLGLSLAGKQOQVET 76  
QY 61 ALKASPETCSYGVWGDGFVVVISRISPNPKCGKNGVGLWKVPVSRQFAAYCYNSSDWT 120  
DB 77 ALKASPETCSYGVWGDGFVVVISRISPNPKCGKNGVGLWKVPVSRQFAAYCYNSSDWT 136  
QY 121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPSTIPAPTTTPAPASTSIPRR 180  
DB 137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPSTIPAPTTTPAPASTSIPRR 196  
QY 181 KKLICVTEVFMTSTMTSTETEPFVFNKAAPFNEAAGFGGVTALLVLALLFFGAAAGLGF 240  
DB 197 KKLICVTEVFMTSTMTSTETEPFVFNKAAPFNEAAGFGGVTALLVLALLFFGAAAGLGF 256  
QY 241 CVKRYVKAPFTNKNQOKEMIEYKVKKEKANDSNPNEESKTKDKNPEESKSPSKTTVR 300  
DB 257 CVKRYVKAPFTNKNQOKEMIEYKVKKEKANDSNPNEESKTKDKNPEESKSPSKTTVR 316  
QY 301 CLEAEV 306  
DB 317 CLEAEV 322

## RESULT 10

US-09-906-618-201

; Sequence 201, Application US/09906618

; Patent No. 6828146

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.







;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 201  
;; LENGTH: 322  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic protein  
US-09-906-646-201

Query Match 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.2e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TRLLVQSLRAEELSIOVSCRMGITLVSKKANQNLNFTKEACRLGLSLAGKQOQVET 60  
Db |||||  
Qy 17 TRLLVQSLRAEELSIOVSCRMGITLVSKKANQNLNFTKEACRLGLSLAGKQOQVET 76  
Db |||||  
Qy 61 ALKASFETCSYGWGDFVVISRISPNPKCGKNGVGLWKVPVSRQFAAYCYNSSDTWT 120  
Db |||||  
Qy 77 ALKASFETCSYGWGDFVVISRISPNPKCGKNGVGLWKVPVSRQFAAYCYNSSDTWT 136  
Db |||||  
Qy 121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPRR 180  
Db |||||  
Qy 137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPRR 196  
Db |||||  
Qy 181 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 240  
Db |||||  
Qy 197 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 256  
Db |||||  
Qy 241 CYVKRYVKAPFTTNKQKQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300  
Db |||||  
Qy 257 CYVKRYVKAPFTTNKQKQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 316  
Db |||||  
Qy 301 CLEAEV 306  
Db |||||  
Qy 317 CLEAEV 322

RESULT 12

US-09-904-462-201  
; Sequence 201, Application US/09904462  
; Patent No. 6878807  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.

;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William, I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: 10466-14  
;; CURRENT APPLICATION NUMBER: US/09/904,462  
;; CURRENT FILING DATE: 2001-07-13  
;; PRIOR APPLICATION NUMBER: 09/665,350  
;; PRIOR FILING DATE: 2000-09-18  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: 2000-02-22  
;; PRIOR APPLICATION NUMBER: US 60/143,048  
;; PRIOR FILING DATE: 1999-07-07  
;; PRIOR APPLICATION NUMBER: US 60/145,698  
;; PRIOR FILING DATE: 1999-07-26  
;; PRIOR APPLICATION NUMBER: US 60/146,222  
;; PRIOR FILING DATE: 1999-07-28  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/20944  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
;; PRIOR FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
;; PRIOR FILING DATE: 1999-11-29  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
;; PRIOR FILING DATE: 2000-01-05  
;; NUMBER OF SEQ ID NOS: 423  
;; SEQ ID NO 201  
;; LENGTH: 322  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-09-904-462-201

Query Match 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.2e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TRLLVQSLRAEELSIOVSCRMGITLVSKKANQNLNFTKEACRLGLSLAGKQOQVET 60  
Db |||||  
Qy 17 TRLLVQSLRAEELSIOVSCRMGITLVSKKANQNLNFTKEACRLGLSLAGKQOQVET 76  
Db |||||  
Qy 61 ALKASFETCSYGWGDFVVISRISPNPKCGKNGVGLWKVPVSRQFAAYCYNSSDTWT 120  
Db |||||  
Qy 77 ALKASFETCSYGWGDFVVISRISPNPKCGKNGVGLWKVPVSRQFAAYCYNSSDTWT 136  
Db |||||  
Qy 121 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPRR 180  
Db |||||  
Qy 137 NSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPRR 196  
Db |||||  
Qy 181 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 240  
Db |||||  
Qy 197 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 256  
Db |||||  
Qy 241 CYVKRYVKAPFTTNKQKQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR 300  
Db |||||

Db 257 CVVKRYKAFPTNKNQOKMIETKVVKEEKANDSNPNESKKTDKNPEESKSPKTTVR 316  
QY 301 CLEAEV 306  
| | | | |  
Db 317 CLEAEV 322

RESULT 13  
US-09-902-736A-201  
; Sequence 201, Application US/09902736A  
; Patent No. 6894148  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/902,736A  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-09-902-736A-201  
  
Query Match 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.2e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQOLNFTTEAKEACRLILGLSLAGKQVET 60  
| | | | |  
Db 17 TRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQOLNFTTEAKEACRLILGLSLAGKQVET 76  
| | | | |  
QY 61 ALKASPETCSYGVWGDGFVVVISRISPNPKCKGKGVGLIWKVPVSRQFAAYCYNSSDTWT 120  
| | | | |  
Db 77 ALKASPETCSYGVWGDGFVVVISRISPNPKCKGKGVGLIWKVPVSRQFAAYCYNSSDTWT 136  
| | | | |  
QY 121 NSCIPEIITTKDPIFNQTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPRR 180  
| | | | |  
Db 137 NSCIPEIITTKDPIFNQTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPRR 196  
| | | | |  
QY 181 KKLICVTEVFMEVETSTMSTETETEPFVENKAAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 240  
| | | | |  
Db 197 KKLICVTEVFMEVETSTMSTETETEPFVENKAAAFKNEAAGFGVPTALLVLALLFFGAAAGLGF 256  
| | | | |  
QY 241 CVVKRYKAFPTNKNQOKMIETKVVKEEKANDSNPNESKKTDKNPEESKSPKTTVR 300  
| | | | |  
Db 257 CVVKRYKAFPTNKNQOKMIETKVVKEEKANDSNPNESKKTDKNPEESKSPKTTVR 316  
| | | | |  
QY 301 CLEAEV 306  
| | | | |  
Db 317 CLEAEV 322  
  
RESULT 14  
US-09-906-722A-201  
; Sequence 201, Application US/09906722A  
; Patent No. 6946262  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: GNE.1618P2C61  
CURRENT APPLICATION NUMBER: US/09/906,722A  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 201  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic protein  
US-09-906-722A-201

Query Match 100.0%; Score 1575; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.2e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TRLLVQSLRAEELSIQVSCRIMGITLVSKKANQOLNFTAKEACRLGLSLAGKQVET	60
Db	17	TRLLVQSLRAEELSIQVSCRIMGITLVSKKANQOLNFTAKEACRLGLSLAGKQVET	76
Qy	61	ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT	120
Db	77	ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT	136
Qy	121	NSCIPEIITKDPINFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI	180
Db	137	NSCIPEIITKDPINFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI	196
Qy	181	KKLCVTEVFMETSTMSTETEPFVENKAAFPKNEAAGFGVPTALLVLALLFFGAAGLGF	240
Db	197	KKLCVTEVFMETSTMSTETEPFVENKAAFPKNEAAGFGVPTALLVLALLFFGAAGLGF	256
Qy	241	CYVKRYVKAFFPTNKNQOKEMIETKVYKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR	300
Db	257	CYVKRYVKAFFPTNKNQOKEMIETKVYKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR	316
Qy	301	CLEARV 306	
Db	317	CLEARV 322	

RESULT 15  
US-09-949-016-7765  
Sequence 7765, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7765  
LENGTH: 344  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7765

Query Match 100.0%; Score 1575; DB 2; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2.4e-151;  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TRLLVQSLRAEELSIQVSCRIMGITLVSKKANQOLNFTAKEACRLGLSLAGKQVET	60
Db	39	TRLLVQSLRAEELSIQVSCRIMGITLVSKKANQOLNFTAKEACRLGLSLAGKQVET	98
Qy	61	ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT	120
Db	99	ALKASFETCSYGVWGDGFVWISRPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT	158
Qy	121	NSCIPEIITKDPINFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI	180
Db	159	NSCIPEIITKDPINFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI	218
Qy	181	KKLCVTEVFMETSTMSTETEPFVENKAAFPKNEAAGFGVPTALLVLALLFFGAAGLGF	240
Db	219	KKLCVTEVFMETSTMSTETEPFVENKAAFPKNEAAGFGVPTALLVLALLFFGAAGLGF	278
Qy	241	CYVKRYVKAFFPTNKNQOKEMIETKVYKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR	300
Db	279	CYVKRYVKAFFPTNKNQOKEMIETKVYKEEKANDSNPNEESKKTDKNPEESKSPSKTTVR	338
Qy	301	CLEARV 306	
Db	339	CLEARV 344	

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Job time : 24.6509 secs

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